SOUVENIR & ABSTRACTS

Proceedings of the 65th
Annual International Conference & School Conclave
of Association of Microbiologists of India (AMI)

PERSPECTIVES OF MICROBES FOR HUMAN WELFARE

11TH, 14TH- 17TH NOVEMBER, 2024




Organized at:

Guru Jambheshwar University of Science & Technology, Hisar, Haryana (125001)

Guru Jambheshwar Ji Maharaj was a great saint, philosopher and environmentalist of the 15th century. He was born in the family of Shri Lohat Ji Panwar and Mata Hansa Devi on Bhadrapada Krishna Paksha Ashtami (Janmashtami), Vikram Samvat 1508 (1451 A.D.) in Pipasar village of Nagaur district of Rajasthan. Guru Jambheshwar Ji Maharaj founded the Bishnoi sect in Vikram Samvat 1542 (1485 A.D.) at Samrathal Dhaura on Kartik Krishna Ashtami. He spent the remaining 51 years of his life spreading his great vision. The first Shabad uttered at the age of 7 years by Guru Jambheshwar Ji is **"Guru Chinho Guru Chinh Purohit"** to a Brahmin called to cure his dumbness. Considering the miraculous powers of Guru Jambheshwar Ji and his teachings, Guru Jambheshwar Ji Maharaj is popularly considered as Vishnu Swarup. His teachings influenced both the ruling class and the common class.

Guru Jambheshwar Ji Maharaj had said - **"Jeev daya palanee, runkh leelo na ghave"**

Which means - "Have compassion for all living beings, and don't cut the green trees".

He raised his voice against the orthodoxies and superstitions prevalent in the contemporary social system. He was a great visionary who had foreseen the consequences of man's actions destroying nature for economic development. He saw the need for environmental protection and weaved his principles into religious commandments so that people could internalise those principles easily. His teachings includes love, peace, kindness, simplicity, honesty, compassion, forgiveness, hard work, ecological consciousness, internal and external purity.

At village Khejarli of Jodhpur State, in Vikram Samvat 1787 (1730 A.D.), under the influence of Guru Jambheshwar Ji Maharaj's teachings, Smt. Amrita Devi Ji and 362 Bishnoi brothers and sisters, sacrificed their lives to save Khejadi trees from being cut by putting their heads in front of moving axes, saying

"Sar Sathe Rukh Rahe, To Bhi Saston Jaan",

Which means "Even if a tree is saved in exchange of a head, it is still a cheaper deal".

The Khejarali village event was the supreme sacrifice worldwide to protect the trees. Khejarali (Jodhpur) is the place where the Chipko movement originated in India Centuries before the S.L. Bahuguna led Chipko movement. This collective sacrifice of human lives to protect the Khejri tree is a unique phenomenon worldwide.

Guru Jambheshwar Ji Maharaj founded 29 rules. Out of these, eight prescribe preservation of biodiversity and encourage good animal husbandry, seven provide directions for healthy social behaviour, and ten are directed towards personal hygiene and maintaining essential good health. The other four commandments provide guidelines for worshipping Lord Vishnu everyday. He expounded his religious philosophy and the essence of these principles in verses. These vibrant and passionate spiritual verses have a vigour of their own and are distinguished by their vivid conversational style and moral exhortation. Guru Ji achieved 'Nirvana' in Vikram Samvat 1593 (1536 A.D.) at Lalasar, in the district of Bikaner, Rajasthan.

A fundamental "Shabad" by Guru Jambheshwar Ji Maharaj runs as -

"Vishnu Vishnu tu bhan re prani, paii key lakh upayun,

Rattan kayo baikunth baaso, tera jara maran bhaya bhajun"

which means, "O human being, recite Vishnu Vishnu continuously so that the recital multiplies in number. This would relieve you from the fear of old age and death."

PROCEEDINGS

of the

65th AMI Annual International Conference & School Conclave

"Perspectives of Microbes for Human Welfare"

November 11, 14-17, 2024

Editor-in-Chief

Prof. Namita Singh

Executive Editor

Dr. Renu Singh

Editors

Prof. Anil Kumar, Dr. Saloni Gupta, Dr. Navnidhi Chhikara, Ms. Renuka Sharma, Mr. Mandeep Nain, Ms. Menal Jain, Ms. Shreya Maheshwari, Ms. Natasha Charaya, Ms. Ayushi Malik, Ms. Kanika

Organized at

Guru Jambheshwar University of Science and Technology

(NAAC-A+)

Hisar, Haryana- 125001, India

Association of Microbiologists of India (AMI)

COPYRIGHT CERTIFICATE

This is to certify that the authors of abstracts published in the *Proceedings of the 65th Annual International Conference of Association of Microbiologists of India (AMI-2024) "Perspectives of Microbes for Human Welfare"* held on **11th, 14th – 17th November 2024** at **Guru Jambheshwar University of Science and Technology, Hisar, Haryana, India**, shall retain full copyright of their respective abstracts.

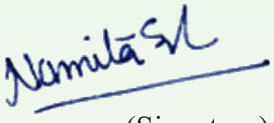
The **Association of Microbiologists of India (AMI)** affirms that:

1. **Copyright Ownership:** The copyright of the submitted abstracts will remain exclusively with the respective authors. The AMI or the conference organizers shall not claim any rights over the intellectual property of the authors.
2. **Publication Rights:** The authors grant permission to the **AMI Annual International Conference 2024** to publish, distribute, and reproduce the abstracts in the official conference *Compendium* in both print and digital formats for academic and archival purposes.
3. **Author Rights:** The authors are free to use, reproduce, or republish their abstracts in other formats, including but not limited to journal publications, book chapters, or institutional repositories, without seeking additional permission from the conference organizers or AMI.
4. **Liability:** The AMI and the conference organizers shall not be held responsible for any copyright disputes arising from the submitted abstracts. Any legal concerns related to authorship, originality, or content shall be the sole responsibility of the submitting author(s).

This certificate serves as an official confirmation that the **copyright of the abstracts remains with the authors**, ensuring their full ownership and freedom for future publication and dissemination.

Issued by: Association of Microbiologists of India (AMI) **Date:** 11-03-2025

Authorized Signatory



(Signature)

Prof. Namita Singh,
General Secretary
Association of Microbiologists of India (AMI)

ISBN Number : 978-81-986392-0-2

Published By:
Association of Microbiologists of India (AMI)

सत्यमेव जयते

Bandaru Dattatraya
Governor, Haryana
बंडारू दत्तात्रेय
राज्यपाल, हरियाणा

Message

It is a matter of great delight that Guru Jambheshwar University of Science and Technology, Hisar, is hosting 65th annual conference of the Association of Microbiologists of India-2024 and an International conference on **"Perspective of Microbes for Human Welfare"** on November 14-17, 2024. During which a broad range of topics of microbial-industrial microbiology. veterinary, agricultural microbiology and microbes for human welfare will be deliberated upon.

There is no denying the fact that microbes play a fundamental role in human welfare, contributing to areas like health, agriculture, industry, and environmental sustainability. Beneficial microbes, including probiotics and gut flora, are essential for human health, aiding in digestion, nutrient absorption. and immunity enhancement.

In agriculture, microbes enhance soil fertility through nitrogen fixation and organic matter decomposition, promoting sustainable farming practices. Industrially, microbes are employed in the production of antibiotics, enzymes. and biofuels, offering eco-friendly solutions and alternative energy sources.

Microbial bioremediation also helps manage environmental pollutants. breaking down toxic substances into harmless by-products. Through these diverse applications, microbes demonstrate their invaluable presence in advancing human welfare, health, and environmental conservation.

My best wishes!

Bandaru Dattatraya

सत्यमेव जयते

Nayab Singh
Chief Minister,
Haryana, Chandigarh

नायब सिंह
मुख्यमंत्री हरियाणा, चण्डीगढ़

Message

It gives me immense pleasure to know that the Association of Microbiologists of India (AMI) and Guru Jambheshwar University of Science and Technology (GJUST), Hisar, are jointly organizing the 65th Annual International Conference on **"Perspectives of Microbes for Human Welfare-2024"** from November 14th to 17th, 2024. I commend the initiative to align this international conference with the annual conclave on the same transformative theme.

Recent breakthroughs in microbiology have significantly influenced key sectors—health sciences, medicine, sustainable energy, and the food industry—while also presenting complex challenges to the scientific community. This conference aligns with the Government of Haryana's commitment to advancing education, fostering research, and promoting sustainable development. Through initiatives like these, the government emphasizes the importance of scientific progress in microbiology to enhance public health, environmental sustainability, and economic resilience.

By encouraging cutting-edge research, innovation, and collaboration, this event will contribute directly to Haryana's objectives of developing human resources and capacity in microbiology and allied sciences, advancing sustainable development goals, and supporting public welfare.

I am confident that the discussions during the conference will deepen participants' understanding of these advancements and strengthen their expertise. Additionally, it will provide an invaluable platform for knowledge exchange, problem-solving, and strategic partnerships, fulfilling the joint commitment of the Government of Haryana and GJUST to drive impactful, research-based solutions for the welfare of society.

My best wishes.

Nayab Singh

Prof. Narsi Ram Bishnoi

Vice Chancellor

Guru Jambheshwar University of
Science & Technology, Hisar

Message

It is my distinct pleasure to welcome each of you to the 65th AMI International Conference on **"Microbes in Human Welfare."** This esteemed gathering provides an invaluable forum for exchanging insights and advancing our understanding of the crucial roles microbes play in promoting human health, agricultural innovation, and industrial development.

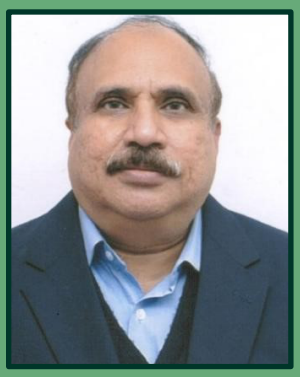
Microorganisms are not just agents of disease but are, in fact, key allies in our quest for sustainable development. Their influence spans far beyond health, contributing immensely to environmental sustainability and helping us achieve the United Nations Sustainable Development Goals (SDGs). From enriching soil fertility and ensuring food security (SDG 2) to promoting health and well-being (SDG 3), microbes are indispensable to building a sustainable future. Their applications are vast; ranging from antibiotic and vaccine production to bioremediation and bio-fertilizer use.

As we convene to explore these essential topics, we celebrate the pioneering research and collaborative efforts that propel the field of microbial science forward. Microorganisms play vital roles in combating climate change, ensuring clean water and sanitation, and supporting sustainable energy solutions; cornerstones of a resilient and sustainable world.

I extend my heartfelt appreciation to the organizing team for their unwavering commitment to making this conference possible. Your dedication to expanding knowledge in this field is invaluable and fosters vital global collaboration.

Let us seize this opportunity to engage in insightful discussions, exchange ideas, and inspire one another to unlock the immense potential of microbes for the welfare of humanity and the planet.

Prof. Narsi Ram Bishnoi



Prof. Sunil K. Khare

FBRS, FNASS, FAMSc.

Director, IISER, Kolkata

President

Association of Microbiologists of India

Message

Greetings to all our esteemed colleagues and cherished friends,

As we gather in the historic city of Hisar for our annual conference, I am honored and privileged to extend a warm welcome to each of you on behalf of the Association of Microbiologists of India (AMI). As we delve into our theme, **"Perspectives of Microbes for Human Welfare,"** this year, I am heartened by the spirit of collaboration and curiosity that defines our vibrant community.

Founded in 1938, AMI has consistently led microbiology research and education in India, influencing our national scientific community and collaborators worldwide. The profound impact of microbes on human welfare spans healthcare, agriculture, and environmental management, highlighting the essential role our field plays in sustainable development.

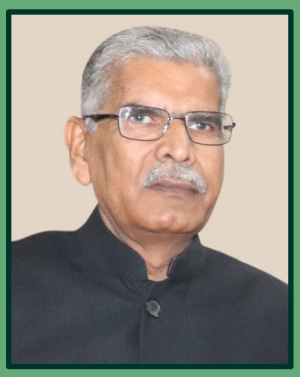
This conference boasts a rich agenda, including diverse sessions, workshops, and keynote addresses covering the latest in microbial biotechnology, medical microbiology, and environmental microbiology. I encourage you to engage deeply, question freely, and build networks that will foster innovative collaborations long after we conclude our proceedings.

Your presence here is a contribution to this conference and a testament to your commitment to advancing microbiology. Let us use this opportunity to exchange ideas, challenge existing boundaries, and envision new possibilities in our field.

Thank you for bringing your expertise and enthusiasm to Hisar. Together, let's make this conference a milestone event filled with engaging discussions and lasting partnerships.

Looking forward to the inspiring days ahead,

Prof. Sunil K. Khare



Prof. Ramesh Chander Kuhad

FNASc, FAMSc, FNAAS, FBRS
Former Vice Chancellor
Central University of Haryana
Mahendergarh,Haryana

Founder Chairman
Indian Academy of Microbiological Sciences

Message

It is a matter of immense delight that Association of Microbiologists of India (AMI) Chapter Hisar and Guru Jambehswar University of Science and Technology, Hisar, Haryana have jointly organized the International conference **"Perspectives of Microbes for Human Welfare"** from 14th Nov to 17th Nov., 2024. The conference will focus upon varied areas like microorganisms for mankind, Climate change, role of Microorganisms in Environmental Management, Microorganisms in production of quality foods and other industrial important products, Plant biomass microbial biotechnology, Microbial diseases, Antimicrobial resistance, human gut Microbiome, Vaccine development, Microbial diagnostics, IPR and Artificial Intelligence in modern microbiology etc.

I am fully confident and feel that the conference will provide a platform to researchers, academicians, policy makers, industrialists, research scholars, students and even common men to utilize this opportunity to learn about microorganisms and their applications for human health and achieving sustainable development goals. Moreover, the International conference will provide a rare opportunity particularly to young and budding researchers to explore prospects of establishing linkage with established researchers from India and aboard. This may also help them to visit their labs and use their facilities. Quite importantly, our UG/PG students may get connectivity for the research Internship. Besides, potential researchers may develop linkage with researchers from industries / research Institutions / higher educational Institutions, Which eventually may result in establishing good collaboration

I am sure that participants will learn a lot and receive an extraordinary experience, which will be helpful throughout their academic and research journey.

I wish the organizers of the International conference on **"Perspectives of microbes for human welfare"** great success towards its organization and completion without any hindrances.

23/10/2024

Prof. Ramesh Chander Kuhad

Prof. Vinod Chhokar

Registrar

Guru Jambheshwar University of Science & Technology, Hisar

Message

It gives me immense pleasure to extend my appreciation and heartfelt congratulations to the Association of Microbiologists of India (AMI) and Guru Jambheshwar University of Science and Technology (GJUST), Hisar, for organizing the 65th Annual International Conference on the highly relevant theme, **"Perspectives of Microbes for Human Welfare'**, scheduled to take place from November 14th to 17th, 2024.

Microorganisms, though often unseen, play a crucial role in many aspects of life, from sustaining ecosystems to fostering health and innovation. In recent years, microbial research has opened doors to ground-breaking applications in healthcare, agriculture, environmental management, and industry. This conference promises to showcase these advancements, highlighting the ways microbes can contribute to sustainable solutions and improve the quality of human life.

Our university is proud to host this conference, providing a unique platform for students, researchers, and scholars in the field of microbiology to showcase their research findings, gain insights from expert lectures, and engage in valuable discussions with leading scientists and professionals from around the world. I am confident that the microbiology community and allied disciplines will gain substantial knowledge and inspiration from the diverse perspectives shared at this event, further advancing the field and encouraging collaborative initiatives.

I am delighted to extend my best wishes to the organizing team for their dedication for a successful and impactful event. Congratulations to AMI, GJUST, Hisar, and all involved in this endeavour for their commitment to making this conference a resounding success.

Prof. Vinod Chhokar

Prof. Namita Singh

Dean International Affairs
Guru Jambheshwar University of Science
& Technology, Hisar

GENERAL SECRETARY,
THE ASSOCIATION OF MICROBIOLOGISTS OF INDIA (AMI)
Executive Secretary, AMSc

Message

Greetings to all our esteemed colleague and guests,

On behalf of the organizing committee, it is my great pleasure to welcome you to the 65th Annual conference of the Association of Microbiologists of India (AMI). This year the AMI and Guru Jambheshwar University of Science and Technology, Hisar are organizing the conference entitled **"Perspectives of Microbes for Human Welfare-2024"** from 14th-17th 2024. The idea to host the AMI each year is to build a research network highlighting the importance of microbiology.

The conference scientific program will foster discussions and hopes to inspire participants to initiate collaborations within and across disciplines for the advancement of microbiology. The various thematic sessions will showcase important scientific advances and highlight the impact of microbes in a world of rapid change and complex interactions. The conference has 12 themes including advanced microbial diagnostics/detection tool, Industrial Microbial Biotechnology, Microbial Nanotechnology, IPR, AI in Microbiological Applications, Pant Microbe interactions, Vaccine development for life, Agricultural Biotechnology. A special session will also be held on 'Child-centric Microbiology (Science for Society)' for schools nationwide in order to promote microbial literacy amongst students.

We have experts from across the field who will be attending the conference for all the four days-sharing their thoughts, knowledge, and opinions with every participant. We welcome all of you to attend the plenaries and oral presentations and to interact with the conference participants. We also encourage participation in discussions through utilization of the digital platforms during the conference.

I wish everyone a successful, safe, and fruitful conference.

Namita Singh

Prof. Namita Singh

Prof. Anil Kumar

Chairperson

Department of Biotechnology

Guru Jambheshwar University of

Science & Technology, Hisar

Message

It is a great pleasure to welcome you all to the 65th Annual Conference of the Association of Microbiologists of India (AMI), centered on the theme **"Perspective of Microbes for Human Health."**

This landmark event marks over six decades of AMI's dedication to advancing the frontiers of microbiology. As we gather to celebrate this milestone, we acknowledge the fundamental role that microbes play in enhancing human health. This conference provides an unparalleled platform to delve into the complex interplay between microbes and human well-being from the exploration of the human micro biome to the development of groundbreaking therapeutic solutions.

Over the next four days, the conference will feature inspiring keynote lectures delivered by renowned global experts, alongside engaging plenary sessions covering critical topics such as micro biome research, infectious diseases, and microbial therapeutics. Participants will also have the opportunity to attend focused symposia, which will delve into important areas like antimicrobial resistance, probiotics, and recent advancements in micro biome engineering. Additionally, poster presentations will showcase innovative and impactful research across various microbiological disciplines, offering insights into the latest developments in the field.

This event provides a unique platform to connect with fellow researchers, clinicians, and industry leaders. It encourages participants to explore the latest advancements, foster meaningful collaborations, and engage in knowledge-sharing. Together, we will address pressing challenges and uncover new opportunities in microbial research, advancing our collective mission to harness the potential of microbes for human health.

My heartfelt appreciation goes out to our keynote speakers, session chairs, participants, and organizers for their invaluable contributions and commitment to making this event a success. Together, let us continue to unlock the transformative potential of microbes for human health and well-being.

Thank you, and may this conference be an inspiring and enriching experience for all.

Prof. Anil Kumar

Prof. Rajesh Gera

Dean
College of Basic Sciences
& Humanities, CCSHAU, Hisar

President
AMI-Hisar Unit, Haryana

Message

I am immense delighted to know that Guru Jambheshwar University of Science and Technology GJUST, Hisar, Haryana and Association of Microbiologists of India (AMI) is organizing an International conference on **"Perspectives of Microbes for Human Welfare"** on November 14th-17th , 2024. It is an ambitious initiative of the University to bring together the Life Scientists from prestigious organizations of the world at one platform to discuss and deliberate the theme of the conference. It will give an opportunity to the young scholars and scientists to interact with the best of the scientists of the world, and shall connect the university fraternity with the outer world.

On this special occasion, I extend my heartfelt compliments to the Vice Chancellor of the University for conceptualizing this international conference at GJUST, Hisar, Haryana. This initiative reflects the strong commitment and visionary leadership of the university, turning challenges into valuable opportunities.

I wish the Organizing Secretary and her dedicated team all the best in successfully organizing the conference and publishing the souvenir and abstracts."

Prof. Rajesh Gera

भारतीय जीवाणुतत्ववेत्त संगठन
Association of Microbiologists of India

Prof. Lilly Ganju
Editor-in-Chief
Indian Journal of Microbiology (Springer)

Prof. Minakshi Prasad
Editor-in-Chief
Indian Journal of Microbiology (Springer)

Message

Dear Colleagues and Esteemed Members of the Microbiology Community, we are delighted to extend a warm invitation to the upcoming 65th Annual International Conference of the Association of Microbiologists of India (AMI), themed **"Perspectives of Microbes for Human Welfare."** This eagerly awaited event, scheduled for November 14th to 17th, 2024, will gather leading scientists, researchers, and thought leaders from across the globe to share and discuss breakthroughs and future directions in microbiology.

As Editor-in-Chief of the Indian Journal of Microbiology (Springer), we are excited about the opportunity this conference provides to showcase the diverse applications of microbial research for advancing human welfare. From addressing public health challenges to enhancing environmental sustainability, and from food security innovations to groundbreaking discoveries in microbial biotechnology, this conference will highlight the extraordinary roles that microbes play in improving quality of life.

` Our journal remains committed to supporting and publishing pioneering work in these areas, and we look forward to seeing many of you present findings that could shape the future of microbiology. With sessions, workshops, and presentations covering 12 key themes such as microbial genetics, disease control, industrial applications, and environmental health, the conference promises to be a valuable platform for knowledge exchange and collaboration.

Please join us in what will undoubtedly be a thought-provoking and inspiring gathering, and let us continue to push the boundaries of microbiological research for a better, more sustainable world. We encourage everyone—scientists, educators, and students alike—to engage fully, learn from one another, and contribute to the growing body of knowledge that will shape our collective future.

Looking forward to seeing you at the conference.

Prof. Lilly Ganju **Prof. Minakshi Prasad**

Prof. Sunil Pabbi

Immediate Past President

Association of Microbiologists of India

भारतीय जीवाणुतत्ववेत्त संगठन
Association of Microbiologists of India

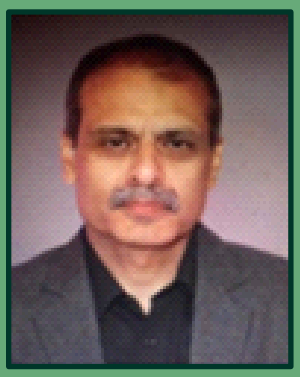
Message

The 65th AMI Annual International Conference on **"Perspectives of Microbes for Human Welfare"**, scheduled for November 14th to 17th, 2024 at Guru Jambheshwar University of Science & Technology, Hisar emerges as a premier international event to showcase, deliberate, discuss and exchange the emerging innovations in microbiological research. The role of microbes in addressing challenges to health, environment, agriculture, food, feed, multiple drug resistance, biotic and abiotic stresses etc. is well stated and the present conference would provide a suitable platform for exchange of latest trends in which microbiological science contributes to the betterment of mankind.

The conference themes will also cover cutting-edge discoveries related to New Techniques/Novel Insights in the development of microbial community structure including microbial diversity data management emphasizing their potential role as a 'Microbiome', their structural and functional aspects with applications for host-pathogen/plant-microbe interactions, climate change, one health perspective and microbial biotechnology. The emerging areas of Intellectual Property Rights and Forensics in Microbiology are rightly included as Special sessions during this conference. It is our dream to make microbiology a household name so that everyone understands that how Microbiology research has paved the way toward incredible advancements and there is no doubt that microbiology touches our life every moment in one way or the other and have a direct bearing on the human condition. The 'Microbiology Literacy Mission for School Students' and the public literacy campaigns for communicating to decision-makers at state, local and community levels to make citizens more aware of the ways that microbiology impacts human life would be a valuable addition to our conference.

The conference will bring together leading researchers, practitioners, and academics from around the world to share and deliberate their latest discoveries and insights in the multiple areas of microbiology. I am sure, it's a perfect blend of modernity and tradition for both young and experienced that will offer an ideal setting for intellectual exchange and professional networking. On behalf of the AMI, I welcome all the distinguished scientists, researchers, students and participants from around the globe to this conference. I congratulate the organizers for their efforts in organizing this conference and wish a great success.

Prof. Sunil Pabbi



Prof. Prince Sharma
Department of Microbiology
Panjab University, Chandigarh

Message

Its indeed a proud feeling to be a part of the Association of Microbiologists of India. The Association for decades has been serving the society untiringly, may it be spreading public awareness about scientific issues, guiding youth to science (microbiology) stream, bringing academia and industry together, uplifting microbiology as a rewarding career. Holding annual conferences at international scale on globally pertinent themes have provided platform to young and veteran scientists and have brought together scientists from world over. The 65th International AMI conference on the theme 'Perspectives of Microbes for Human Welfare' to be held at GJUST, Hisar, is one such successive endeavour to bring together microbiological community to discuss various glaring issues about environment, energy, health, industry, new syllabi and so on.

My heartiest best wishes go to the organisers for the stupendous success of this conference.

I call upon the students, young faculty, scientists, industry experts, policy makers, to join the conference wholeheartedly with fervour.

Let Science Triumph Over Global Concerns

Prof. Prince Sharma

Prof. R. S. Paroda

(Padma Bhushan Awardee)

Chairman, TAAS

and Former Secretary,

DARE and Director General,

ICAR Former President, AMI

Message

I am delighted to learn that the 65th AMI International Conference on **"Perspectives of Microbes for Human Welfare"** is proposed to be organized by the Association of Microbiologists of India (AMI) in collaboration with the Department of Biotechnology at Guru Jambheshwar University of Science and Technology, Hisar, Haryana on 14-17 November, 2024. The Conference is being organized very timely on a highly relevant theme and I am confident that in-depth deliberations will highlight the important role of microbiologists in the post COVID scenario as well as reveal clearly the beneficial - contributions of microbes in the service of humanity.

I also believe that this Conference will serve as an important platform for researchers, scientists, and industry professionals alike to share their latest research findings, exchange innovative ideas, and foster collaboration with microbiologists across the country. I am confident that in-depth deliberations during the conference will help in exchanging the scientific knowledge in the field of microbiology and its diverse applications. It will surely help in suggesting a Way Foreword to harness the tangible benefits from microbes for human welfare.

I wish the conference a great success.

RS Paroda

Dr. Tapan K. Adhya

FNA, FNASc, FNAAS, FWAST, FAMI

Professor, Biotechnology

Kalinga Institute of Industrial Technology (KIIT)

Bhubaneswar, Odisha, India

Message

It gives me immense pleasure to write a message for the forthcoming 65th International Conference of the Association of Microbiologists of India (AMI) on **"Perspectives of Microbes for Human Welfare"** to be held at the Guru Jambheshwar University of Science and Technology, Hisar, Haryana from 14-17th November 2024. AMI which began its journey way back in 1938 is one of the oldest and reputed scientific organizations of the country devoted to popularization of research and studies in Microbiology and developing awareness in the Society about Microbiology. In the terms of Microbiology, the association which started with initial attachment to the society by microbiologist-to-microbiologist adhesion, has developed into a closely knit matrix and a mature biofilm to envelop entire country in the discipline of Microbiology, with connections from abroad.

Obviously, this progress has not been made in a few years and had been nurtured constantly with nutrients and incubations by great Microbiologists like Profs. G. Rangaswamy, J.B. Bhat, V.V. Modi, P. Tauro, K.V.B.R. Tilak, Manju Sharma, Bhavadish Johri, K.R. Dadarwal, S. Ayyappan, R.C. Kuhad to name a few. I feel myself lucky to give my input for the betterment of the society during 2014-15. The society is doing great and has developed international links with many famous microbiological societies abroad. Science of Microbiology has changed a great deal during the last decade and our young leaders are certainly capable of leading the Society into the future.

I wish all success to the 65th International Conference of AMI.

Dr. Tapan K Adhya

Prof. P. Gunasekaran

Ph.D., D.Sc.

Former Head, School of Biological Sciences

Madurai Kamaraj University, Madurai, Tamil Nadu

Former Vice Chancellor VIT Bhopal University,Madhya Pradesh

Former Vice Chancellor, Thiruvalluvar University, Tamil Nadu

Past President, AMI

Message

I am immensely pleased to learn that the 65th International Conference of Association of Microbiologists of India (AMI) is organized at the Department of Biotechnology, Guru Jambheshwar University of Science and Technology, Hisar during 14th to 17th November 2024. Association of Microbiologists of India (AMI) is one of the oldest academic societies established earlier in our country. Annual conference is an important activity of the AMI which brings together students, researchers, eminent scientists in microbiology and allied fields and provides an overview of current microbiological research and discoveries. This 65th Annual conference theme is appropriately entitled as **"Perspectives of Microbes for Human Welfare".** I am privileged to associate myself with AMI several years in various capacities including as president of the Association (2009) and organizing secretary of the 32ndAnnual conference of AMI at Madurai (1992).

Everyone understands that microorganisms play an important role in every walk of our life. The application of microbiology covers all discipline of science, environment, industry, agriculture, medical, veterinary science, engineering and technology. Further, the employability is increased with skill and expertise to work in various disciplines of science and technology. The theoretical and practical knowledge of advanced Microbiology techniques and intelligent systems will help to understand the human health and cognitive capabilities. Microbiologists develop advanced research methods to analyze and solve health and medical problems.

I am confident that this 65th International Conference of Association of Microbiologists of India would provide a common platform for all students, scientists and researchers in the area of Microbiological Sciences to have discussion and share their knowledge and experience. It is with great honor and pleasure I extend my cordial welcome all the delegates and participants of the Annual conference of AMI. I also extend my hearty congratulations to the organizing secretary and organizing team of the conference for their great initiative and I wish the conference a great success.

Prof. P. Gunasekaran

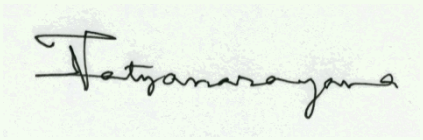
Prof. T. Satya Narayana

Deptt. of Microbiology,
University of Delhi South Campus
Benito Juarez Road
New Delhi-110021, India

Message

It gives me immense pleasure that Guru Jambheswar University, Hisar will be organizing 65th AMI Annual meeting and International conference in Nov. 2024. This gives an excellent opportunity to meet Microbiologists from Universities and Institutes in India and abroad, and get to know recent developments and opportunities in microbiology.

Best wishes for a successful organization of the event,



Prof. T. Satya Narayana

65th Annual International Conference of Association of Microbiologists of India (AMI)

ORGANIZED BY :

GURU JAMBHESHWAR UNIVERSITY OF SCIENCE & TECHNOLOGY (GJUST)
ASSOCIATION OF MICROBIOLOGISTS OF INDIA (AMI)
ACADEMY OF MICROBIOLOGICAL SCIENCES (AMSC)

PERSPECTIVES OF MICROBES FOR HUMAN WELFARE

14th - 17th November, 2024

HIMEDIA For Life is Precious

Department of Biotechnology

Venue : CRS Auditorium, GJUST, Hisar, Haryana, India
Visit us at : https://amiindia.info/amiconf/index.html, (https://www.gjust.ac.in)
Contact Us : ami2024hisar@gmail.com, +91-1662263312 (9:30 am - 5:30 pm)
+91-1662263165 , +91 9653564750

CONTENT

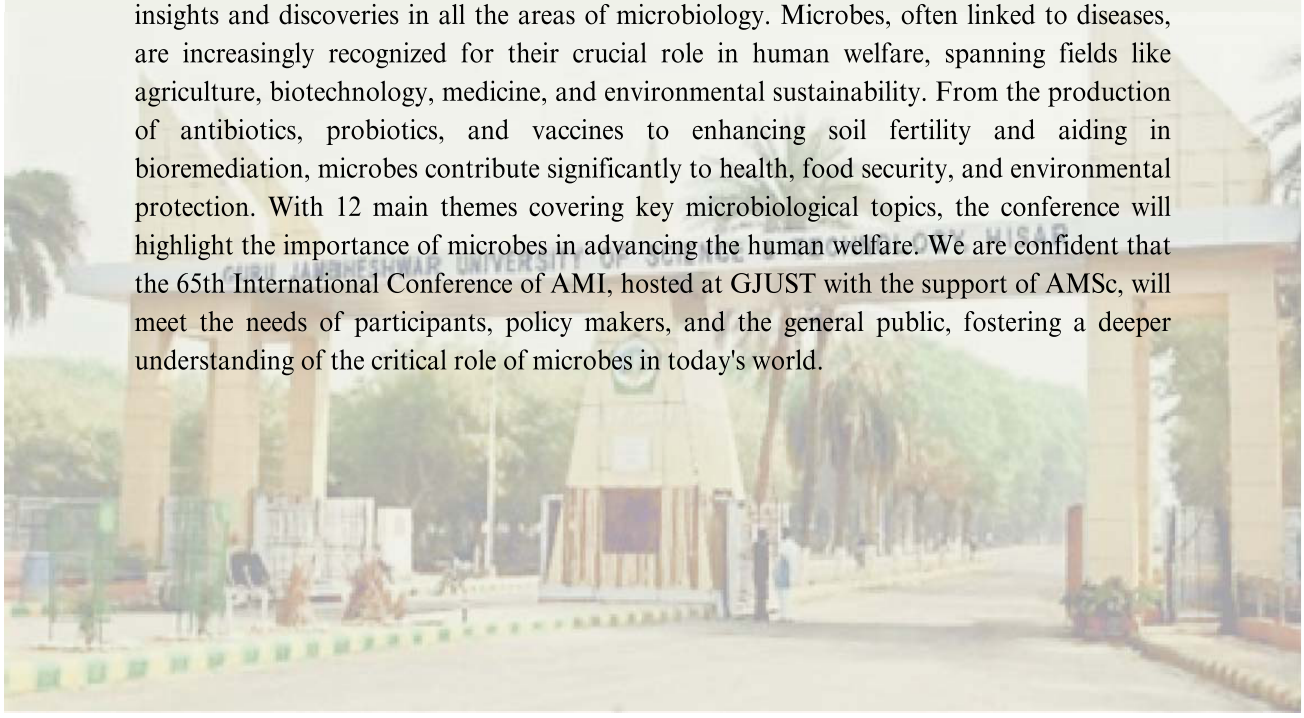
65th International Conference of Association of Microbiologists of India

INVITATION

Guru Jambheshwar University of Science and Technology (GJUST), Hisar in association with Association of Microbiologist of India (AMI) and Academy of Microbiological Sciences (AMSc) is organizing 65th Annual International Conference of AMI on “Perspectives of Microbes for Human the Welfare”during 14th -17th November 2024 . On behalf of GJUST and associated organizations, we the members of organizing committee cordially invite all the members of the Association, faculty members, researchers, students, progressive farmers, thinkers, policy makers, government officials, industry personnel to participate in this international conference. We assure you that the forum will provide an excellent opportunity to all the participants for fruitful scientific deliberations, by the esteemed international and national renowned speakers/researchers who will be addressing the delegates. We welcome all the scientific fraternity to attend this event and make this a grand success.

ABOUT THE 65th INTERNATIONAL CONFERENCE:

The 65th International Conference of the Association of Microbiologists of India, hosted by Guru Jambheshwar University of Science and Technology in collaboration with the Academy of Microbiological Sciences, will focus on the theme "Perspectives of Microbes for Human Welfare." This conference promises to deliver high-quality scholarly activities, making it a valuable opportunity for students, researchers, and industry professionals alike. Given the diverse and advanced research themes selected, this international event will bring together leading scientists, researchers, and scholars from across the globe to share their insights and discoveries in all the areas of microbiology. Microbes, often linked to diseases, are increasingly recognized for their crucial role in human welfare, spanning fields like agriculture, biotechnology, medicine, and environmental sustainability. From the production of antibiotics, probiotics, and vaccines to enhancing soil fertility and aiding in bioremediation, microbes contribute significantly to health, food security, and environmental protection. With 12 main themes covering key microbiological topics, the conference will highlight the importance of microbes in advancing the human welfare. We are confident that the 65th International Conference of AMI, hosted at GJUST with the support of AMSc, will meet the needs of participants, policy makers, and the general public, fostering a deeper understanding of the critical role of microbes in today's world.



ABOUT HISAR

Hisar, a city located in west part of Haryana, India, is rich in history and culture. With a population of over 300,000 people, it is famously known as the "grain bowl of Haryana" due to its strong agricultural roots. Established by Firoz Shah Tughlaq in 1354, Hisar features historical treasures such as the Hisar Fort, Gujri Mehal, archeological, sites, etc. The city's lively cultural landscape encompasses festivals and local cuisine, showcasing its hospitable charm.

Hisar serves as a prominent educational center, accommodating institutions such as Chaudhary Charan Singh Haryana Agricultural University (CCS HAU) and Guru Jambheshwar University of Science and Technology (GJUST). It is also home to research establishments like the Central Institute for Research on Buffaloes (CIRB), which contributes to advancements in buffalo genetics and dairy industry practices. Hisar is renowned for its focus on equine research and veterinary education, hosting institutions like the National Research Centre on Equines (NRCE) and Lala Lajpat Rai University of Veterinary and Animal Sciences (LUVAS).

Hisar enjoys excellent road and railway connections from various parts of the country. It harmoniously combines its rich historical legacy with modern amenities, offering an attractive destination for tourists, scholars, and entrepreneurs alike.

HOW TO REACH

ByAir :

The nearest airport is Indira Gandhi International airport, New Delhi is at a distance of 160 km from Hisar

ByTrain :

Hisar Junction is well-connected by a reliable railway network. Trains that stop at this station include the Gorakhdham Express, Delhi Express, Kisan Express, Sri Ganganagar Delhi Express, Tripura Sundari Express, Ajmer Amritsar Express, and Ludhiana Express.

ByBus :

Hisar is on the National Highway No. 09 and has excellent bus connections to all the cities and towns of the neighboring states.

ABOUT THE ORGANIZATIONS

ABOUT ASSOCIATION OF MICROBIOLOGISTS OF INDIA

The AMI, established in 1938, is one of the oldest and reputed scientific organizations of the country. Since its inception, it has contributed significantly towards the development of microbiology, particularly in areas of research and teaching in the country. At present, there are more than 5580 life and annual members and about 450 corporate members of the Association. The Association publishes a quarterly journal, "Indian Journal of Microbiology" (INJM) for the last 64 years and holds a National convention annually at one of the well-established centers of microbiology in the country. INJM, by publishing peer reviewed original research findings and research reviews from researchers in India and abroad, has acquired a respectable status among national and international scientific community and research periodicals in the world.

ABOUT ACADEMY OF MICROBIOLOGICAL SCIENCES :

The discoveries over the last few decades have established microbiology as a very important scientific discipline because of its practical ramifications in agriculture, medicine, environment, industry, genetic engineering and other fields. It is now clear that the role of microbe in nature is all encompassing. In view of the extreme microbial diversity, it is also well understood now that the process of mining microbial genetic variations for newer applications will continue long into the future. Also, the rapid rate of microbial evolution ensures that there will be no permanent solutions to problems posed by microbes. These problems will demand a continual stream of creative and new approaches of management that evolve along with the microbes. Thus, the excitement of microbiology will continue long into the future. However, these opportunities are imperatives and demand a deep understanding of basic microbial physiology, genetics, and ecology.

Major challenges that lay ahead are to impart broad and state of art training to enable the next generation of microbiologists, and to educate the public and government representatives about the continued and critical importance of this field for health, environment and economy. This is our road map for creation of' Academy of Microbiological Sciences (AMSc)' under the aegis of Association of Microbiologists of India (AMI), which has been into existence for more than eighty years now.

ABOUT GURU JAMBHESHWAR UNIVERSITY OF SCIENCE & TECHNOLOGY :

Guru Jambheshwar University of Science & Technology (GJUST), established in 1995 by an Act of the Legislature of the State of Haryana, is dedicated to fostering studies and research in emerging areas of higher education, focusing on technology, pharmacy, environmental studies, non-conventional energy sources, and management studies, while striving for excellence in these areas. Currently holding an A+ Grade NAAC accreditation from 18.10.2022 to 17.10.2027 with a CGPA of 3.38 in the fourth cycle, the University has achieved notable recognition. In the Atal Ranking of Institutional Innovations and Achievements (ARIIA-2020) by the Education Ministry, Govt. of India, it secured a position in Band-A between 6-25th among government and government aided universities. The University has attained graded Autonomy of Category-II, a distinction shared by only 21 State Universities in the country. Additionally, it has been accepted for the third time into the prestigious Global Initiative Academic Network (GIAN) Phase-III Scheme by MIIRD. Notable accolades include ranking 409th globally and 16th in India in UI Green Matric World University Rankings by the University of Indonesia. Jakarta in 2023, and winning the first prize at the State level for raising awareness about "Prevention of Alcoholism and Substance Abuse". The University has fostered interdisciplinary collaboration and research, with faculty publishing 4129 research papers in peer-reviewed journals listed in SCOPUS, garnering over 86000 citations. The University has received grants from the DST under the FIST program and the SAP program by UGC. Furthermore, it has successfully completed the DST- PURSE program, receiving a grant of Rs. 10.25 Crore.

CONFERENCE VENUE :

Ch. Ranbir Singh Auditorium is having large and expansive installs with exhaustive audio -visual integration fare, and there have also been some unique and innovative weaving of audio visual environments. The Ch. Ranbir Singh Auditorium on the campus of GJUST, Hisar, Haryana, the 'Steel City' of Haryana, however, scores a different note altogether.A large, impressive, and multi-purpose building stands out with many unique design features, combining both structure and texture, all brought together in a new and eye-catching way that also engages the senses of sight and sound.

MESSAGE FROM CHAIRPERSON

Dear Participants,

On behalf of the Organizing Committee we are looking forward to welcome you to Hisar for the 65th International Annual Conference of Association of Microbiologists of India (AMI) which takes place between 14th to 17th November. The conference is jointly organized by the GJUST in association with AMI and AMSc. The main theme of the conference is '**Prespectives of Microbes for Human Welfare-2024**'. The event is taking place at Ch. Ranbir Singh Auditorium, GJUST, Hisar, Haryana, India. The aim of the conference is to delve into the manifold ways in which microbial sciences contribute to the betterment of humanity. Microbes and their activities have a vast and often unexpectedly profound impact on human health, well-being, and the functioning of the entire biological world, including the Earth's atmosphere.

While many misconceptions about microbes persist, it is crucial to dispel these swiftly. Although some microbes have no impact on our lives, many are beneficial, and only a small fraction are harmful. Unfortunately, pathogens receive the most attention and are the most widely known. However, microbes should be viewed as allies, helping to address key challenges such as improving food production and offering numerous benefits to society. To maximize these benefits, microbes must be considered in both day-to-day decisions and those made at the community, national, and global levels regarding health and sustainability.

Despite the importance of microbes, public and decision-makers' understanding of microbiology remains limited, in contrast to fields like health, economics, and transportation, which are well understood. This international conference aims to bridge this knowledge gap by exploring various aspects of microbiology across major sectors such as food, agriculture, pharmaceuticals, and industry. It will provide a platform for sharing the latest technical advancements, high-quality research findings, and new developments in the field of microbiology. Moreover, it will promote discussions and the formulation of future priorities and directions for creating a better society.

We are honored to welcome several renowned speakers from around the world, and we hope you find the event both informative and engaging.

Prof. S.K. Khare
President, AMI Director,
IISER, Kolkata, West Bengal

Prof. R.C. Kuhad
Chairman, AMSc, Former VC,
CUH Mahendergarh, Haryana

MESSAGE FROM ORGANIZING SECRETARY & CONVENERS

Dear Delegates,

On behalf of the Organizing Committee, it is our distinct pleasure to extend a warm invitation to you for the 65th Annual and International Conference of Association of Microbiologists of India (AMI), scheduled to be held from November 14th – 17th, 2024.

This year the conference will be hosted jointly by Guru Jambheshwar University of Science and Technology, Hisar and Association of Microbiologists of India in Hisar, India. With the theme "**Perspectives of Microbes for Human Welfare**," the conference aims to delve into the manifold ways in which microbial sciences contribute to the betterment of humanity.

The conference will provide a platform for leading researchers, academicians, and practitioners from around the globe to share their latest findings, exchange ideas, and foster collaborations in the dynamic field of microbiology. We are confident that your expertise and insights would greatly enrich our discussions and contribute to the success of the event.

The conference program will include keynote lectures, plenary sessions, poster presentations, and workshops covering a wide range of topics such as microbial biotechnology, environmental microbiology, veterinary/medical microbiology, and industrial microbiology, among others.

Furthermore, we are organizing special sessions dedicated to emerging trends and challenges in the field, providing an opportunity for in depth exploration and dialogue among participants.

Your presence at the conference would not only honour us but also inspire fellow researchers and students alike. We believe that your valuable contributions and active participation will significantly enhance the academic exchange and networking opportunities at the event.

We eagerly anticipate your presence.

Organizing Secretary

Prof. Namita Singh
Dept. of Biotechnology,
GJUST, Hisar

Conveners

Prof. Anil Kumar
Dept. of Biotechnology,
GJUST, Hisar

Prof. Rajesh Gera
Dept. of Microbiology,
CCS HAU, Hisar

65th International Conference of Association of Microbiologists of India

AMI OFFICE BEARERS

President
Prof. Sunil K. Khare
Director, IISER, Kolkata,

Chairman, AMSc
Prof. R.C. Kuhad
Ex-VC, CUH, Mahendergarh

Immediate Past President
Prof. Sunil Pabbi
IARI, New Delhi

Past President
Prof. Praveen Rishi
Panjab UniversityChandigarh

General Secretary
Prof. Namita Singh
GJUST, Hisar

Joint Secretary
Dr. Anil Panghal
CCS HAU, Hisar

Treasurer
Dr. Livleen Shukla
ICAR-IARI, New Delhi

Central Council Members

Prof. Shamsher Singh Kanwar
HPU, Shimla

Prof. Minakshi Prasad
NRCE, Hisar

Prof. Lilly Ganju
Former Associate Director,
DIPAS, DRDO, New Delhi

Prof. Meenu Saraf
Director, Gujrat University
Ahemdabad.

Prof. N. Vasudevan
Anna UniversityChennai

Editor - in - Chief (INJM)

Prof. Minakshi Prasad
NRCE, Hisar

Prof. Lilly Ganju
Former Associate Director,
DIPAS, DRDO, New Delhi

AMI - Hisar Unit

President
Prof. Rajesh Gera
CCS HAU, Hisar

Secretary-cum-Treasurer
Prof. Namita Singh
GJUST, Hisar

Executive Council Members
Dr. Alka Sharma
GJUST, Hisar
Dr. Navnidhi Chhikara
GJUST, Hisar
Dr. Kamla Malik
CCS HAU, Hisar
Dr. Swati
LUVAS, Hisar
Dr. Shikha Mehta
CCS HAU, Hisar
Dr. Monika Kayasta
CCS HAU, Hisar

HONORARY ADVISORY MEMBERS

- Padma Bhushan Prof. R.S. Paroda, Past President, Association of Microbiologists of India
- Padma Bhushan Prof. Manju Sharma, Past President, Association of Microbiologists of India
- Padma Shri Prof. Vijayraghvan, Former Secretary, Department of Biotechnology, New Delhi
- Padma Shri Prof. S. Ayyappan, Past President, Association of Microbiologists of India
- Padma Shri Prof. R. C. Sobti, Ex-Vice Chancellor, Punjab University, Chandigarh
- Padma Shri Prof. Sudhir K Sopory, Ex-Vice Chancellor, JNU, New Delhi
- Prof. M. Jagadesh Kumar, Chairman, University Grants Commission
- Prof. AbhayKarandikar, Secretary to the Government of India, Department of Science & Technology, New Delhi
- Dr. Rajesh S Gokhale, Secretary, Department of Biotechnology, New Delhi
- Dr. (Mrs.) N. Kalaiselvi, Director General, CSIR & Secretary, DSIR
- Shri G. Kamala Vardhana Rao, Chief Executive Officer, FSSAI, New Delhi
- Prof. K.C. Sharma, Chairperson, Haryana State Higher Education Council, Panchkula
- Dr. Sanjeev Khosla, Director, IMTECH, Chandigarh
- Dr. Soumya Swaminathan, Chief Scientist, World Health Organization
- Dr.Tarun Kumar Bhattacharya, Director, ICAR-National Research Centre on Equines, Hisar
- Dr. Tirtha Kumar Datta, Director, ICAR-Central Institute for Research on Buffaloes, Hisar
- Prof. D. P. Singh, Chancellor, Tata Institute of Social Sciences
- Prof. Yogesh Singh, Vice-Chancellor, Delhi University, Delhi
- Prof. Tankeshwar Kumar, Vice-Chancellor, Central University of Haryana, Mahendergarh, Haryana
- Prof. Rajbir Singh, Vice-Chancellor, Maharishi Dayanand University, Rohtak
- Prof. Dinesh Kumar, Vice Chancellor, Gurugram University, Gurugram
- Sh. Raj Nehru, Vice-Chancellor, Shri Vishwakarma Skill University (SVSU), Gurugram
- Prof. B. R. Kamboj, Vice-Chancellor, CCS Haryana Agriculture University, Hisar
- Dr. Vinod Kumar Verma, Vice-Chancellor, Lala Lajpat Rai University of Veterinary and Animal Sciences (LUVAS), Hisar
- Prof. Ajmer Singh, Vice-Chancellor, Chaudhary Devi Lal University, Sirsa
- Prof. S.K. Tomar, Vice-Chancellor, J.C. Bose University of Science & Technology, YMCA, Faridabad
- Prof. Sudesh, Vice-Chancellor, BhagatPhool Singh MahilaVishwavidyalaya, Khanpur Kalan,Sonepat
- Prof. SK Singh, Vice-Chancellor, Rajasthan Technical University, Kota
- Prof. J. P. Yadav, Vice-Chancellor, Indira Gandhi University, Meerpur
- Shri Gajendra Chauhan, Vice-Chancellor, PanditLakhmi Chand State University of Performing and Visual Arts, Rohtak
- Prof. Ranpal Singh, Vice-Chancellor, Chaudhary Ranbir Singh University, Jind
- Prof. S. P. Singh, Vice-Chancellor, DeenbandhuChhotu Ram University of Science and Technology, Murthal
- Prof. Deepti Dharmani, Vice Chancellor, Chaudhary Bansi Lal University, Bhiwani
- Dr. Suresh K Malhotra, Vice Chancellor, Maharana Pratap Horticultural University, Karnal
- Dr. Anita Saxena, Vice Chancellor, Pt. Bhagwat Dayal Sharma University of Health Sciences, Rohtak, Haryana
- Prof. Deepak Pental, Ex-Vice Chancellor, University of Delhi, N Delhi
- Prof. P. Tauro, Past President, Association of Microbiologists of India
- Prof. B.N. Johri, Past President, Association of Microbiologists of India
- Prof. K. Laxaminaryana, Past President, Association of Microbiologists of India
- Prof. Dalel Singh, Past President, Association of Microbiologists of India
- Prof. B.S. Kundu, Past President, Association of Microbiologists of India
- Prof. P. Gunasekaran, Past President, Association of Microbiologists of India
- Prof. Gaya Prashad, Past President, Association of Microbiologists of India
- Prof. L.V. Rao, Past President, Association of Microbiologists of India
- Prof. Sunil Khanna, Past President, Association of Microbiologists of India
- Dr. Renu Swarup, Former Secretary, Department of Biotechnology, New Delhi
- Prof. Ashutos Sharma, Former Secretary, Department of Biotechnology, New Delhi

INTERNATIONAL ADVISORY COMMITTEE

- Prof. Arthur Riedacker, France
- Prof. Avigad Vonshak, Israel
- Prof. Trinad Chakraborty, USA
- Prof. Oleksandr Tashyrev, Ukrain
- Dr. Jabborova Dilfuza, Uzbekistan
- Prof. Peter R Williamson, USA
- Prof. K. Yutaka, Japan
- Prof. Barry T Rouse, USA
- Prof. Vijay Thakur, United Kingdom
- Prof. Ajay Singh, Canada
- Prof. Adriano Gomes da Cruz ,Brazil
- Dr. Tukasz Drewniak, Poland
- Dr. Dror Minz, Israel
- Prof. Brett Pletschke, South Africa
- Dr. Sanjay Nagarkar, Hong Kong
- Dr. Harshini Mukundan, USA
- Dr. Paramjeet Singh Bagga, New Jersey
- Prof. Rajesh Sani, USA
- Prof. (Dr.) Santasree Banerjee, China
- Dr. Minaxi Sharma, China
- Dr. Gaurav Rajauria, Ireland
- Dr. Nikhil Bhalla, United Kingdom
- Prof. Helen Treichel, Brazil
- Prof Mortaza Aghbashlo, Iran
- Dr Ajeet Kaushik, Lakeland, FL
- Prof Ahmed M. Abdel-Azeem, Egypt
- Prof Jiri Damborsky, Czech Republic
- Prof. Dr. Sudip K. Rakshit, Canada
- Dr. Lahiru Jayakody, Carbondale, Illinois
- Prof. Meisam Tabatabaei, Malaysia
- Prof. Vijai Kumar Gupta, Ireland
- Dr Vaibhav Srivastava, Sweden
- Prof. Mark Stadler, Germany
- Prof. Dr.Rer.nat.hesham A. Malaysia
- Prof. Samantha C. Karunarathna, China
- Prof. Turgay Çakmak, Istanbul, Türkiye
- Dr. Eddie Cytryn, Israel
- Prof. Kiminori Shimizu, Japan
- Dr. Zainul Akmar Zakaria, Malaysia

NATIONAL ADVISORY COMMITTEE

- Prof. Sunil Pabbi, Past President, Association of Microbiologists of India
- Prof. Praveen Rishi, Past President, Association of Microbiologists of India
- Prof. D.K. Singh, Past President, Association of Microbiologists of India
- Prof. Yogender Singh, Past President, Association of Microbiologists of India
- Prof. J.S. Virdi, Past President, Association of Microbiologists of India
- Prof. Appa Rao Podile, Past President, Association of Microbiologists of India
- Prof. Amulya K. Panda, Past President, Association of Microbiologists of India
- Prof. Sunil Khanna, Past President, Association of Microbiologists of India
- Prof. T. Satyanarayana, Past President, Association of Microbiologists of India
- Prof. Tapan Adhya, Past President, Association of Microbiologists of India
- Prof. S.S. Dudeja, Past President, Association of Microbiologists of India
- Prof. Rup Lal, Past President, Association of Microbiologists of India
- Dr. R. K. Behl, SSARM
- Dr. R. S. Sangwan, Former Director-AcSIR, Ghaziabad
- Dr. K. C. Bansal, Former Director-NBPGR, New Delhi
- Dr. Neelam Sangwan, Professor, Central University of Haryana
- Dr. S. D. Attri, Member Technical at Commission for Air Quality Management in NCR and Adjoining Areas, New Delhi.
- Prof. K. D. Sharma, Dean, Post Graduate Studies, CCS Haryana Agriculture University, Hisar
- Prof. K K Kapoor, Former Emeritus Professor, Dept of Bio & Nano Technology, Guru Jambheshwar University of Science & Technology, Hisar, Haryana
- Mr. Soshil Kumar Jain, Executive Chairman of the Board, Panacea Biotec
- Dr. Sanjay Mishra, Scientist-'G' DBT government of India
- Dr. Gulshan Vadhwa Scientist DBT

65th International Conference of Association of Microbiologists of India

LOCAL ADVISORY COMMITTEE

Prof. Yogesh Chaba,
Dean, Academic Affairs, GJUS&T, Hisar

Prof. Asha Gupta,
Dean, Faculty of Environmental and Bio Sciences & Technology, GJUS&T, Hisar

Prof. N.K, Bishnoi
Dean, Faculty of Religious Studies, GJUS&T, Hisar

Prof. Karam Pal Narwal,
Dean, Haryana School of Business, GJUS&T, Hisar

Prof. Sandeep Kumar Arya,
Dean, Faculty of Engineering & Technology, GJUS&T, Hisar

Prof. Sumitra Singh,
Dean, Faculty of Medical Sciences, GJUS&T, Hisar

Prof. Vandana Punia,
Dean, Faculty of Education, GJUS&T, Hisar

Prof. Rajiv Kumar,
Dean, Faculty of Law, GJUS&T, Hisar

Prof. Neeraj Dilbaghi,
Dean, Research & Development, GJUS&T, Hisar

Prof. Mukesh Kumar Sharma,
Dean, Alumni, GJUS&T, Hisar

Prof. Mukesh Kumar,
Director PDUCIC, GJUS&T, Hisar

Prof. Manoj Dayal,
Director, Abdul Kalam Centre for Ancient Indian Science, GJUS&T, Hisar

Prof. Vinod Kumar,
Director, Haryana School of Business, GJUS&T, Hisar

Prof. Ashish Agarwal,
Director, IQAC, GJUS&T, Hisar

Prof. Munish Ahuja,
Director, CIL, GJUS&T, Hisar

Prof. Vishal Gulati,
Director, PDUIIC, GJUS&T, Hisar

Prof. Dalbir Singh,
Director, Public Outreach & Relations, GJUS&T, Hisar

Prof. Sunita Rani,
Director, MMTTC, GJUS&T, Hisar

Prof. Khujan Singh,
Director, Center for Distance and Online Education, GJUS&T, Hisar

Dr. Pratap Singh Malik,
Director, Training & Placement Cell, GJUS&T, Hisar

Dr. Mahavir Parshad,
Director, Hospitality, GJUS&T, Hisar

Prof. Aradhita Burman Ray,
Chairperson, Department of Food Technology, GJUS&T, Hisar

Perspectives of Microbes for Human Welfare-2024

65th International Conference of Association of Microbiologists of India

CONFERENCE THEMES

1. Advanced Microbial Diagnostics/Detection Tools
2. AI in Microbiological Applications
3. Climate Change and Agroecosystem: Effect on soil microbial diversity
4. Entrepreneurship and IPR
5. Environmental Microbiology
6. Food and Industrial Microbiology
7. Microbial Nanotechnology
8. Microbial Therapeutics and Anti-Microbial Resistance
9. Microbiology for Mankind
10. Microbiology for Sustainable Development
11. Plant Microbe Interactions
12. Vaccine Development for Life
13. Sponsored Session

Perspectives of Microbes for Human Welfare-2024

65th International Conference of Association of Microbiologists of India

Participation and Registration: All the delegates must register to participate in the 65 International Conference in prescribed google form https://forms.gle/iatKGcgsDtPNPUwK9 . No abstract will be accepted without registration. For conference participation, registration and submission of oral and poster session abstracts, please contact us at **ami2024hisar@gmail.com** .

REGISTRATION FEE DETAILS

Category	Category	Early Bird Registration (upto 10 October)	Late Registration (upto 31st October)	On the Spot Registration** (max. Limit 100 person)
AMI Members	Faculty/Post-Doctoral	4500	5000	5000
	Students	2500	3000	3000
	Accompanying (Spouse/guest)	2500	3000	3000
Non-AMI Members	Faculty/Post-Doctoral	5000	5500	5500
	Students	3000	3500	3500
	Accompanying (Spouse/guest)	2500	3000	3000
Industry/corporate		10000	12000	12000
Foreign Delegates		USD 400	USD 450	USD 450
Accompanying (spouse/guest)		USD 250	USD 275	USD 275
SAARC Countries Delegates		USD 200	USD 250	USD 250
Accompanying (spouse/guest)		USD 100	USD 125	USD 125

COMBO OFFER

Category	Fees
Faculty/Post-Doctoral	**8850/- {Lifetime membership (3850/-) + Conference registration(5000/-)}**
Students	**6850/- {Lifetime membership (3850/-) + Conference registration(3000/-)}**
Individual Life Membership for a person working in Corporate/Industry/Private Sector	**15000/- {Lifetime membership (5000/-) + Conference registration(10000/-)}**
SAARC Country	**USD 500 {Lifetime membership (USD 300) + Conference registration (USD 200)}**

Mode of Payment

Payment can be remitted via GooglePay/ Paytm/ PhonePay/ UPI ID.

Bank : Punjab National Bank
Branch : GJUS&T, Hisar
IFSC Code: PUNB0467400
Swift Code : PUNBINBBHIS

IMPORTAN LINKS :

Registration: https://forms.gle/iatKGcgsDtPNPUwK9

Accommodation: https://forms.gle/UMcKyQWrGxSJsPoG8

Travel: https://forms.gle/sj5B7FtyAuAwgukd7

ACCOMMODATION : Registration fee do not include accommodation charges. However, stay arrangements for all the participants have been made in the nearby hotels, University Guest house, Hostels. Therefore, all the delegates are requested to ensure their accommodation through pre-booking.

OPPORTUNITIES AT THE CONFERENCE....

Guidelines For Abstract Submission

We invite abstracts (not exceeding 300 words) of original research for poster presentations. Please include the title, names of all authors, complete postal address, and email address of the corresponding author in the abstract. The name of the presenting author should be underlined. Abstracts must be formatted in Microsoft Office Word, using Times New Roman font (size 12pt) with 1.5-line spacing. The deadline for abstract submission is October 25, 2024. Full-length articles will be considered for publication in Scopus-indexed journals with a minimal article processing fee. **Selected articles will be published in a SCOPUS listed journal with a nominal charges.**

Poster Presentations-Award Competition

Dimensions: 120 cm (length) x 90 cm (width). Font sizes: Title - 80 pt, Authors - 50 pt, Subheadings - 46 pt, Text - 24 pt, Captions - 18 pt. The poster should feature the following sections: Title, Name, Theme, Address, Introduction, Materials and Methods, Results, Conclusion, and References.

Oral Presentations-Award Competition

The presentation should be limited to 10 slides and completed within 5 minutes. The first slide should include the title, name, theme, and address. The following slides should cover the introduction, materials and methods, results, and conclusion.

Content of the Poster

1. ORIGINAL Research Work (a declaration from the authors will be required)
2. The poster should include a title, name, and affiliation of all the authors.
3. Content should be appropriately sectioned. The title and subheadings should be written in bold. Multiple fonts should be avoided. Poster Font size:>=16.
4. At the footer/bottom part of the poster, it should be noted: **Presented at 65th Annual International Conference on "Perspectives of Microbes for Human Welfare"2024.**

NOTE :

- Presenting author name should be bold and underlined. It is mandatory for the presenting author to register for the conference.
- Other author may register. Certificates will be issued to all registered authors of each oral and poster presented in the conference.

AMI- AWARDS

- AMI - Prof. G. S. Rangaswamy
- AMI - S. R. Vyas Memorial award
- AMI - Soshil Kumar Jain Panacea Biotech Award
- AMI - Prof. B. N. Johri Award
- AMI - Louis Pasteur Award
- AMI - Dr. J. V. Bhatt Award
- AMI - Young Scientist Award
    - Agricultural Microbiology
    - Dairy and Food Microbiology
    - Environmental Microbiology
    - Industrial Microbiology
    - Medical & Veterinary Microbiology
    - Molecular Microbiology
- AMSc Fellow
- AMI - Dr. R. S. Rana Memorial Award (Best Poster award for 65 AMI Conference)
- AMI - Dr. Manvika Sahgal Best Poster Award (Agricultural, Soil and Environmental Microbiology)
- AMI - Student Travel Award (20)
- Springer - AMI award- 12 each in poster and oral presentations
- AMI - Best poster award one in each category
  (Agricultural Microbiology, Dairy and Food Microbiology, Environmental Microbiology, Industrial Microbiology, Medical & Veterinary Microbiology, Molecular Microbiology)

65th International Conference of Association of Microbiologists of India

EMINENT SPEAKERS

PADMA BHUSHAN PROF. NIRMAL KUMAR GANGULY
Former Director General, ICAMR New Delhi and Former President of National Academy of Medical Sciences

PADMA BHUSHAN DR. MANJU SHARMA
Executive Director, Indian Institute of Advanced Research in Gandhinagar, Gujrat and Former Secretary DBT, India

PROF. AVIGAD VONSHAK
Ben-Gurion University, Negev, Israel

PROF. BHARAT K. C. PATEL
Adjunct position-QUT Visiting Professor-IRD, Univesite de Marseille, France and National University of Singapore Honorary position - University of New England, Australia.

PROF. THIERRY REGNIER
Tshwane University of Technology, pretoria, South Africa

PROF. VIJAY KUMAR GUPTA
School of Biotechnology, University of Dublin, Ireland

PROF. LUKASZ DREWNIAK
Faculty of Biology, University of Warsaw, The Institute of Biology, Jan Kochanowski University, Kielce, Poland

PROF. BARRY T. ROUSE
University of Tennessee, USA

PROF. DR. BARBARA SPELLERBERG
Ulm University Medical Center, Germany

PROF. RAJESH SANI
Department of Chemical and Biological Engineering, South Dakota, USA

DR. MOHD ULUL ILMIE BIN AHMAD NAZRI
Universiti Malaysia Terengganu (UMT), Malaysia

DR. ULRICH BERK
President, German Association of Homa Therapy

DR. ZAINUL AKMAR BIN ZAKARIA
Universiti Teknologi Malaysia (UTM), Malysia

DR. APARNA BANERJEE
Universidad Autónoma de Chile

PROF. SARMAN SINGH
Director Medical Research and Institutional Collaboration, AVMC, Pondicherry

PROF. BHABATOSH DAS
Professor & Coordinator Centre for Microbial Research, Translational Health Science and Technology Institute, NCR Biotech Science Cluster, Faridabad

PROF. DAYANAND AGSAR
Vice-Chancellor: Gulbarga University, Kalaburagi, Karnataka

DR. NALLUSAMY SIVAKUMAR,
Sultan Qaboos University, SQU, Oman

65th International Conference of Association of Microbiologists of India

PROF. YOGENDER SINGH
Department of Zoology, University of Delhi

PROF. R.C. KUHAD
Founder Chairman AMsc and Former Vice Chancellor, CUH, Mahendergarh, Haryana

DR. AVIJIT DAS
Marie Skłodowska-Curie Postdoctoral Fellow (MSCA PF), Tel Aviv University (TAU), Isreal

PROF. SUHAIL AHMAD
Professor, Department of Microbiology, Faculty of Medicine, Kuwait University, KUWAIT

DR. MANJU BALHARA
International Flavors & Fragrances Inc. (IFF) Denmark

DR. DILFUZA JABBOROVA
Uzbekistan Academy of Sciences

DR. SONAM PALIYA
Alexander von Humboldt Fellow
RWTH Aachen University, Germany

PROF. AMITA GUPTA
Professor and Head of Department of Biochemistry
Director, CIIDRET, University of Delhi
Director, DSSEED, University of Delhi

DR. SUNIL MUNDRA
Department of Biology, United Arab Emirates University, UAE

DR. BELLE DAMODARA SHENOY
CSIR-NIO Regional Centre in Visakhapatnam, Andhra Pradesh

DR. MINAXI SHARMA
University of Nottingham Ningbo China (CBI-UNNC), China

PROF. OM PRAKASH
Symbiosis International, Pune

PROF. RAGINI GOTHALWAL
Professor and Head SUB-DIC, DBT, Department of Biotech BU. Bhopal, MP

PROF. SUNIT K. SINGH
Director Dr. B R Ambedkar Center of Biomedical Research (ACBR), University of Delhi, Delhi

PROF. SIVAKUMAR UTHANDI
Dean, TNAU, Coimbatore

DR. (MRS) BECKY M THOMAS
Director at Shriram Institute for Industrial Research (SRIFIR), Gurugram

DR. GITANJALI YADAV
Scientist, NIPGR, New Delhi Adjunct Professor, Dept. of Data Science, IISER, Bhopal and University of Cambridge, U.K

DR. SANJAY MISHRA
Advisor DBT, Scientist F'Govt. India

PROF. RAMAKRISHNA WUSIRIKA
Department of Biochemistry and Dean Incharge Academics in Central University of Punjab, Bathinda

PROF. SURENDER SINGH
Department of Microbiology, CUH, Mahendergarh, Haryana

65th International Conference of Association of Microbiologists of India

DR. D.L.N RAO
Indian Institute of Soil Science (IISS) Soil Biodiversity and Biofertilizers

DR. JAVED N. AGREWALA
Professor , CBME, Indian Institute of Technology, Ropar, India

DR. SANJAY KUMAR
IISER, Tirupati

DR. BANWARILAL
Senior Director, TERI, New Delhi

PROF. JYOTI PRAKASH TAMANG
Senior Prof. Department of Microbiology at Sikkim Central University

DR. VIJAY K. CHAUDHARY
NASI-Senior Scientist
CIIDRET, University of Delhi
Advisor (Hon.), DSSEED, University of Delhi

DR. PRAGYA D. YADAV
ICMR, National Institute of Virology, Pune

DR. PANKAJ SETH
Prof. & Scientist VII, NBRC, Manesar, Haryana

PROF. RUPLAL
INSA Senior Scientist
Acharya Narendra Dev College, University of Delhi, New Delhi-110019

DR. YOGENDRA S PADWAD
CSIR - Institute of Himalayan Bioresource Technology, (IHBT) Pharmacology and Toxicology

PROF. BISHWAJIT KUNDU
Kusuma School of Biological Science, IIT Delhi

DR. D JOSEPH BAGYARAJ
INSA Hon. Scientist & Chairman, CNBRCD, Bengaluru

PROF. HARI S MISRA
Distinguished Professor of Biological Science, NMIMS deemed University, Mumbai

PROF. PRINCE SHARMA
Department of Microbiology, Panjab University, Chandigarh

DR. SWAPAN GHOSH
Molecular Myca pathology Cancer Research Unit, Ram Krishan Mission, Kolkata

DR. G. VELMURUGAN
KMCH Research Foundation, Coimbatore, Tamil Nadu

DR. SANDIP KUMAR DASH
Berhampur University, Odisha

PROF. VEENA PANDE
Department of Biotechnology, Kumaun University Sir J.C.Bose Technical Campus, Bhimtal, Nainital(Uttarakhand)

PROF. PRADEEP VERMA
Department of Microbiology
Central University of Rajasthan
Bandersindri Kishangarh Ajmer Rajasthan

PROF. NAVEEN KANGO
Harisingh Gour University, Sagar, M.P.

65th International Conference of Association of Microbiologists of India

PROF. SUNIL KHARE
Director, IISER Kolkata and Former Dean of R&D at IIT Delhi and President AMI

PROF. APPA RAO PODILE
Senior Professor, University of Hyderabad
Former Vice Chancellor Central University of Hyderabad

PROF. SUNITA VARJANI
Senior Associate Professor, UPES, Dehradun, India, Professor (Adjunct)- Korea University, Republic of Korea and Director-Institute of Chartered Waste Managers, India

DR. SENTHIL KUMAR
Staff Scientist, Integrative Structural Biology Laboratory, National Institute of Immunology, New Delhi

PROF. BALJEET SINGH SAHARAN
Department of Microbiology, Chaudhary Charan Singh Haryana Agriculture University, Hisar

DR. GULSHAN WADHWA
Scientist `G' DBT Technology, Capacity & Partnerships.

DR. DEEPTI PARASHAR
Head of the Diagnostic Reagent Facility ICMR-National Institute of Virology, Maharashtra

DR. ANJU PAPPACHAN
Professor, School of Life Sciences, Central University of Gujarat

DR. AMULYA K PANDA
Associate Director, Panacea Biotec Ltd and Former Director, National Inst of Immunology, New Delhi

PROF. ARUN S. KHARAT
School of Life Sciences, Jawaharlal Nehru University, New Delhi

DR. MUKESH KUMAR YADAV
Department of Microbiology, Central University of Punjab, Bhatinda 151401, Punjab, India

DR. ANIL KUMAR
National Institute of Immunology, New Delhi

DR. RADHA PRASANNA
Head Division of Microbiology, ICAR-IARI, New Delhi

PROF. SHEETAL BHASIN
Maharaja Ranjit Singh College of Professional Sciences, Indore, M.P

DR. DINESH A. NAGEGOWDA
Chief Scientist & Scientist In-Charge
CSIR-CIMAP Research Centre, Bengaluru

DR. INDRANI GHOSH
CSIR-IPU, New Delhi

DR. YAMINI SINGH
DIPAS, DRDO,
Ministry of Defence,Timarpur, Delhi.

PROF. GUNJAN GOEL
Department of Microbiology, Central University of Haryana

PROF. URMI BAJPAI
Delhi University

DR. GAYA PRASAD
Former Vice-chancellor of Sardar vallabh bhai Patel University of Agriculture and Technology, Modipuram, Meerut,

65th International Conference of Association of Microbiologists of India

MS. NAMRATA JOSHI
Faculty of Biology, University of Warsaw, Poland

DR. SANJAY RAJPUT
Additional Prof. AIIMS, Bhatinda

PROF. RAM CHANDRA
Department of Environmental Microbiology,
Babasaheb Bhimrao Ambedkar University, Lucknow

PROF. NAVEEN GUPTA
Chairperson, Department of Microbiology
Panjab University, Chandigarh

DR. K. K. SHARMA
Department of Microbiology

PROF. BIJENDER SINGH
Department of Biotechnology, Central
University of Haryana, Mahendergarh, Haryana

DR. SONU GANDHI
Scientist E, DBT-National Institute of Animal
Biotechnology, Hyderabad

DR MAHAVEER P SHARMA
Indian Institute of Soybean Research, Indore

PROF. MD. IMTAIYAZ HASSAN
Centre of Interdisciplinary Research in Basic Sciences
Jamia Millia Islamia, New Delhi

DR. RAVI MISHRA
Principal Scientist
CSIR-INSTITUTE OF MICROBIAL
TECHNOLOGY, Chandigarh

DR. SANJAY K.S. PATEL
Associate Professor, Hemvati Nandan Bahuguna
Garhwal University (A Central University)

PROF. BHIM PRATAP SINGH
Head, Department of Agriculture and
Environmental Sciences, NIFTEM Kundli,
Haryana

DR. NEETU KUMAR KAMRA
Associate Prof. NIFTEM, Sonipat

PROF. N. RAGHU RAM
School of biotechnology, GGS, I.P.University,
New Delhi

PROF. PRAVEEN RISHI
Department of Microbiology, Panjab University,
Chandigarh

DR. JASKARAN SINGH
Dean Research,
Geeta University, Panipat, Haryana

DR. ANJU MANUJA
Principle Scientist NRCE, Hisar

DR. RAHUL TANEJA
Scientist, Patent Information Center, HSCST

DR. SHRUTI SUKHLA
Associate Prof. NEHU, Shillong

DR. MEENAKSHI PARSHAD
ICAR-SCIENTIST E, NRCE, HISAR

65th International Conference of Association of Microbiologists of India

PRE-CONFERENCE WORKSHOP & LECTURES

MICROBIAL FORENSICS AND APPLICATION

14th November, 2024

Dr. Minakshi Parsad,
NRCE, Hisar

Dr. Jaskaran Singh,
Head & Associate Prof.
Geeta University

INTELLECTUAL PROPERTY RIGHTS

14th November,2024

Dr. Rahul Taneja,
Scientist,
Patent Information Center ,DST

Dr. Ashvani,
GJUST, Hisar

*Registration Fee:
Rs. 1000/- (UG/PG/Ph.D)
Rs.2000/- (Faculty)

*NO Registration Fee

Nanomaterials for Drugs & Diagnosis Application

14th November, 2024

Prof. Neeraj Dilbaghi
Dean Research & Development
GJUST,Hisar

Dr. Anju Manuja
Principal Scientist
NRCE,Hisar

Dr. Dadarwal Memorial Lecture:

Genetically diverse and symbiotically efficient Nitrogen-fixing rhizobia are root nodule symbionts of various wild/native and invasive legumes found in different agro-climatic conditions of India

15th November, 2024

PROF. H.S. GEHLOT
ICAR-Emeritus Scientist,
HSSc, Bhopal

DR. SS DUDEJA
Past President of AMI
Prof. (Retd.) CCSHAU, Hisar

65th International Conference and Conclave of Association of Microbiologists of India

CONFERENCE AND CONCLAVE ON,
PERSPECTIVES OF MICROBES FOR HUMAN WELFARE

Organized by

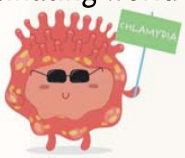
Guru Jambheshwar University of Science & Technology, Hisar, Haryana

in collaboration with

ASSOCIATION OF MICROBIOLOGISTS OF INDIA

Microbe Vision: Children Specific Activities

The School Conclave at the 65th Annual International Conference of the Association of Microbiologists of India (AMI), titled "Perspective of Microbes for Human Welfare," aims to inspire young minds to explore the fascinating world of microbes.



Objectives of the Conclave :-

- The primary objective is to introduce school children from class 8th to 12th to the fascinating world of microbes.
- Demystify the microbial world.
- Showcase their positive applications in food production, agriculture, medicine, waste management and clean & green environment.
- Promote their interest and STEM (Science, Technology, Engineering and Mathematics) and the SDG (Sustainable Developement Goals).
- Addressing microbes role in global challenges such as climate. change, public health, soil health and sustainable development.

November 11th, 14th to 17th 2024

Events :-

- Poster making
- Essay writing
- Slogan writing
- Quiz
- Model on the perspective of microbes for Human welfare
- Rangoli making

No Registration Fees

65th International Conference of Association of Microbiologists of India

IMPORTANT INFORMATION

Abstract: Send your abstract to Google Form:
https://docs.google.com/forms/d/1NsqjEQQg9v1fKp8GdsWXT3j-96p5d9Vmw_iNPXmkJ5E/edit
on or **before 10th October 2024** No abstract will be accepted after the last date **i.e.'10/10/2024**
Registration: Open for all Students, Scholars, Delegates, and Industry personnel **Late Registration ends on 31st October 2024.**

Early bird Registration CLOSING ON.... 31st October, 2024

On the Spot Registration
(LIMIT TO 100 ONLY, 14th November, 2024)

Visit Us : https://www.gjust.ac.in **E-mail Us on : ami2024hisar@gmail.com**
https://amiindia.info/amiconf/index.html/

Contact us:

Ms. Taruna Sheoran	**+91-76268 50255 (For Registration)**
Ms. Shreya Maheshwari	**+91-82185 97390 (For Abstract Acceptance)**
Mr. Mandeep	**+91-89505 25215 (For Accommodation & Transportation)**
Mr. Yuvansh Anjna	**+91-7011964796 (Hospitality & Accommodation)**
Mr. Sandeep	**+91-91420 15420 (For Travel Query)**
Ms. Renu Sheokand	**+91-88160 23910 (General Assistance)**
Ms. Shalu	**+91-70152 10977 (General Assistance)**
Ms. Renuka Sharma	**+91-7206259130 (Only the invited Speakers)**
Mr. Amit	**+91-7840025159 (Payment only for Accommodation related)**

For Specific Queries:

Dr. Anita Rani Gill	**+91-94166 46870**
Dr. Krishan Dutt Rawat	**+91-90343 75246**
Dr. Nayan Tara	**+91-82955 15695**
Dr. Rakesh Yadav	**+91-81683 55706**
Dr. Ravinder Kumar	**+91-94667 48271**
Dr. Renu Singh	**+91-94668 60066**
Dr. Saloni Gupta	**+91-99910 91374**
Dr. Anil Panghal	**+91-99880 49760**
Dr. Anita Kirolia	**+91-90504 17740**
Dr. Sapna Grewal	**+91-94165 97896**
Dr. Rajesh Thakur	**+91-94681 90092**
Dr. Santosh Kumari	**+91-88180 23060**
Prof. Namita Singh	**+91-94169 28883 (Only in case Emergency)**
Prof. Anil Kumar	**+91- 94165 33004 (Only in case Emergency)**
Prof. Rajesh Gera	**+91- 94169 61450 (Only in case Emergency)**

SPECIAL CULTURAL ATTRACTION

Rakhi Garhi

Rakhi Garhi, an Indus Valley Civilization archaeological site in Haryana's Hisar District, is about 150 km northwest of Delhi and dates back to 2600-1900 BCE.

Agroha Dham

Agroha Dham is a revered temple dedicated to Goddess Mahalaxmi, built by Maharaja Agrasen and maintained by Agroha Vikas Trust. The complex houses three temples: one for Goddess Mahalaxmi, one for Goddess Saraswati, and one for Maharaja Agrasen, the spiritual leader.

Shri Devi Bhawan Mandir

Shri Devi Bhawan Mandir, one of Hisar's most significant religious sites, was built by Maharaja Amar Singh of Patiala in 1770, following the split of the West Jamuna canal. The temple houses numerous statues of Hindu deities and is one of the city's most historic and revered places of worship.

Jindal Tower

Jindal Tower in Hisar, standing 90 meters tall, features a sturdy core with stairs and an elevator, supported by three slanted structures. At the top, a circular platform offers panoramic views. Built using submerged arc welding, it's surrounded by a landscaped park and gifted by industrialist O.P. Jindal to Haryana.

Kajla Dham

Kajla Dham, a Hindu temple dedicated to Lord Hanuman, is located in Kajla village, 16 km west of Hisar, Haryana. It attracts numerous devotees throughout the year.

Sanctuary National Park

Sanctuary National Park is a bird watcher's haven, offering clear views of the lake where birds can be spotted wading, swimming, or flying. Annually, around 90 species of migratory birds arrive, with winter being the prime season, though some species also visit in summer.

Kurukshetra

Kurukshetra, in Haryana, is famous as the setting of the *Mahabharata*. The Kurukshetra Panorama and Science Centre showcases the epic's battle through a large diorama. Nearby Jyotisar is a key pilgrimage site where *Lord Krishna* delivered the *Bhagavad Gita*.

Gujri Mahal

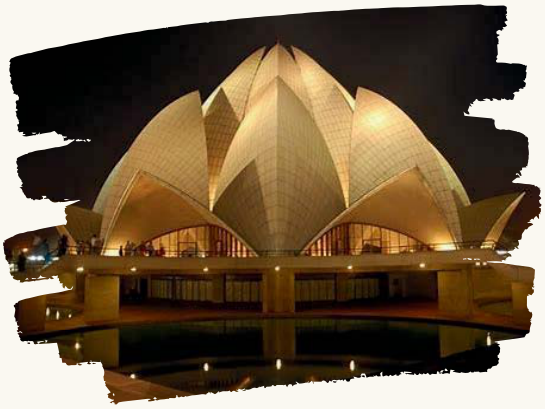
Gujri Mahal, located in Hisar, Haryana, was built by Firoz Shah Tughlaq in the 14th century for Queen Gujri. Part of Hisar Fort, this palace showcases Indo-Islamic architecture with impressive gates, intricate patterns, and stone construction. Though partially in ruins, it retains its grandeur and once featured a garden and water reservoir, reflecting its royal past.

NEAR BY PLACES

AMER FORT, JAIPUR

KANGRA FORT, KANGRA

TAJ MAHAL, AGRA



LOTUS TEMPLE, NEW DELHI

RED FORT, DELHI

GOLDEN TEMPLE, AMRITSAR

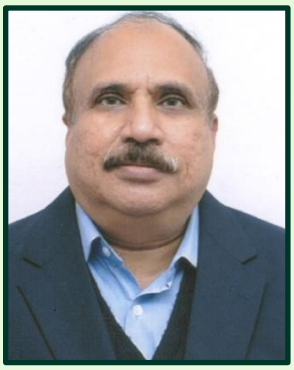
SPONSORSHIP OPPORTUNITIES

We are offering several sponsorship opportunities, including but not limited to:

1. Diamond Sponsor (₹7,00000 and above)
   - Acknowledgment as the Diamond Sponsor in conference materials
   - Logo placement on the conference website, banners, and brochures
   - Complimentary exhibition booth
   - Seven complimentary conference registrations
   - Opportunity to speak at the conference platform
   - Brand mention on the website post event one year
2. Platinum Sponsor (₹5,00,000 -₹699999)
   - Acknowledgment as the Platinum Sponsor in conference materials
   - Logo placement on the conference website, banners, and brochures
   - Complimentary exhibition booth
   - Five complimentary conference registrations
   - Opportunity to speak at the conference platform
   - Brand mention on the website post event 6 month
3. Gold Sponsor (₹3,00,000 - ₹4,99,999)
   - Acknowledgment as the Gold Sponsor in conference materials
   - Logo placement on the conference website, banners, and brochures
   - Complimentary exhibition booth
   - Three complimentary conference registrations
   - Brand mention on the website post event 3 month
4. Silver Sponsor (₹2,00,000 - ₹2,99,999)
   - Acknowledgment as the Silver Sponsor in conference materials
   - Logo placement on the conference website and brochures
   - Two complimentary conference registrations
   - Brand mention on the website post event 1 month
5. Bronze Sponsor (₹1,00000 - ₹1,99,999)
   - Acknowledgment as the Bronze Sponsor in conference Compendium
   - Logo placement on the conference website and brochures
   - One complimentary conference registration
6. Shining Star: (₹50,000 - ₹99,999)
   - Acknowledgment as the Shining Star Sponsor in conference Compendium
   - Logo placement on the conference website and brochures
   - One complimentary conference registration
7. Star: (₹25,000-- ₹50,000)
   - Acknowledgment as the Star Sponsor in conference Compendium
   - Logo placement on the backdrop for all days during the conference
8. Kind: We accept sponsorship in Cash as well as in Kind.

ACKNOWLEDGEMENT: **General Secretary-AMI** acknowledge contribution of **Mr. Sahil Barak, BTech CSE (AI & ML) GJUS&T, Hisar, Haryana, India** for designing conference Brochure

Scan for LinkedIn ID



Prof. Sunil K. Khare

FBRS,FNASS,FAMSc,

President

Association of Microbiologists of India

भारतीय जीवाणुतत्ववेत्त संगठन
Association of Microbiologists of India

PRESIDENTIAL ADDRESS - 65th AMI ANNUAL CONFERENCE

Good morning/afternoon,

Esteemed colleagues, respected members of the Association of Microbiologists of India (AMI) and distinguished guests.

It is my great honor to stand before you today as the President of AMI, an organization that has long been at the forefront of promoting microbiological research and education in India. Over the next 30 minutes, I would like to share with you our vision, the progress we've made, and the essential role microbiology plays in shaping a sustainable and innovative future.

As we all know, microbiology touches every aspect of life—from healthcare to environmental conservation, biotechnology to agriculture. In the 21st century, it is more critical than ever that we, as microbiologists, harness the power of microbes not only for research and industrial applications but also for addressing global challenges like climate change, public health crises, and food security. AMI, founded in 1938, has served as a beacon for scientific collaboration, knowledge dissemination, and the advancement of microbiological sciences in India. With over 5,000 active members, AMI has successfully fostered an environment where scientific inquiry and innovation thrive, bridging the gap between academia and industry to ensure that the research we promote is not only academically sound but also practically applicable.

Through our annual conferences, symposia, and publications such as the Indian Journal of Microbiology (INJM), AMI has played a pivotal role in promoting excellence in microbiological research. Moreover, our efforts have extended beyond academia into influencing policy, education, and research initiatives at national and international levels. Our recent focus on sustainability, biotechnology, and the application of extremophiles and bioengineering exemplifies our commitment to addressing the needs of humanity's future.

Microbiology education in India has also evolved tremendously over the years. It is now a core subject in many premier institutions at both undergraduate and postgraduate levels, where students receive a blend of theoretical knowledge and practical training. However, we face the challenge of ensuring that students are equipped with state-of-the-art skills and knowledge to meet the demands of a rapidly advancing field. To achieve this, we need more investment in infrastructure, hands-on research opportunities, and stronger alignment with industry needs. AMI is committed to enhancing the quality of microbiology

education by fostering interdisciplinary research, strengthening academia-industry collaborations, and providing mentorship for the next generation of scientists. Our goal is to ensure that microbiology education remains dynamic, inclusive, and capable of empowering students to drive innovation in India and beyond.

One of the most significant challenges we face today is the rise of antibiotic-resistant bacteria. The misuse and overuse of antibiotics have given rise to resistant strains such as Acinetobacter baumannii and Staphylococcus aureus, which are becoming increasingly difficult to treat with conventional therapies. In response, researchers are now exploring promising alternative solutions like phage therapy, which utilizes naturally occurring viruses to target and eliminate bacteria. While still facing certain challenges, such as ensuring the efficacy of phage cocktails and navigating regulatory hurdles, phage therapy presents an exciting avenue for the treatment of resistant infections.

In addition to the healthcare sector, microbiology is making tremendous strides in addressing the problems posed by biofilms—complex communities of microorganisms that form on surfaces in medical and industrial settings. Recent breakthroughs have introduced novel methods to disrupt biofilms, such as quorum-sensing inhibitors like Furanone C-30, derived from marine algae, and Savarin, a synthetic molecule targeting *Staphylococcus aureus.* Enzymes like DNases, proteases, and dispersin B are helping degrade the biofilm matrix, making embedded bacteria more susceptible to antibiotics, while silver nanoparticles are proving effective in penetrating biofilms with their broad-spectrum antimicrobial properties.

Our growing understanding of the human microbiome continues to reveal how interconnected we are with the microbial world. Emerging research on the gut-brain axis has shown how the trillions of microbes living in our intestines influence mental health, potentially offering new avenues for treating conditions such as depression and anxiety. This intricate relationship underscores the importance of the microbiome in personalized medicine, where treatments can be tailored based on an individual's unique microbial profile.

At the same time, extremophiles—organisms that thrive in extreme environments—are offering innovative solutions across industries. The enzymes produced by these resilient microbes are prized for their ability to remain stable and active under extreme conditions, making them ideal candidates for industrial processes ranging from biofuel production to bioremediation. The global enzyme market increasingly reflects the demand for these extremophilic enzymes, particularly for their applications in pharmaceuticals, food processing, and the creation of heat-resistant polymers and biocompatible materials.

Our advancements in microbiology are powered by leaps in sequencing technology, which has evolved dramatically over the past decades. We began with first-generation sequencing, where methods like Sanger sequencing enabled us to read DNA, but at a slow and costly pace. This was followed by second-generation sequencing, or next-generation sequencing (NGS), which revolutionized the field by allowing massively parallel DNA sequencing, offering faster, more affordable, and high-throughput results. Now, we are in the era of third-generation sequencing technologies, like nanopore sequencing and single-

molecule real-time (SMRT) sequencing, which allow for the direct reading of long DNA or RNA molecules, providing greater accuracy and insights into genetic diversity. These innovations have accelerated our ability to explore microbial genomes, track microbial evolution, and apply this knowledge to therapeutic developments and biotechnology.

When paired with the advances in CRISPR-Cas9 gene-editing technology, we can now manipulate microbial genomes with unprecedented precision. This confluence of sequencing and gene-editing technologies offers us new tools to develop targeted therapies, engineer microbes for industrial applications, and address sustainability challenges.

As microbiologists, we are uniquely positioned to contribute to the creation of a more sustainable future. Whether through the discovery of novel microbes, the bioengineering of enzymes, or the development of innovative biotechnologies, we are making significant strides toward responsible resource use and environmental preservation. At AMI, we are focused on strengthening the role of microbiology in shaping this sustainable world.

As I reflect on these advancements, I am filled with immense pride in our collective achievements. It is clear that the work of microbiologists is more important than ever. At AMI, we are fully committed to fostering this spirit of innovation, advancing microbiological sciences, and inspiring the next generation of scientists to explore new frontiers.

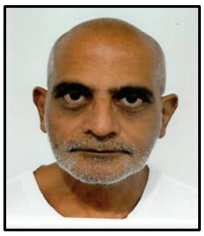
As I conclude, I want to express my sincere thanks to all of you—our members, supporters, and collaborators—for your unwavering dedication to microbiology. It is your passion, innovation, and commitment that continue to drive this community forward. Together, we can push the boundaries of scientific discovery and make meaningful contributions to society through the transformative power of microbiology.

Thank you.

Prof. Sunil K. Khare

BRIEF BIOGRAPHY
OF
INVITED SPEAKERS

Invited International Speakers



Prof. Bharat K. C. Patel

Queensland University of Technology, Brisbane, Australia

Prof. Bharat K. C. Patel has held an adjunct position at QUT since January 2017. He completed his Ph.D. on New Zealand extreme thermophiles at Waikato University in 1985. Following his Ph.D., he held research and teaching roles, including overseeing a 650-liter small-scale fermentation facility. He later worked on ethanol production from wood using thermophilic bacteria and held a tenured scientist position at Ruakura Agricultural Research Station, Ministry of Agriculture and Fisheries (MAF), where he established a laboratory for monoclonal antibodies and cell cultures. In 1988, he joined Griffith University as a lecturer, eventually becoming a professor in 2006. He has held visiting professor positions in France, Singapore, and Australia. An expert in extremophiles and extremozymes, he has published over 140 peer-reviewed papers and maintains a unique collection of Australian thermophilic microbes.

Prof. Abu Salim Mustafa

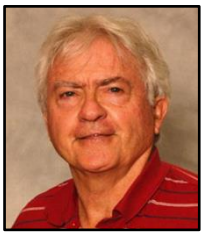
College of Medicine, Kuwait University, Kuwait

A Ph.D. (1980) and FRCPath (1998) holder, **Prof. Abu Salim Mustafa** has been a Full Professor at the College of Medicine, Kuwait University since 1996, with extensive experience as Chairman of the Microbiology Department (2019–present) and Accreditation Committee Chair (2021–present). Previously, he served as Microbiology Research Coordinator, Graduate Program Director, and Director of Research Core Facility at Kuwait University. With over 250 published papers, three edited books, and 25 national and international research awards, he has executed 51 research grants and reviewed 81 projects for funding. An editorial board member for six international journals and a member of 11 scientific societies, he has supervised 28 graduate theses and spoken at 65 conferences. His recent research focuses on the molecular biology and immunology of mycobacterial diseases, including bacterial and viral genome sequencing analyzed through bioinformatics.

Dr. Sunil Mundra

United Arab Emirates University, Al Ain, United Arab Emirates

Dr. Sunil Mundra is an Associate Professor in the Department of Biology at United Arab Emirates University, holding a Ph.D. in Molecular Microbial Ecology from the University of Oslo, Norway. He leads the "Microbial Ecology and Environmental Genomics" lab, focusing on the effects of climate and environmental changes on soil-plant-microbial interactions across diverse ecosystems, including forests and arid regions. His research employs advanced genomic and multi-omics techniques, such as metagenomics and machine learning, to explore the relationships between microbial diversity and ecosystem functionality. Dr. Mundra aims to translate fundamental research into practical applications to enhance agricultural productivity and environmental sustainability, particularly in arid environments. He has published over 60 papers in leading microbial ecology journals and supervises several Master's and Ph.D. students at UAEU. Additionally, he received the prestigious Abu Dhabi Young Investigator Award.



Prof. Barry T. Rouse

University of Tennessee, Knoxville, USA

Prof. Barry T. Rouse earned his Bachelor's from the University of Bristol (1965), M.Sc. from the University of Guelph (1967), and Ph.D. from the Walter and Eliza Hall Institute of Medical Research (1970). He also received an honorary D.Sc. from Bristol in 1997. Currently the Lindsay Young Distinguished Professor at the University of Tennessee, he has published over 400 research papers and book chapters. His research focuses on Herpes Simplex Virus (HSV), particularly its effects on tissues like eye and nervous system, and on herpes stromal keratitis (SK). He received the American Veterinary Medical Association's Lifetime Achievement Award in 2018 and is ranked among the top 2% of scientists globally for research citations (2021). His recent work includes virology, immunometabolism, and applying COVID-19 technology to livestock vaccines.

Prof. (Emeritus) Avigad Vonshak

Ben-Gurion University Institutes for Desert Research, Israel

Prof. Avigad Vonshak, a former faculty member at the Jacob Blaustein Institutes for Desert Research (BIDR) at Ben-Gurion University of the Negev, served as BIDR's Director from 2002 to 2010. He founded and directed the International School for Desert Studies from 1998 to 2003 and later became the Dean for International Academic Affairs (2010-2012). His research focuses on environmental stress in microalgae, particularly adapting dense algal cultures to drylands. He is internationally recognized for his work on large-scale cultivation of *Spirulina* (cyanobacteria) and has published over 100 works, including a book on *Spirulina*.

Prof. Thierry Regnier

Arcadia campus, Pretoria, South Africa

Dr. Thierry Regnier, is a professor in the Department of Biotechnology and Food Technology and holds a C2 rating from the National Research Foundation (NRF), reflecting his significant contributions to the field. His research focuses on innovative solutions to global and regional challenges, including alternative protein sources, cellular agriculture, and phytoremediation. He is also working on plastic degradation technologies, particularly tailored to address Africa's environmental issues. Through his work, Prof. Regnier is driving the development of sustainable food systems and environmental restoration methods, making a profound impact on biotechnology and sustainability. In addition to his research, Prof. Regnier has authored more than 100 scientific publications and has mentored numerous master's and Ph.D. students, contributing to the development of the next generation of researchers. His expertise is sought after on various advisory boards, where he plays a strategic role in advancing biotechnology and food safety initiatives. As the Global Harmonization Initiative (GHI) ambassador for South Africa, he is involved in promoting global food safety standards, further demonstrating his leadership and influence in both academic and applied scientific communities.

Dr. Harshini Mukundan

Lawrence Berkeley Laboratory's Office of National and Homeland Security, Berkeley, USA

Dr. Harshini Mukundan is a scientist and program manager for chemical and biological technologies at Lawrence Berkeley Laboratory's Office of National and Homeland Security, where she contributes to advancing bioscience initiatives with national impact. Formerly the group leader of physical chemistry and applied spectroscopy at Los Alamos National Laboratory, Dr. Harshini has a distinguished background in developing diagnostics and surveillance technologies for national and homeland security. Her work has involved collaborations with multiple government agencies, including the Department of Homeland Security, National Institutes of Health, and Defense Advanced Research Projects Agency. She has authored over 100 peer-reviewed publications and holds 8 patents, with her innovations earning 2 R&D 100 awards, including a prestigious gold award for corporate social responsibility. She has numerous recognitions including being a Fellow and IF/THEN Ambassador of the American Association for the Advancement of Science (AAAS), as well as receiving honors like the Sievers International Award and New Mexico Tech Council's Women in Technology Award. Her achievements in innovation are highlighted by several accolades, such as R&D 100 Universal Bacterial Sensor award and 2022 R&D100 award for PEGASUS. Her commitment to science policy and public health has made her a valued Senior Policy Advisor at the Council on Strategic Risks.

Prof. (Dr.) Barbara Spellerberg

Institute of Medical Microbiology and Hygiene University, Ulm, Germany

Dr. Barbara Spellerberg, after studying medicine, Barbara Spellerberg began her career in pediatrics at the University Hospital of RWTH Aachen. During her postdoc at Rockefeller University, she focused on the molecular biology of streptococci. Returning to Aachen, she completed her residency in medical microbiology and led a research group on streptococcal pathogenicity. In 2002, she became Associate Professor for Medical Microbiology at the University of Ulm. Her lab researches alternative antibacterial substances and streptococcal biology. She has supervised numerous Ph.D., medical, and graduate students, and serves on editorial boards for several scientific journals. She has published over 100 peer-reviewed papers.

Dr. Manju Balhara

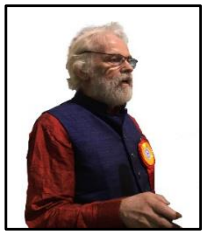
International Flavors & Fragrances Inc. (IFF), Denmark

Dr. Manju Balhara is a Quality and Food Safety Specialist at International Flavors & Fragrances Inc. (IFF) in Denmark. Her career in food safety began in 1998 after mustard oil poisoning incident in Delhi, which prompted her to focus on food safety issues. She earned her Ph.D. on "Aflatoxin Contamination and Seed Deterioration in Rapeseed Mustard During Storage," working with the Directorate of Sugar & Edible Oils and University of Delhi to establish post-harvest management guidelines. Dr. Balhara conducted postdoctoral research at Aarhus University, collaborating with the University of Geneva and Royal Botanic Gardens, Kew, on environmental sustainability and phylogeny of palms. She holds a professional bachelor's degree in Chemical and Biotechnical Food Process Technology from Business Academy Aarhus and completed a specialized course in Strategic Procurement. Her expertise covers food supply chain management and safety challenges from farm to fork. Dr. Balhara has worked with Denmark's largest grocery group on ethical sourcing and served as Supplier Assurance Manager at Arla Foods, ensuring compliance with BRC and FSSC 22000 standards. At IFF, she sets product specifications per European Food Safety Authority (EFSA) guidelines and participates in BRC audits, also being a member of the Food Safety Management Team at IFF's European Global Office.

Prof. (Dr.) Hab. Łukasz Drewniak

University of Warsaw and Jan Kochanowski University, Poland

Dr. Hab. Łukasz Drewniak is a microbiologist and environmental biotechnologist, serving as a professor at the University of Warsaw and Jan Kochanowski University in Kielce. He earned his Ph.D. in 2009, habilitation in 2017, and professorship in 2022. His research focuses on biohydrometallurgy, bioremediation, and bio-preparations for agriculture and industry, with 60 JCR-indexed articles and an H-index of 18. Prof. Drewniak holds 11 patents and has co-founded several academic-spin-offs, including BHUMI Sp. z o.o. He has served as Vice-Dean for Finance at the University of Warsaw and received multiple awards for his scientific and implementation achievements. Prof. Drewniak has been recognized with numerous awards, including multiple Rector's Prizes for scientific achievements and the Minister of Science and Higher Education's team award for significant implementation achievements in 2019. His dedication to both science and education continues to drive his contributions to the fields of microbiology and environmental biotechnology.



Dr. Ulrich Berk

Haldenhof, Mühlingen, Germany

Dr. Ulrich Berk is a leading expert in Agnihotra and Homa Therapy, with a Ph.D. in Natural Sciences. His research bridges ancient Vedic rituals and modern environmental science, focusing on Agnihotra's effects on air purification, soil regeneration, and pollution reduction. He has contributed to global Homa Organic Farming initiatives that improve crop yields and soil health without chemical inputs. Dr. Berk shares his knowledge through international conferences, workshops, and publications, promoting how spiritual practices can address environmental challenges. His seminars on practical applications of Homa Therapy have been instrumental in spreading awareness of how ancient spiritual practices can address modern environmental challenges. His work has earned him numerous awards, and he is recognized for engaging diverse audiences worldwide in Agnihotra techniques.

Dr. Aparna Banerjee

Universidad Autónoma de Chile, Chile

Dr. Aparna Banerjee, born in Asansol, West Bengal, India, in 1990, completed her primary education in 2007 before pursuing undergraduate and master's degrees in biotechnology, followed by a Ph.D. in Botany. In 2018, she received the Young Investigator Award from the Indian Science Congress Association. After completing her Ph.D., she became a postdoctoral researcher in Chile and later secured a Fondecyt Initiation Project as an Assistant Professor. Currently, a full Professor and Research Coordinator at Universidad Autónoma de Chile, Dr. Banerjee has led two Antarctic expeditions and participated in a significant international project in the Atacama Trench. She oversees multiple research projects, holds a Fondecyt Regular Project awarded in 2023, and has over 60 indexed publications. Additionally, she is involved in 2 doctoral programs and serves as a reviewer for several journals, with research interests in extreme microbiology, microbial biotechnology, and bioinformatics.

Dr. Zainul Akmar Bin Zakaria

Universiti Teknologi Malaysia (UTM), Malaysia

Dr. Zainul Akmar Bin Zakaria is an Associate Professor of Environmental Technology under the Faculty of Chemical and Energy Engineering, Universiti Teknologi Malaysia (UTM) where he works on waste treatment and resource recovery. He has a Scopus H-index of 23 and has published 2 Research Books and 9 Edited Books with one of his research books has been awarded the "National Book Award 2018" under the biochemistry category. Dr. Zainul is currently the Associate Editor for the *Environmental Quality Management* journal under Wiley Publishers, USA. He has been involved as Project Leader in various research projects with cumulative amount of RM1.9million. He also has had the opportunity to serve as *Visiting Scientist* to Argentina, Mexico, Indonesia, China and India as well as being the *Program Head* for the UTM-CONICET, Argentina R&D Program (2015-2018).

Dr. Gaurav Rajauria

University College Cork, Ireland

Dr. Gaurav Rajauria holds a Ph.D. in Food & Bio Analytical Science from Technological University Dublin (2013), an M.Sc. in Biotechnology from Agra University, India (2006), and a B.Sc. in Biological Science from the same university (2004). Currently, a Senior Lecturer at University College Cork, he has held academic positions at Munster Technological University and University College Dublin, where he served as Senior Nutrition Biochemist. His research has garnered €7.4 million in funding and produced over 100 scientific publications. He is an inventor of three technologies related to sustainable food production and has been recognized as one of the world's top 2% scientists by Stanford University. Dr. Rajauria is involved in several significant projects, including EPA-funded "JustACE" and "RefineTEXT," and DAFM-funded "FEDERI." He coordinates multiple initiatives focused on sustainable bioprocesses and is active in teaching and mentoring students at various academic levels. His engagements extend to international collaborations, keynote speaking, and editorial responsibilities across several scientific journals. Dr. Rajauria has received several awards, including recognition from MIT for his innovative research and was recently nominated for UCC's Early-Stage Researcher of the Year, 2023.

Prof. Suhail Ahmad

Kuwait University, Kuwait

Prof. Suhail Ahmad completed his Ph.D. in 1982 from Aligarh Muslim University, India. He was awarded with various esteemed fellowships like of Research Fellow, C.S.I.R., New Delhi, India (1979-1983), Postdoctoral Fellow, SUNY, Binghamton, NY, USA (1983-1985), Postdoctoral Fellow, University of Florida, Gainesville, FL, USA (1985-1988) and Postdoctoral Fellow, McMaster University, Hamilton, Canada (1988-1990). His professional appointments includes Associate Professor, Department of Microbiology, Faculty of Medicine, Kuwait University, Kuwait (1999-2006), Visiting Associate Professor, Bio-Medical Center, University of Texas Health Center at Tyler, USA (July-Aug. 2000), Assistant Professor, Department of Microbiology, Faculty of Medicine, Kuwait University, Kuwait (1997-1999), Research Scientist, International Centre for Genetic Engineering and Biotechnology, New Delhi, India (1993-1997) and Research Associate, Department of Biochemistry and Molecular Biology, University of British Columbia, Canada (1990-1993).

Dr. Sushma Bharrhan

Louisiana State University (LSU) Health, Louisiana, USA

Dr. Sushma Bharrhan is an immunologist and Staff Scientist-Specialist at Louisiana State University (LSU) Health in Shreveport, Louisiana, with over 20 years of experience in immune responses to microbial infections. She obtained her B.Sc., M.Sc., and Ph.D. in Medical Microbiology from Panjab University, Chandigarh, focusing on endotoxin-mediated hepatotoxicity. Her postdoctoral research at the Albert Einstein College of Medicine advanced her expertise in host immune responses to *Mycobacterium tuberculosis* (Mtb), where she developed conditional knockout mouse models in a BSL3 facility. At LSU Health, Dr. Bharrhan has established immunophenotyping protocols and optimized spectral flow cytometry panels, utilizing advanced technologies like the Aurora Cytometer and Isospark proteomics system to enhance data quality. Her research is published in high-impact journals, and she has received several awards, including Best Manuscript Award and an NIH Institutional Training Grant, underscoring her significant contributions to the scientific community

Dr. Avijit Das

Tel Aviv University, Israel

Dr. Avijit Das is an Indian molecular biologist specializing in phage biology, with over ten years of research experience. He earned his Ph.D. from the Birla Institute of Technology and Science, Pilani, where he studied the antirepressor protein's role in the lysogenic-lytic switch of *Staphylococcus aureus* phage Phi11. His pioneering research identified a unique regulatory mechanism and host genes involved in phage development, recognized in 'The Journal of Biochemistry'. Currently, Dr. Das is a Marie Skłodowska-Curie Postdoctoral Fellow at Tel Aviv University, investigating the lysogeny-lytic switch in Listeria monocytogenes and the role of the late lytic gene activator (llgA). He previously held a TAU Postdoctoral Fellowship and worked as a DBT Research Associate at Bose Institute, Kolkata, focusing on bacterial mechanisms and whole-cell bioreporters. Dr. Das has published numerous articles in high-impact journals and has received several fellowships, travel grants, and awards. He co-founded the Rosalind Franklin Council of Scientific Research, promoting science outreach and researcher empowerment. Committed to mentoring, he has supervised multiple graduate and undergraduate students while contributing to scientific inquiry and community initiatives.

Dr. Rohit K. Jangra

Louisiana State University (LSU) Health, Louisiana, USA

Dr. Rohit K. Jangra is an Assistant Professor in the Department of Microbiology & Immunology at Louisiana State University (LSU) Health in Shreveport, specializing in emerging RNA viruses. His research focuses on viral and host factors affecting hantavirus susceptibility, developing high-throughput virus entry analysis systems, and exploring direct-acting antivirals for hemorrhagic fever viruses. He leads several NIH-funded projects on hantavirus entry glycoproteins and antivirals for hantaviruses and Ebola. Dr. Jangra holds a Bachelor of Veterinary Science and Animal Husbandry from Choudhary Charan Singh Haryana Agricultural University (CCS HAU), a Master's in Veterinary Science in Veterinary Virology from the Indian Veterinary Research Institute, and a Ph.D. in Microbiology and Immunology from The University of Texas Medical Branch. He has published over 57 peer-reviewed articles in leading journals, holds multiple patents, and has developed pseudotyped virus systems for studying BSL3/4 viruses in BSL2 settings. He has mentored numerous students and frequently presents his work at international conferences. At this conference, he will present his research on integrating artificial intelligence (AI) and receptor binding studies to identify potential reservoir hosts for Ebola viruses.

Dr. Nallusamy Sivakumar

Sultan Qaboos University, Oman

Dr. Nallusamy Sivakumar has completed his Ph.D. from Bharathidasan University. He is working as an Assistant Professor in the Department of Biology, Sultan Qaboos University, Oman. His research areas are microbial fermentation, bioprocessing and bioactive compounds. He has published more than 25 papers in reputed journals. He has published more than 25 papers in reputed journals. His research areas are microbial fermentation, environmental microbiology, antimicrobials, bioprocessing, microbial molecular biology and microbial ecology. He has a significant h-index of 28.

Prof. (Dr.) Vijai Kumar Gupta

Dublin City University, Glasnevin, Dublin, Ireland

Dr. Vijai Kumar Gupta, an Associate Professor at the School of Biotechnology, Dublin City University, since January 2024, previously led research at the Biorefining and Advanced Material Research Centre and Centre for Safe and Improved Foods at SRUC, Edinburgh. With over 15 years of teaching and research experience, his expertise includes biomass valorization, microbial engineering, fermentation technologies, and bioactive natural products. Following his Ph.D. in 2009, he worked at renowned universities in India, Ireland, Estonia, Morocco, and the UK. He is a Fellow of multiple prestigious societies, including Linnean Society and Academy of Microbiological Sciences, India. He has mentored numerous students and edited journals and books in his field. His research, widely cited, includes publications in *Lancet*, *Nature*, and *Trends-Cell Press* journals, with a Google Scholar h-index of 85.

Ms. Namrata Joshi

University of Warsaw, Poland

Ms. Namrata Joshi is pursuing a Ph.D. in environmental microbiology and biotechnology at the University of Warsaw, Poland. She holds an M.Sc. in Microbiology and a B.Sc. in Biological Sciences from Indian universities. Her research focuses on microbial processes and developing biopreparations for environmental and industrial applications, with expertise in gene cloning, enzyme characterization, and advanced biotechnological tools like HPLC and GC-MS. As a Product Manager at BHUMI sp. z o.o. in Warsaw, she leads research on microbiological products on a semi-industrial scale. Previously, she was a Senior Research Fellow at the Centre of Innovative and Applied Bioprocessing in India, contributing to enzyme discovery and biomass processing. Ms. Namrata has received several accolades, including a silver medal at INTARG® 2023 and a diploma from the University of Warsaw. Her work has resulted in multiple publications and patents, reflecting her commitment to advancing sustainable biotechnology solutions.

Prof. (Dr.) Santasree Banerjee

Jilin University, Changchun, China

Dr. Santasree Banerjee (Indian citizen), presently working as Professor in the Department of Genetics, College of Basic Medical Sciences, Jilin University, Changchun, 130021, China. He was working as a Principal Investigator/Research Group Leader/International Expert in Genetic Counseling in world's largest and biggest genomics research institution, BGI-Research Institute, Shenzhen, China. He was also working as a full-time professor in the Department of Medical Genetics, College of Basic Medicine, Jilin University, China. He has done his Ph.D. in Biochemistry and Molecular biology. During his Ph.D., he did his research work on human medical genetics and genomics and publish several articles in peer reviewed journal. Moreover, during his postdoctoral studies, he also continued his research on medical genetics and genomics (genetics of rare disease, hereditary cancer and sporadic cancer) and published several articles in BGI-Research Institute. Until today, he has published more than 30 research articles in SCI/international peer-reviewed journal (24 articles as a first/co-first or corresponding/co-corresponding author). Further, there are several articles which are "under review" presently. He is also involved in reviewing scientific articles for several high impact journals. Currently, he is working as a principal investigator/research group leader/ International expert in Genetic Counseling at BGI-Research Institute, Shenzhen, China. His present work involves newborn screening, screening of all the inherited mendelian diseases, screening of mitochondrial disease, carrier screening, PGD/PGS, Molecular Genetic Screening and Diagnostic services for all the rare diseases, hereditary cancers and sporadic cancers by using high-throughput sequencing technology.

Prof. (Dr.) Rajesh Sani

South Dakota School of Mines and Technology, South Dakota, USA

Dr. Rajesh Sani is a Distinguished Professor in the Department of Chemical and Biological Engineering at the South Dakota School of Mines and Technology. For 18 years, his research has focused on extremophilic bioprocessing, biopolymers, biofuels, and advanced synthetic biology. He led the NSF-funded BuG ReMeDEE consortium, focusing on methane regulation in extreme environments. Dr. Sani has secured $68.2 million for 56 projects and published over 100 peer-reviewed articles. He holds 125 invention disclosures and 3 patents. Additionally, he has developed biological engineering courses, promoted diversity in STEM, and contributed to K-12 education. He had been committee member and technical session chair for AIChE, SIMB, and ASM annual meetings and national/international advisory boards.

Dr. Aniket Kumar Gade

Nicolaus Copernicus University, Torun, Poland

Dr. Aniket Kumar Gade is a POLONEZ-BIS Fellow at the Department of Microbiology, Nicolaus Copernicus University, Torun, Poland, and an Associate Professor in Biological Sciences and Biotechnology at the Institute of Chemical Technology, Mumbai, India. With a distinguished academic and research background, he has held faculty roles across prominent institutions, including Sant Gadge Baba Amravati University and Vidya Pratishthan's College, Baramati. His expertise spans bioinformatics, nanobiotechnology, and microbial technology, demonstrated through his postdoctoral research at Utah State University and significant

contributions to mycofabrication of silver nanoparticles. Dr. Gade has co-led numerous projects funded by prestigious organizations like UGC, DST, and DRDO, focusing on applications of nanotechnology in antimicrobial agents, rapid pathogen detection, and bio-nanotechnology. Dr. Gade's accomplishments are extensive, with over 100 research publications, 25 international book chapters, and several high-impact patents, including innovative antimicrobial formulations. Recognized with awards such as the Young Scientist Award, INSA Fellowship, and listing among Stanford's top 2% most influential scientists, he has presented at over 50 international forums and contributed substantially to research outreach through M.Sc. and Ph.D. mentorship. Dr. Gade's technology transfer efforts have led to products like Silver Nano-Mask, highlighting his commitment to impactful scientific advancements.

Prof. Mohammed Bello Yerima

Sokoto State University, Nigeria, Africa

Prof. Mohammed Bello Yerima is a faculty member in the Department of Microbiology at Sokoto State University, Nigeria, with 29 years of experience in teaching and research in Microbial Biotechnology. His work focuses on utilizing microorganisms to enhance human welfare. Currently serving as Deputy Vice Chancellor (Academic), he is also a visiting professor at various Nigerian universities and he was immediate past president of both Biotechnology Society of Nigeria and Nigerian Society for Microbiology, where he is a recognized Fellow. Prof. Yerima is an external examiner for numerous universities and an external assessor for academic promotions. He has received the TeTfund National Research Fund grant in 2022 and numerous national and international awards. With over 100 publications, including 38 indexed in Scopus, he is an active reviewer and editorial board member for several reputable journals. He has presented over 100 scientific papers at conferences, often as a keynote or invited speaker, and has established collaborations with research groups in China and India. Currently, his research interests include algal biotechnology, genomics, and public health microbiology, and he is a part of a continental core team working on genome editing projects to combat hunger in Africa. Prof. Yerima is also the MD/CEO of YeriMBel NextGen Technologies, an indigenous biotech company.

Dr. Minaxi Sharma

University of Nottingham Ningbo China, China

Dr. Minaxi Sharma, is an Assistant Professor in Food Science and Technology at the China Beacons of Excellence Research and Innovation Institute, University of Nottingham Ningbo China. With 9 years of experience, her research focuses on advanced food processing technologies, nanoencapsulation, and green extraction methods for food waste valorization to create smart and functional foods. Dr. Sharma has worked internationally in India, Estonia, Belgium, and China, receiving the Young Scientist Award and BEWARE Fellowship (2021-2024). She is recognized among the World's Top 2% Scientists by Elsevier and Stanford University (2023). With an h-index of 35, she has published approximately 150 peer-reviewed articles in reputable journals.

Dr. Dilfuza Jabborova

Uzbekistan Academy of Sciences, Kibray, Uzbekistan

Dr. Dilfuza Jabborova is an expert in plant microbe interaction, plant growth promoting bacteria, medicinal plant research and plant physiology. She was awarded the China Great Wall Fellowship in 2010, to conduct research in South China Agricultural University, Guangzhou. In 2014, she got awarded DAAD (German Academic Exchange Service) Research Scholarship, to conduct research in Leibniz Centre Agricultural Landscape Research (ZALF), Müncheberg, Germany. In 2020, she got DBT-TWAS Postdoctoral Fellowship, 2020-2021 to conduct research in Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi, India. She has more than 40 peer reviewed international publications and has delivered numerous invited speaker presentations in numerous international conferences. Additionally, she is an editorial board member of Frontiers in microbiology, Annals of Phytomedicine, Plant Archives and Turkish Journal of Agriculture and Forestry. She is also a member of the Association of Microbiologists of India, American Society of Microbiology (ASM), Society for Environmental Sustainability, Plant Biochemistry and Biotechnology (SPBB), and International Society of Environmental Botanists (ISEB). She is a recipient of many prestigious awards and honors from various research societies. In 2023, she has received the Global Scientist Award-2023 from Agricultural Technology Development Society (ATDS) Ghaziabad, Uttar Pradesh, India.

Dr. Mohd. Ulul Ilmie Bin Ahmad Nazri

Universiti Malaysia Terengganu, Malaysia

Dr. Mohd. Ulul Ilmie Bin Ahmad Nazri earned his Ph.D. in Physiology in 2021 and focuses on nervous system regeneration in marine animals and zoonotic diseases like leptospirosis. At Universiti Malaysia Terengganu (UMT), he leads research on antibacterial agents from silver nanoparticles derived from marine animals. He teaches biology at the STEM Foundation Centre and was Head of the Biology Unit for two years. Dr. Ilmie was selected as one of 35 global participants for the RIKEN Brain Science Institute Summer Programme in 2009. He has received multiple awards, including the Pro-Chancellor Award (2021) and Hope Alumni Icon (2024), and has won gold, silver, and bronze medals in both international and national innovation competitions.

Dr. Sunita Varjani

Korea University, Seoul, South Korea

Dr. Sunita Varjani, is a Senior Associate Professor at UPES, Dehradun, India, and holds adjunct professor status at Korea University. She is also the Director of the Institute of Chartered Waste Managers, India, and has previously worked as a visiting fellow at City University of Hong Kong and as a Scientific Officer at the Gujarat Pollution Control Board. Her research focuses on industrial and environmental biotechnology, wastewater treatment, bioremediation, and waste management, with an emphasis on developing circular waste-based biorefineries for sustainable chemical and fuel production. Dr. Varjani has authored over 475 publications, achieving an h-index of 73 and a recognition as a Highly Cited Researcher by Clarivate (2022) and Elsevier (2020-present). She has received numerous accolades, including Environmental Sciences Leader Award for 2024 and Rising Star of Science Award for 2023. She was elected to National Academy of Sciences, India (NASI) in 2021. Additionally, she has won multiple Young Scientist Awards and is actively involved in editorial roles for various scientific journals. Dr. Varjani has also served on the Management Council of the Biotech Research Society and is a member of the Executive Committee of the International Society for Energy, Environment and Sustainability.

Dr. Sonam Paliya

RWTH Aachen University, Germany

Dr. Sonam Paliya is an Alexander von Humboldt Fellow at RWTH Aachen University, Germany, with over eight years of experience in Biological and Environmental Science. She earned her Ph.D. from CSIR-National Environmental Engineering Research Institute, focusing on the bioremediation of persistent organic pollutants and waste valorization. She has received several awards, including the Best Young Researcher Award (2020) and National Postdoctoral Fellowship (2022) by DST-SERB. Dr. Paliya's research has been published in high-impact journals and she has edited over 4 books with leading publishers. Her contributions to sustainable waste management and environmental science are recognized internationally through her participation in conferences and publications.

Invited National Speakers

Prof. Pradeep Verma

Central University of Rajasthan (CURAJ), Ajmer, Rajasthan, India

Professor Verma is a Group Leader at the Bioprocess and Bioenergy Laboratory in the Department of Microbiology at CURAJ, Bandersindri, Kishangarh, Ajmer, Rajasthan. He is a Fellow of several prestigious organizations, including Mycological Society of India (2020), Biotechnological Research Society of India (2021), and Association of Microbiological Sciences, India (2021). His accolades include Ron-Cockcroft Award from Swedish Society and UNESCO Fellow ASCR Prague. He has held postdoctoral and visiting positions in Prague, Germany, and Japan, including a recent Bridge Fellow JSPS award in 2022 at Kyoto University. His expertise includes microbial diversity, bioremediation, and biomass-based biorefinery. Prof. Verma holds international patents related to microwave-assisted biomass pretreatment and bio-butanol production. He has authored over 94 peer-reviewed publications with 6,946 citations, a cumulative impact factor of 286.6, an h-index of 44, and an i-index of 106. His work also includes 62 book chapters and 20 edited books published by Springer, Elsevier, CRC, IWA, and De-Gruyter.

Prof. D Joseph Bagyaraj

INSA Hon. Scientist and Chairman
Centre for Natural Biological Resources and Community Development (CNBRCD), Bengaluru, Karnataka, India

Prof. D. Joseph Bagyaraj, an expert in Agricultural Microbiology, earned his Ph.D. from the University of Agricultural Science, Bangalore, where he later became a professor. He has undergone post-doctoral training in several countries and has served as a Visiting Scientist in New Zealand and at Oregon State University. Currently, he is an INSA Hon. Scientist and Chairman of the Centre for Natural Biological Resources and Community Development (CNBRCD) in Bengaluru. With 58 years of teaching experience, he has mentored around 65 M.Sc. and Ph.D. students and has been recognized as a pioneer in Arbuscular Mycorrhizal Fungi (AMF) research in India. He has published 434 research papers, 117 review articles, and authored 11 books. Prof. Bagyaraj holds fellowship in multiple national academies and is the current President of the National Academy of Biological Sciences and Indian Society of Soil Biology and Ecology. He has also served on various funding agency committees. Among his numerous accolades, he received the Distinguished Asian Mycologist Award in 2019 and contributed to the Global Atlas on Soil Biodiversity for the European Commission in 2016. A mycorrhizal fungus is named in his honor, *Glomus bagyarajii*.

Prof. Dayanand Agsar

Hon'ble Vice-Chancellor
Gulbarga University, Kalaburagi, Karnataka, India

Prof. Dayanand Agsar is the Vice-Chancellor of Gulbarga University, Kalaburagi, with over 34 years of teaching experience. He has held various administrative roles, including Registrar, Chairman, and Student Welfare Officer at the university, and serves as Coordinator for VGST GoK Programmes. He has also been a Visiting Professor at SFIT, EPFL, Switzerland, and an Invited Professor at the University of Helsinki, Finland, with collaborative research at Sun Yat-sen University, China. With 38 years of research experience, Prof. Agsa has guided 23 Ph.D. and 9 M.Phil. students. He has chaired several projects, including CSIR IICT-GUK ADBT Collaborative Research Project. His accolades include the Fellowship of the Academy, KSTA, GoK (2021), Research Publication Award from VGST, GoK (2018), and Best Presentation Award at an International Conference (2012).

Prof. Nandula Raghuram

Guru Gobind Singh Indraprastha University (GGSIP University), New Delhi, India

Prof. Raghuram is an expert in nitrogen use efficiency, with broader interests in sustainability, public health, and science policy. He has published 66 journal articles, 14 books, 32 book chapters, 8 microarrays, 16 sequences, 10 book reviews, and 31 additional articles, with over 3,550 citations globally. As Editor-in-Chief of *Physiology and Molecular Biology of Plants*, he has elevated it to one of Asia's top plant journals. He co-founded Indian Nitrogen Group, led the Indian and South Asian nitrogen assessments, and, as Chair of the International Nitrogen Initiative (2019-2022), co-led the global nitrogen assessment. Prof. Raghuram was

instrumental in organizing three International Nitrogen Conferences, including chairing the 2024 event, and facilitated the first UN resolution on Sustainable Nitrogen Management. He has taught 20+ courses, mentored 88 theses, and secured over Rs. 60 million in research grants, contributing significantly to academic and policy advancements in nutrient management.

Prof. Dr. Pragya D. Yadav

National Institute for One Health, Nagpur, Maharashtra, India and Indian Council of Medical Research-National Institute of Virology (ICMR-NIV), Pune, Maharashtra, India

Dr. Pragya D. Yadav is the Director-in-charge of the National Institute for One Health in Nagpur and serves as Scientist 'F' and Head of Asia's first Biosafety Level-4 laboratory at the Indian Council of Medical Research-National Institute of Virology (ICMR-NIV) in Pune, India. She earned her Ph.D. in Virology from Savitribai Phule Pune University in 2004 and has been instrumental in researching emerging viral infections in India. Her work spans multiple areas, including human and animal virology, epidemiology, and public health, with significant contributions to the study of viruses like Nipah, SARS-CoV-2, Zika, and Ebola. Dr. Yadav has led efforts in outbreak investigations, developed diagnostic assays, and facilitated technology transfer for commercial production. Notably, during COVID-19 pandemic, she isolated SARS-CoV-2 virus, which contributed to the development of COVAXIN™, India's first indigenous vaccine. With over two decades of experience in high-risk pathogens, she is committed in enhancing virology and biosafety training in public health laboratories across India.

Dr. Ravi Mishra

CSIR-Institute of Microbial Technology, Chandigarh, India

Dr. Ravi P.N. Mishra is a Principal Scientist at CSIR-Institute of Microbial Technology in Chandigarh, India, leading Vaccine and Biotherapeutics R&D. He has over 15 years of global experience in vaccine and biotherapeutic discovery and process development. Dr. Mishra earned his Ph.D. from Banaras Hindu University in 2005 and has held post-doctoral positions at the University of Montpellier and Harvard Medical School. He has published extensively in journals like PNAS and Vaccine and holds several international patents. Previously, he worked as a Research Scientist at Novartis Vaccines Research Centre (2007-2013) and as General Manager-R&D at Biological E. (2014-2018), where he helped to develop Typhoid Vaccine conjugate TYPHIBEV, launched in 2019. Currently, he is developing a next-generation protein subunit vaccine against COVID-19 and is leading a project to establish National Repository of GMP-compliant Cell Banks for Biopharmaceutical Products (NRGCBIO) under National Biopharma Mission-BIRAC to enhance biomanufacturing in India.

Dr. Deepti Parashar

ICMR-National Institute of Virology, Pune, Maharashtra, India

Dr. Deepti Parashar heads the Diagnostic Reagent Facility at ICMR-National Institute of Virology, Pune, focusing on research related to dengue and chikungunya viruses. Her work includes antiviral testing, drug delivery systems, and pioneering research in RNA interference, developing an RNA interference agent to inhibit chikungunya virus, which has been patented in multiple countries. She has identified anti-dengue and anti-CHIKV activity in bioactive plant compounds and FDA-approved drugs like resveratrol and doxorubicin. As facility head, she oversees the production and distribution of diagnostic kits for dengue, chikungunya, and Japanese Encephalitis across India. Dr. Parashar has received several accolades, including Endeavour Executive Fellowship (Australia) and ICMR-International Fellowship (USA). She has over 80 publications in high-impact journals and has contributed to various workshops and training sessions in molecular virology.

Dr. Sonu Gandhi

DBT-National Institute of Animal Biotechnology, Hyderabad, Telangana, India

Dr. Sonu Gandhi is a Scientist E at the National Institute of Animal Biotechnology, Hyderabad, Telangana, India, specializing in biosensor development and the diagnostic applications. She earned her Ph.D. from IMTECH, Chandigarh, and completed her postdoctoral research at IFOM-IEO in Milan, Italy, and as a visiting scientist at University of Washington, Seattle. Dr. Gandhi has received numerous national and international awards, including the prestigious 2023 Connect Fellowship from the Alexander von Humboldt Foundation and the ICAR Panjabrao Deshmukh Award (2022). Her accolades also include SERB Women Excellence Award (2021), SERB Early Career Research Award (2016), and Best Young Investigator Award at IIT-BHU. She was

featured in "SHE IS - 75 Women in Chemistry" and has been elected as a Fellow of the Royal Society of Chemistry and a Young Associate of the Indian Academy of Sciences. With 93 peer-reviewed publications, her research has been highlighted in various prestigious platforms, including PIB and Nature India News.

Prof. Avnesh Verma

Kurukshetra University, Kurukshetra, Haryana, India

Prof. Avnesh Verma holds a B.E., M.Tech, and Ph.D. (Engineering) with nearly 30 years of experience, including a decade in academic administration. He is presently working as Professor in the Department of Instrumentation, Kurukshetra University, Kurukshetra. He served as Registrar at Guru Jambheshwar University of Science & Technology, Hisar (2020-2023), and was Head of Electrical Engineering Department for six years. Recognized with a "Lifetime Achievement Award" by Science Fathers in 2024 for innovative research, he has also received the "Jan Seva Ratan Samman" for social welfare contributions and various honors from national academic bodies.
Prof. Verma is a member of prestigious academic councils and served as a nominee of the Chancellor and Governor in appointments across several universities. He participated in Japan's JICA Youth Invitation Program, led research projects with institutions like IIT Bombay, and has published two patents, two books, and numerous research papers. Supervising five Ph.D. scholars and guiding 11 M.Tech dissertations, he is also on the editorial board of IAPAAR Journal, has reviewed for 10 international journals, delivered 32 expert lectures, and attended 28 workshops. His research interests include VLSI, power electronics, and motor control, and he is affiliated with professional bodies such as ISTE and the Institute of Engineers, India.

Prof. Ramakrishna Wusirika

Central University of Punjab, Bhatinda, Punjab, India

Prof. Ramakrishna Wusirika is a Professor of Biochemistry and Dean Incharge Academics at the Central University of Punjab, Bathinda. With over 30 years of research and 20 years of teaching experience, he previously served at Michigan Technological University and as a postdoctoral fellow at Purdue University. He has published 90 papers in prestigious journals and secured over ₹10 crores in research funding. His research focuses on plant-microbe interactions, nanoparticles, and anticancer properties of plant compounds. Prof. Wusirika has an h-index of 40 and nearly 7,000 citations. Prof. Wusirika's research areas include omics approaches to understand interactions between plant growth promoting bacteria (PGPB), nanoparticles and their host plants and biochemical and molecular mechanisms regulating anticancer activity by plant natural compounds.

Dr. Asha Chaubey

CSIR-Indian Institute of Integrative Medicine Jammu, Jammu & Kashmir, India

Dr. Asha Chaubey is the Senior Principal Scientist and Head of the Fermentation and Microbial Biotechnology Division at the CSIR-Indian Institute of Integrative Medicine, Jammu. With over 20 years of expertise in fermentation technology, Dr. Chaubey specializes in exploring microorganisms from unique Himalayan niches for producing bioactives, enzymes, and biopharmaceuticals. She earned her Ph.D. from LLRM Medical College, Meerut, focusing on biosensors for healthcare applications, which led to high-impact publications and patents. Her contributions span industrial enzyme production, biotransformation, and biosensor development, including COVID-19 detection devices. Dr. Chaubey is an expert on national committees, a coordinator for the CSIR Jigyasa program, and has received prestigious awards such as the BOYSCAST Fellowship and the Bharat Ratna Rajiv Gandhi Gold Medal. Actively involved in student mentorship and skill development programs, she also advances organic farming and participates in exhibitions to promote institutional innovations.

Prof. Surender Singh

Central University of Haryana, Mahendragarh, Haryana, India

Prof. Surender Singh obtained his M.Sc. and Ph.D. in Microbiology from the Indian Agricultural Research Institute (IARI), New Delhi, in 2005 and 2009, respectively. After serving as a Scientist (ARS) at IARI, he joined the Central University of Haryana in 2018. His research specializes in developing multi-stress tolerant bioinoculants and recycling organic matter, including bioethanol production from lignocellulosic materials. He was awarded the Endeavour Research Fellowship in 2011 for research at the University of South Australia and has

received several honors, including the Young Scientist Award from the Association of Microbiologists of India (2015), the Young Scientist Award from the National Academy of Agricultural Sciences (2015-16), and the Haryana Yuva Vigyan Ratan Award (2018). Prof. Singh has led nine extramural research projects, supervised six doctoral scholars, and guided 20 postgraduate dissertations. He has authored over 10 research articles, two books, and 20 book chapters, while also serving as an active reviewer for prominent microbiological journals. He is on the editorial boards of the Electronic Journal of Biotechnology, Science Progress, and Frontiers of Microbiology, and is a life member of the Association of Microbiologists of India and the Indian Science Congress.

Dr. Mahaveer P. Sharma

Indian Institute of Soybean Research, Indore, Madhya Pradesh, India

Dr. Mahaveer P. Sharma is a Principal Scientist in Agricultural Microbiology at the Indian Institute of Soybean Research, Indore, under ICAR-DARE, Ministry of Agriculture & Farmers Welfare, Government of India. He earned his B.Sc. and M.Sc. in Agriculture from Rajasthan Agricultural University, Bikaner, and his Ph.D. from Gwalior, receiving a gold medal during his master's program. Dr. Sharma began his career in mycorrhizal research at the University of Delhi and TERI, New Delhi, where he worked for 11 years before joining ICAR as a Senior Microbiologist. He specializes in soil microbiological research, focusing on plant growth-promoting microbes, particularly Arbuscular Mycorrhizal Fungi (AMF), to enhance plant growth, soil carbon sequestration, drought tolerance, and crop productivity. He has received multiple awards for best paper presentations, travel grants, and external research grants from DBT, DST, and ICAR. Additionally, he was honored with the DBT-CREST Award in 2013 for research on fatty acid biomarkers related to AMF and soil microbial community changes. Dr. Sharma has published approximately 105 research articles in reputable journals and has microbial accessions in the NCBI database and cultures deposited in international microbial repositories.

Dr. Indrani Ghosh

CSIR-IPU, New Delhi, India

Dr. Indrani Ghosh is a seasoned expert with a Ph.D. in Biotechnology and nearly 20 years of experience as a Registered Patent Agent with the Government of India. She has managed over 1,000 patent applications for CSIR, both domestically and internationally. Her expertise includes patent searching, drafting, filing, prosecution, and providing strategic patent counseling, especially in Molecular Biology and Biotechnology. Dr. Ghosh's diverse background includes research at CSIR-Institute of Microbial Technology and patent experience with prestigious organizations like WIPO, Austrian Patent Office, and IIM Ahmedabad. She also participated in an advanced patent program at US Patent and Trademark Office. Beyond her patent work, she trains researchers, consults, and lectures on intellectual property rights.

Prof. Prince Sharma

Panjab University, Chandigarh, India

Prof. Prince Sharma (FAMSc) is a former Dean of the Faculty of Science at the Department of Microbiology, Panjab University, Chandigarh, and a Fellow of the Academy of Microbiological Sciences, India. He is the President Elect of the Association of Microbiologists of India. His research interests include reverse vaccinology, antimicrobial resistance, and the engineering of industrial enzymes and biosensors for microbial diagnostics. He has published 119 research papers, with an h-index of 36 on Scopus and 43 on Google Scholar, and has completed 14 research projects with DBT, DST, UGC, ICMR, and DFS. He has guided 29 Ph.D. students, with 8 currently under his supervision. Prof. Sharma has received several awards, including the Glaxo Smith Kline Vaccine Award for his reverse vaccinology work, with a notable paper being in the top 100 of *Scientific Reports* in 2017. He received the Best Research Publication Award from the Smt. Prem Lata and Prof. DVS Jain Research Foundation (2020-21) and was named among the top 2% of scientists globally by Stanford University in 2022. Prof. Sharma has three patents and has transferred enzyme technologies to Cadilla, India, and New England Biolabs, USA. He serves as an advisor to AINovoTM Biotech Inc., USA, and collaborates on projects with L'Oréal Paris, Panacea Biotec, AINovoTM Biotech Inc., and Invigorate Biotechnologies LLP.

Dr. Sanjay Mishra

Department of Biotechnology, Ministry of Science and Technology, Government of India

Dr. Sanjay Mishra is working as Scientist `H', Technology, Capacity & Partnerships (Scientific Decision Unit), Department of Biotechnology, Government of India. He has two decades of teaching, research and academic management experience from India, the UK, the USA and Australia along with 10 years of working in Government of India. Furthermore, he possesses significant experience in strategic planning, designing, and implementation of policy, programs in areas of education, science, technology, innovation, STEM, gender advancement, climate change and biotechnology, often in partnership with industry, research institutions, non-government-organisations and academia. He is passionate about initiating, designing and engaging youth, early career academic, women, industry and Not-For-profit organisation for partnership programs with government. He is fully aware of academic and research landscape of India and Australia (brief experience in the UK and the USA) and is an expert in extra mural grant management and new program design. He consistently seeks innovative ideas to make positive impact in society through interventions.

Prof. Ragini Gothalwal

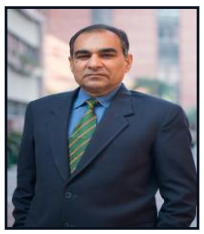
Barkatullah University, Bhopal, Madhya Pradesh, India

Prof. Ragini Gothalwal is the Professor and Head of the Departments of Biotechnology and Pharmacy, and Coordinator of the Bioinformatics Centre at Barkatullah University, Bhopal. With a Ph.D. in Microbiology (1991), she has 36 years of research and 26 years of teaching experience. Her expertise includes environmental biotechnology, microbial physiology, and protein engineering. She has guided 25 Ph.D. students and published 106 research papers. Prof. Gothalwal has received several awards, including the Young Scientist Award, JRF, SRF and RA from various government agencies and has been involved with numerous academic and professional organizations, serving on various boards, committees, and as a reviewer for journals.

Prof. Sanjay Kumar Singh Patel

Hemvati Nandan Bahuguna Garhwal University, Uttarakhand, India

Dr. Sanjay K. S. Patel holds a B.Sc. in Chemistry from Banaras Hindu University, an M.Sc. in Biotechnology from Himachal Pradesh University, and a Ph.D. in Biotechnology from CSIR-IGB, New Delhi. He served as Senior Assistant Professor at Kankuk University, South Korea (2013-2024) and is currently an Associate Professor at Hemvati Nandan Bahuguna Garhwal University, Uttarakhand. A life member of AMI and BRSI, Dr. Patel has authored over 126 publications, 7 book chapters, and holds 24 international patents. With an h-index of 55 and 7500+ citations, he is listed among the top 2% of world scientists since 2019. His research focuses on bioenergy, bioremediation, microbial biotechnology, protein engineering, and nanotechnology.



Dr. Banwari Lal

The Energy and Resources Institute (TERI) and ONGC TERI Biotech Ltd (OTBL), New Delhi, India

Dr. Banwari Lal is the Senior Director of the Environmental and Industrial Biotechnology Division at TERI, New Delhi, and Managing Director of ONGC TERI Biotech Ltd (OTBL). He specializes in Petroleum Biotechnology and has developed three patented and commercialized technologies: "Oilzapper" for oil spill bioremediation, "Microbial Enhanced Oil Recovery," and technology for preventing paraffin deposition in oil wells. He holds 9 patents, has published 107 research papers, authored 2 books, and contributed to multiple book chapters. His work has been cited 9,028 times, with an h-index of 40 and an i10-index of 175. Dr. Lal has received several awards, including the Tata Innovation Fellowship (2010) and the National Bioscience Award (2004). He is actively involved in scientific communities, serves on advisory committees for DBT and DST, and is a life member of the Association of Microbiologists of India (AMI).

Dr. Om Prakash Sharma

Symbiosis Centre for Climate Change and Sustainability (SCCCS), Pune, Maharashtra, India

Dr. Om Prakash Sharma is Deputy Head and Associate Professor at the Symbiosis Centre for Climate Change and Sustainability (SCCCS), Pune, with over 25 years of interdisciplinary research in anaerobic microbiology, climate change, greenhouse gas

emissions, and environmental health. He previously curated the anaerobic facility at the National Centre for Microbial Resource and the National Centre for Cell Science in Pune. He earned his Ph.D. in Microbiology from the University of Delhi and completed five years of postdoctoral training in the USA. Currently, he chairs the Subcommittee on Methanogenic Archaea of the International Committee on Systematics of Prokaryotes and was recently elected to the Community Building Committee of the Microbiology Society in London. Dr. Prakash has received several awards, including the DST-SERB International Grant for a talk in China, a Senior-INSA visiting fellow award, and the Best Mentor award from Florida A&M University. He has published over 100 articles in high-impact journals, accumulating more than 4,300 citations.

Prof. Naveen Gupta

Panjab University, Chandigarh, India

Prof. Naveen Gupta serves as the Chairperson of the Department of Microbiology at Panjab University, bringing 28 years of extensive experience in research and teaching. Throughout his career, Prof. Gupta has made significant contributions to microbiology, evidenced by his 6 granted patents, including 3 international and 3 national. His research has led to over 70 publications in esteemed journals, reflecting his dedication to advancing the field. Prof. Gupta has also successfully transferred one developed technology for broader application, with two additional technologies currently under evaluation. As a mentor, he has guided 14 Ph.D. students, fostering new generations of researchers in microbiology.

Prof. Ram Chandra

Babasaheb Bhimrao Ambedkar University, Lucknow, Uttar Pradesh, India

Professor Ram Chandra is a senior professor in the Department of Environmental Microbiology and Director of the Internal Quality Assurance Cell (IQAC) at Babasaheb Bhimrao Ambedkar University, Lucknow. With a Ph.D. from Banaras Hindu University, he spent over 23 years as a scientist at CSIR-Indian Institute of Toxicology Research before joining B.B. Ambedkar University in 2011. His research focuses on bioremediation, particularly in the degradation of distillery and lignocellulosic waste. He has identified several bacterial strains for these purposes and has published 240 research papers and 8 books. With an h-index of 60, 10,511 citations, and 3 patents, Professor Chandra is recognized among the world's top 2% scientists by Stanford University. He is a fellow of several prestigious societies and has presented his research internationally.

Prof. Rajesh Dhankar

M. D. University, Rohtak, Haryana, India

Dr. (Mrs.) Rajesh Dhankhar is Professor in Department of Environmental Science and presently Dean of the Life Sciences since 2022 at M. D. University, Rohtak, Haryana. She has completed her Ph.D. in the field of Environmental Bioremediation for the bio-amelioration of saline soils from Department of Biosciences, Maharshi Dayanand University, Rohtak in Oct. 1992. She has 32 years of research experience in the field of Eco-toxicology; 32 years teaching experience in Postgraduate classes of Botany and Environmental Sciences; 7 years of teaching experience in undergraduate classes at IGNOU centre and 5 years of teaching experience in UG classes (Pharmacy Deptt.). She has guided and supervised 26 Ph.D. in Eco-toxicology; presently 7 fellows are under her supervision. She has more than hundred publications in different national and international peer journals of high impact factors and has three books on Environmental Sciences. She is the member of more than 10 scientific bodies and different N.G.Os. Furthermore, she has been the resource person in different refresher courses, N.S.S. camps, Conferences, Environmental awareness programs organized by different universities and co-ordinator of UGC Innovative programme 2012-2017. She has also been the co-ordinator of DST- FIST programme 2012-2013; convener of Green Audit Committee at M.D.U. Campus Rohtak; member of E-waste management committee at M.D.U. Campus Rohtak; co-ordinator for establishment of "Bioinformatics Infrastructure facility" under BTIS net programme; coordinator of ESM Cell of the University from 2017-2022 and was also having additional charge of Director, Centre for Bio- informatics and Provost Girls from Aug. 2016 to January 2020. Moreover, she has been the member of steering committee for climate change, biodiversity and wildlife constituted by Govt. of Haryana 2012-2013; member of National Academic bodies UGC, DST, MHRD for various committees; member of Executive Council of Maharshi Dayanand University and member of Finance Committee of Maharshi Dayanand University.

Prof. Bhim Pratap Singh

National Institute of Food Technology Entrepreneurship & Management (NIFTEM), Kundli, Sonepat, Haryana, India

Dr. Bhim Pratap Singh is a Professor in the Department of Agriculture and Environmental Sciences at the National Institute of Food Technology Entrepreneurship & Management (NIFTEM), India. He holds a Ph.D. from the National Bureau of Agriculturally Important Microorganisms (ICAR-NBAIM) and completed post-graduate training at ICAR-NBPGR, New Delhi. Previously, he was a Research Associate at NRCPB and served as an Assistant Professor at Mizoram University, where he established a Molecular Microbiology and Systematics laboratory. With over 100 peer-reviewed publications and six edited books, Dr. Singh has guided 4 Ph.D. and 3 M.Phil. students. He received a DBT Overseas Fellowship for training in natural compounds isolation at the University of Aberdeen, Scotland, and is a member of several professional organizations, earning numerous awards in microbial diversity. He has led 10 externally funded projects, including a notable Indo-Russia project worth ₹1.70 crore. His research primarily focuses on postharvest disease management and enhancing the shelf life of fresh commodities to reduce food loss.

Prof. Gunjan Goel

Central University of Haryana, Mahendragarh, Haryana, India

Prof. Gunjan Goel, a Full Professor at the Central University of Haryana since 2018, specializes in Food Microbiology and Microbial Gut Ecology. He earned his PhD from ICAR-National Dairy Research Institute and completed postdoctoral studies in Germany and Belgium. His research, funded by several prestigious organizations, focuses on probiotics, gut health, and functional foods. He has guided multiple PhD scholars and postdoctoral fellows and collaborates internationally. His lab has developed an innovative in vitro gut simulation model. Dr. Goel has authored over 90 research papers and three books, with around 4,500 citations.

Prof. (Dr.) Jyoti Prakash Tamang

Hon'ble Vice-Chancellor, Sikkim University, Gangtok, Sikkim

Prof. Jyoti Prakash Tamang, FNA, FNASc, FNAAS, is a distinguished microbiologist known for his extensive research in the field of food microbiology, with a particular focus on fermented foods. He is currently acting Vice-Chancellor of Sikkim University. He has made significant contributions to understanding the role of beneficial microorganisms in traditional fermented foods of the Himalayan region and beyond. Dr. Tamang's research is highly regarded in the scientific community, especially in the areas of food safety, nutrition, and microbial diversity. He has been elected as a Fellow of several prestigious scientific academies, including: FNA, FNASc and FNAAS. Dr. Tamang has published numerous research papers and books and is recognized internationally for his contributions to microbiology, fermented food studies, and sustainable food systems. He has also played an important role in promoting the value of traditional food knowledge in modern food science.

Prof. Veena Pande

Kumaun University, Nainital, Uttarakhand, India

Dr. Veena Pande is a Professor in the Department of Biotechnology at Sir J.C. Bose Technical Campus, Kumaun University, Bhimtal, Nainital, with 24 years of experience in teaching and research, specializing in Plant Biotechnology and Biochemistry. She earned her Master's degree in Biochemistry from G.B. Pant University of Agriculture and Technology and her Ph.D. in Plant Biotechnology from Kumaun University. Dr. Pande has been instrumental in the development of the Department of Biotechnology since its inception in 2000, securing DBT support and establishing significant infrastructure and research facilities. She served as the Head of the Department until March 2023 and has held numerous administrative roles, including Coordinator of the IPR Cell and Dean of Students Welfare. She is a lifetime member of various academic societies and has served as Associate Editor of the *SAR Journal of Medical Biochemistry*. Dr. Pande has completed several research projects as a Principal Investigator with funding from agencies like UCOST, CSIR, and DIBER. Her accolades include the Lupin Fellow award (2010), Governor's Best Researcher Award (2016, 2017), and the Leading Women Researcher Award (2022). She holds a US patent, has over 300 research publications, and has contributed to 20 book chapters. Dr. Pande has guided 32 PhD students (including two TWAS fellows), with eight more currently under her supervision. She has also organized over 60 academic events and remains actively engaged in academic and societal initiatives.

Dr. Neetu KumraTaneja

National Institute of Food Technology Entrepreneurship & Management (NIFTEM), Kundli, Sonepat, Haryana, India

Dr. Neetu Kumra Taneja is the Associate Head of CFRA and Senior Assistant Professor of Microbiology in the Department of Basic and Applied Sciences at NIFTEM, Kundli, under the Ministry of Food Processing Industries, Government of India. She holds a PhD in Biotechnology from AIIMS, New Delhi, and completed her post-doctorate in Microbiology from North Carolina, USA. Since joining NIFTEM in 2012, she has focused on food safety, developing technologies for detecting and controlling foodborne pathogens, and using probiotic bacteria for food fortification. Dr. Taneja has developed label-free technologies using plant-based antimicrobials to extend the shelf life of beverages and invented a layered silver-iron oxides nanocomposite for rapid bacterial pathogen elimination, for which she holds a national patent. She has also developed a unique biostain for Gram-negative bacteria. She established the Centre for Food Nano-biotechnology at NIFTEM and co-heads the Centre for Food Research Analysis, a commercial food testing lab. Dr. Taneja has led a global food safety program with Nestlé, and serves on expert panels such as FSSAI and BIS. She has received IAFP Travel Awards in 2022 and 2024.

Prof. Naveen Kango

Dr. Harisingh Gour University, Sagar, Madhya Pradesh, India

Prof. Naveen Kango is the Head of the Department of Microbiology and Director of Academic Affairs at Dr. Harisingh Gour University, Sagar, Madhya Pradesh, India. Since joining as an Assistant Professor in 1997, he has over 25 years of experience in teaching and research. Dr. Kango holds a M.Sc. (Gold Medal, 1996), NET-JRF (1995), and a Ph.D. (2003) in Applied Microbiology and Biotechnology from the same university. His postdoctoral work includes research on thermophilic fungal enzymes at Durban University of Technology, South Africa, and the University of Helsinki, Finland. With 71 peer-reviewed papers, 13 book chapters, a textbook, and five completed research projects, Dr. Kango has supervised 12 Ph.D. students and is currently guiding six more. His Google Scholar metrics include a citation index of 2242, h-index of 29, and i10 index of 51. A fellow of the Mycological Society of India (MSI), he received the MSI V. Agnihothrudu Memorial Award in 2021 and serves as Associate Editor of *Frontiers in Microbiology* and *Kavaka* and Chief Editor of *Madhya Bharti*.

Dr. Radha Prasanna

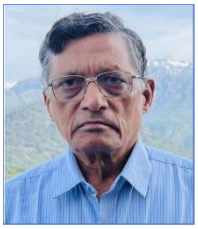
ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India

Dr. Radha Prasanna is a leading researcher in cyanobacteria, exploring their interactions with eubacteria, fungi, and plants. She is currently serving as Head, Principal Scientist, ICAR-Indian Agricultural Research Institute (IARI), New Delhi. Her work emphasizes their role in enhancing plant metabolism and the soil microbiome, showcasing their potential as plant growth promoters, biocontrol agents, and biofortifying agents. She has developed innovative microbial formulations that save 20-30% nitrogen and improve crop yields and soil nutrient availability. Expanding the application of cyanobacteria beyond rice, Dr. Prasanna has demonstrated their effectiveness in crops such as wheat, maize, cotton, legumes, and vegetables. Her team has conducted comprehensive studies on cyanobacterial diversity in various Indian agro-ecologies and developed markers for their soil establishment and plant colonization. Additionally, she has optimized nursery mixes with cyanobacteria for disease management and soil health restoration. Dr. Prasanna has authored over 300 research papers (h-index of 67 and 13,967 citations) and deposited more than 250 sequences in NCBI. Her contributions to agricultural microbiology have earned her numerous accolades, including fellowships from NAAS and the Academy of Microbiological Sciences, and prestigious awards like the ICAR Panjabrao Deshmukh Outstanding Woman Scientist Award.

Dr. G. Senthil Kumar

National Institute of Immunology, New Delhi, India

Dr. G. Senthil Kumar currently working as a Staff Scientist at the National Institute of Immunology in New Delhi, India. Dr. Kumar earned his Ph.D. from Molecular Biophysics Unit at IISc, Bangalore. Following this, he undertook extensive postdoctoral research in the United States, beginning as a Post-Doctoral Fellow at Northwestern University in Evanston, Illinois. After this he held positions as a Research Associate and later as an Assistant Professor (Research) at Brown University in Providence, Rhode Island. Additional academic roles include Research Assistant Professor at the University of Arizona in Tucson and Assistant Professor (In-Residence) at the University of Connecticut Health Center in Farmington, Connecticut.



Prof. Rup Lal

Acharya Narendra Dev College, University of Delhi, New Delhi, India

Prof. Rup Lal, born in Village Kanoh, Hamirpur, and educated at Government High School Bani, is currently an INSA Senior Scientist at the Acharya Narendra Dev College, University of Delhi. He is a Fellow of several prestigious organizations, including the American Academy of Microbiological Sciences and the Indian National Science Academy. Prof. Lal served as the ASM Ambassador for India from 2012 to 2015 and currently represents India in ISME and FEMS, as well as the International Microbial Literacy Initiative-South Asia Centre. He began his academic career at Sri Venkateswara College in 1979 and moved to the University of Delhi's Department of Zoology in 1992, where he held several leadership positions until his retirement in 2018. He has been a visiting scientist at numerous esteemed institutions worldwide and has received multiple fellowships and awards, including the Alexander von Humboldt Fellowship and the ASM Moselio Schaechter Distinguished Service Award. Recently, he was awarded the INSA Distinguished Lecture Fellowship for 2024. Prof. Lal has supervised over 75 Ph.D. students and has published more than 250 research papers with over 11,000 ISI citations, achieving an h-index of 54. He has also introduced outreach programs to promote microbiology in schools and has conducted over 350 lectures and 100 workshops on various microbiology topics. Additionally, he is the Honorary Director of the start-up PhiXgen Pvt. Ltd. and actively works to enhance microbial literacy through lectures and workshops targeting students and children.

Dr. Shruti Shukla

North-Eastern Hill University (NEHU), Shillong, Meghalaya, India

Dr. Shruti Shukla is an Associate Professor in the Department of Nanotechnology and a DBT-Ramalingaswamy Awardee at NEHU. She holds a Ph.D. in Life Science and has over 12 years of teaching and 13 years of research experience. Her research interests include developing nano-diagnostic sensors for the food, agricultural, environmental, and medical sectors, as well as nano-toxicology, safety regulations, nano-coatings, nano-packaging, and nano-functional food products. Dr. Shukla has supervised three Ph.D. candidates and has three more ongoing. She is an adjunct faculty member at the TERI School of Advanced Studies and has served as a girls' hostel warden. Her collaborations span several national institutions, including TERI, NIFTEM, and IIT-BHU, as well as international universities in South Korea, Spain, Poland, and the USA. Currently, she works as a Senior Scientist at the TERI-Deakin Nanobiotechnology Centre and was awarded the DBT-Ramalingaswamy Re-Entry Fellowship in 2019. With over 100 publications in prestigious SCI-indexed journals, she has played a key role in developing biogenic nano-products for agriculture and has secured a DBT-NER Mega research grant for creating functional non-toxic nano-coatings to enhance the shelf life of fruits and vegetables. Dr. Shukla has also been recognized as a Highly Cited Researcher by Stanford University and serves on the Food Safety Standards Authority of India's National Biohazard Team.

Dr. Sandip Kumar Dash

Berhampur University, Berhampur, Odisha, India

Dr. Sandip Kumar Dash, Assistant Professor (Stage-II) in the Department of Zoology at Berhampur University, Odisha, focuses on nanotechnology and molecular diagnosis of bacterial and viral diseases. With over ten years of research and teaching experience, he has published multiple research articles, book chapters, and edited books. He holds two patents and has led or been involved in three research projects, including a World Bank-funded project worth 3.0 crores. Currently, he supervises three Ph.D. scholars and has guided numerous M.Phil. and M.Sc. theses. Dr. Dash has received several awards, including the N.K. Sahu Memorial Medal (2008), Best Thesis Award (2014), and Faculty of the Year (2015). He is a life member of various scientific societies like ISZS, IAAM, ISCA, AMI, and SBC, and serves as an editor/reviewer for journals such as *Acta Scientific Microbiology*, *Talanta*, and *Journal of Physical Chemistry Solids*.

Prof. Bijender Singh

Central University of Haryana, Mahendragarh, Haryana, India

Dr. Bijender Singh is currently working as Professor in the Department of Biotechnology, Central University of Haryana, Mahendragarh. He is working in the field of Applied and Microbial Biotechnology with major emphasis on exploring thermophilic moulds for multifarious applications. Dr. Bijender Singh has obtained his Doctoral degree from Department of Microbiology, University of Delhi, South Campus, New Delhi in 2008. Dr.

Singh has been awarded DST-Fast Track Young Scientist award and Young Scientist Award in Industrial Microbiology by AMI. Dr. Singh is also featuring in top 2% Scientists of India in a study by Stanford University of USA since 2020. Dr. Singh has completed nine research projects funded by various funding agencies of India like UGC, DBT, CSIR, HSCST etc. Dr. Singh has published more than 100 research publications with a cumulative Impact Factor of more than 400. Dr. Singh has Edited one book and published more than 25 book chapters. Dr. Singh has H-index of 37.

Prof. Md. Imtaiyaz Hassan

Jamia Millia Islamia, New Delhi, India

Prof. Md. Imtaiyaz Hassan is a prominent Full Professor at the Center for Interdisciplinary Research in Basic Sciences, Jamia Millia Islamia, New Delhi, specializing in structural biology and drug discovery. With over 15 years of research experience, he focuses on identifying and validating novel drug targets and pioneering structure-based drug design. His extensive research has resulted in approximately 520 publications in high-impact peer-reviewed journals, accumulating over 18,000 citations and an h-index of 62. Prof. Hassan is particularly dedicated to discovering potent and selective kinase inhibitors, utilizing a multidisciplinary approach that integrates experimental and computational techniques. His work includes thorough validation of therapeutic potentials through cytotoxicity and in vivo studies. Recognized for his contributions to molecular biology and biochemistry, he has been elected a Fellow of the Royal Society of Chemistry and the Royal Society of Biology in the UK. Beyond research, he is a passionate educator committed to advancing scientific knowledge and mentoring future generations.

Prof. Arun S. Kharat

Shivaji University, Kolhapur, Maharrashtra, India

Prof. Arun S. Kharat earned an M.Sc. in Microbiology from Shivaji University, Kolhapur (1993), and a Ph.D. from the Indian Institute of Science, Bangalore, focusing on beta-glucoside utilization genes in Shigella. He completed two postdoctoral fellowships: one at the University of Grenoble Alpes (France) and another at Rockefeller University (USA) studying host-pathogen interactions with *Streptococcus pneumoniae*. Since 1994, he has taught Microbiology and Biotechnology at institutions such as Abasaheb Garware College, Dr. Babasaheb Ambedkar Marathwada University, and Jawaharlal Nehru University. He has supervised three foreign students and ten Indian Ph.D. candidates. With over 40 publications and three books, his expertise encompasses microbiology, host-bacterium interactions, medicinal microbiology, agricultural microbiology, environmental microbiology, microbiomes, biofilms, and cancer research.

Dr. Yogendra S Padwad

CSIR-IHBT, Palampur, Himachal Pradesh, India

Dr. Yogendra S Padwad holds a Ph.D. in Biochemistry (Virology & Immunology) from DIPAS (DRDO), New Delhi (2007), an M.Sc. in Biotechnology from Amravati University (2001), and a B.Sc. in Biology from the same institution (1998). He is currently a Principal Scientist at CSIR-IHBT, Palampur, where he has served in various roles, including Senior Scientist and Scientist. His post-doctoral experience includes work at the Medical University of South Carolina and a DBT Post-Doctoral Fellowship at IIT Madras. He serves on several committees, including the Management Council and as Chairman of the Institutional Animal Ethics Committee. His accolades include multiple research prizes and a summer undergraduate scholarship from Dr. B.R. Ambedkar Center. He has supervised 11 Ph.D. candidates, currently has four registered, and has published 110 papers with five patents. His research impact includes 3,512 citations, an h-index of 33, and an i10-index of 77.

Dr. K. K. Sharma

Maharshi Dayanand University (MDU), Rohtak, Haryana, India

Dr. Krishna Kant Sharma specializes in Biocatalysis, Biorefinery, and Gut Microbiology, with a Google Scholar H-index of 33 and recognition among Stanford's World Top 2% scientists in 2023. He currently serves as Associate Dean of Research & Development, Department of Microbiology, MDU, Rohtak and has over 20 years of teaching and research experience. Dr. Sharma earned his Ph.D. in Microbiology from the University of Delhi South Campus in 2008. His accolades include the DST Young Scientist Award (2012), INSA Visiting Scientist Fellowship (2017-2018), and multiple awards for his research and teaching excellence. He has supervised 8 Ph.D. students and a national postdoctoral fellow, with over 60 international publications. Dr. Sharma has led research projects funded by national agencies like DST, DBT, ICMR, and UGC and coordinates the DST-FIST Program.

Dr. (Mrs.) Becky M Thomas

Shriram Institute for Industrial Research (SRIFIR), Gurugram, Haryana, India

Dr (Mrs) Becky M Thomas is the Director at Shriram Institute for Industrial Research (SRIFIR), Gurugram. Prior to joining SRIFIR, Dr Thomas was Professor & Director Doctoral Programs & Research Promotions at the ATLAS SkillTech University Mumbai. Dr Thomas holds a Ph.D. in Immunology from the National Institute of Immunology, JNU, New Delhi and has done her Management course from IIM-Calcutta. She has extensive R&D experience with Indian Pharmaceutical industries such as Dabur Research Foundation, Reliance Life Sciences and Piramal Healthcare Ltd. Dr Thomas subsequently moved into academics and has worked in organizations such as D Y Patil University, Amity University Mumbai, Director & Dean Research at Somaiya Vidyavihar University, Mumbai and Professor & Head Research at the CHRIST (Deemed to be University), Pune Lavasa. She has successfully filed 62 patents both globally and in India with 15 granted patents to her credit. Dr Thomas has peer-reviewed publications in both National and International Journals and has participated in both oral and poster presentations in National and International conferences.

Dr. Vijay K Chaudhary

Infectious Disease Research, Education, and Training (CIIDRET), University of Delhi, New Delhi, India

Dr. Vijay Kumar Chaudhary is a NASI-Senior Scientist at the Centre for Innovation in Infectious Disease Research, Education, and Training (CIIDRET) and an Honorary Advisor at the Delhi School of Skill Enhancement & Entrepreneurship Development (DSSEED) at the University of Delhi. A former Professor and Head of the Department of Biochemistry at the University of Delhi South Campus, he served for 25 years. He is dedicated to developing innovative healthcare solutions tailored to Indian needs and mentoring young scientists. He founded CIIDRET in 2015, which later inspired the creation of DSSEED. His research group has developed several antibody-based diagnostics, including the NEVA-HIV test for HIV detection and TBConfirm for tuberculosis. More recently, his team created an immunization-free antibody discovery platform for COVID-19 treatment and snakebite therapy. Dr. Chaudhary has received multiple awards, including the Biotech Product and Process Development Award (thrice), the NRDC Award, the WIPO Medal for Best Invention, and the Visitor's Award for Innovation from the President of India.

Prof. Amita Gupta

University of Delhi, New Delhi, India

Dr. Amita Gupta is a Professor and Head of the Department of Biochemistry at the University of Delhi, where she also serves as Director of both the Delhi School for Skill Enhancement & Entrepreneurship Development (DSSEED) and the Centre for Innovation in Infectious Disease Research, Education, and Training (CIIDRET), University of Delhi. With a Master's and PhD in Biochemistry from the University of Delhi, she has made significant contributions to infectious disease research, earning several prestigious awards including the Visitor's Award for Innovation and the INSA Young Scientist Medal. Dr. Gupta's research focuses on developing novel diagnostics and therapeutics for diseases like tuberculosis, COVID-19, and HIV, including work on drug-resistant TB and the toxin-antitoxin systems in *Mycobacterium tuberculosis*.

Dr. Puja Yadav

Central University of Haryana, Mahendragarh, Haryana, India

Dr. Puja Yadav is an Assistant Professor in the Department of Microbiology at Central University of Haryana, where she has served since 2016. She completed postdoctoral fellowships at the University of Texas and Harvard Medical School, and earned her Ph.D. from Jamia Millia Islamia, specializing in infectious diseases. Dr. Yadav has received numerous awards, including the WISER grant, SERB International Research Experience Award, and Distinguished Microbiologist Award. Her research focuses on host-pathogen interactions, antibiotic resistance, and biofilm formation. She has authored 20 publications, with an H-index of 14 and 1155 citations, and supervises 02 Ph.D. and 28 M.Sc. students.

Dr. Yamini Singh

Defence Research and Development Organisation (DRDO), New Delhi, India

Dr. Yamini Singh, Scientist F, at Defence Institute of Physiology & Allied Sciences, DRDO, Ministry of Defence, India, holds a Ph.D. in Biotechnology from Jiwaji University, Gwalior. With a background in Applied Microbiology and Zoology, Botany, and Chemistry, her expertise spans molecular biology, genetics, genomics, and mitochondrial research. Her work includes DNA barcoding for bird species identification, high-altitude acclimatization studies, and COVID-19 pathogenesis. She has received numerous accolades, including Scientist of the Year 2020 at DIPAS and has authored 40 publications, 4 patents, and guided 03 PhD and 35 MSc students. Dr. Singh is a member of several professional societies including Associate Member of the Aeronautical society of India (ASI), Indian Academy of Biomedical Sciences (IABS) and Biological chemists (India).

Prof. Hari S Misra

Narsee Monjee Institute of Management Studies (NMIMS), Mumbai, Maharashtra, India

Prof. Hari S. Misra, a Distinguished Professor of Biological Sciences at NMIMS University, Mumbai, holds an M.Sc. in Chemistry and a Ph.D. in Biochemistry and Microbiology. Formerly Head of the Molecular Biology Division at Bhabha Atomic Research Centre (BARC), Mumbai, his research focuses on molecular and cellular responses to stress, particularly DNA damage and repair. He made significant contributions to understanding DNA damage response mechanisms in *Deinococcus radiodurans*, challenging the traditional LexA/RecA-mediated SOS response model. Prof. Misra has supervised many PhD students, published over 100 high-impact papers, and received national awards, including the Fulbright-Nehru Senior Scholarship. He is a Fellow of several prestigious academies.

Dr. Swapan Ghosh

Ramakrishna Mission Vivekananda Centenary College, Kolkata, West Bengal, India

Dr. Ghosh, an Associate Professor at Ramakrishna Mission Vivekananda Centenary College, Kolkata, established a Cancer Research Unit in 2012 after returning from Harvard University. His work focuses on cancer drug development using edible and medicinal mushrooms. He has supervised 13 research projects and six PhD scholars, with seven former scholars now awarded PhDs, some in postdoctoral research in the USA. With 207 publications, including 92 in international peer-reviewed journals, he also holds two Indian patents. Dr. Ghosh has delivered 25 invited talks and received 11 national and international awards, including "Excellence in Research" from UNICEF in 2021.

Dr. Anil Kumar

National Institute of Immunology, New Delhi, India

Dr. Anil Kumar is presently working as Staff Scientist in the National Institute of Immunology, New Delhi. His research interest focuses on microbiota-derived metabolites such as Trimethylamine N-oxide (TMAO), Indoxyl Sulfate, Trimethylamine etc. which have been implicated in human health and disease, and their early detection in the body fluids is thought to be significant in understanding pathogenesis and treatment of colorectal cancer and other diseases. His group is also studying the link of gut microbes in colorectal cancer causation. As an inventor, he credits more than granted 50 patents for developing product & processes useful indifferent industries. He also has published 75 research publications in international journals. He had participated in the development of biosensor which has been transferred to industry. In 2012, one of his patents has been selected for CSIR Technology Award 2012 and other US patent won Merck Millipore India Innovation Award 2012. He is also heading the IPR division in the National Institute of Immunology.

Dr. Anju Pappachan

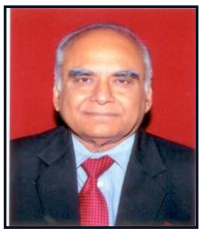
Central University of Gujarat, Gandhinagar, Gujarat, India

Dr. Anju Pappachan is a Structural Biologist and Assistant Professor at the School of Life Sciences, Central University of Gujarat. She earned her Ph.D. in Molecular Biophysics from the Indian Institute of Science, Bangalore. Her research focuses on the structural and functional characterization of proteins from pathogens and industrial organisms using various biophysical, biochemical, and computational methods. Current projects include studying proteins from *Leishmania donovani* and molecular mechanisms of translational fidelity. Dr. Pappachan has led several externally funded projects and published extensively in reputed journals.

Prof. Sunit K. Singh

University of Delhi, New Delhi, India and Banaras Hindu University (BHU), Varanasi, Uttar Pradesh, India

Prof. Sunit K. Singh is the Director of the Dr. B. R. Ambedkar Centre of Biomedical Research (ACBR) at the University of Delhi and a Professor of Molecular Immunology & Virology at Banaras Hindu University (BHU). He was a faculty member at CSIR-Centre for Cellular and Molecular Biology (CCMB), Hyderabad. With a Ph.D. from the University of Wuerzburg, Germany, and postdoctoral training at Yale and UC Davis, Chonbuk National University (South Korea), and the University of Geneva (Switzerland) his research focuses on infectious diseases, particularly neurotropic viruses. Prof. Singh has held leadership roles at BHU and CSIR-CCMB and has published extensively, receiving multiple national awards, including the Dr. B. C. Roy Award. He is a Fellow of several prestigious scientific academies.



Prof. Nirmal Kumar Ganguly

Padma Bhushan, Government of India

Prof. Nirmal Kumar Ganguly, M.D., Ph.D. former President of the National Academy of Medical Sciences, Indian Science Congress, and JIPMER - Puducherry, Prof. Nirmal Kumar Ganguly is a distinguished medical scientist and former Director General of the Indian Council of Medical Research. He has held leadership roles at PGIMER Chandigarh and the National Institute of Biologicals and has been awarded six honorary Doctorate of Science degrees by Indian universities. A fellow of Imperial College and the Royal College of Pathologists, Prof. Ganguly was part of the COVID-19 Advisory Committee to the Ministry of Health. He has served on boards for the Canada Innovation Fund, the Indian Pharmacopeia Commission, and various international health organizations, including the WHO and NIH. He chairs several prestigious scientific advisory committees and is the president of multiple research societies. With over 800 publications and 21 book chapters, he has guided more than 130 PhD students and received 9 international and over 114 national awards. In recognition of his significant contributions to medical sciences, he was awarded the Padma Bhushan by the President of India in 2008.

Dr. Rajnikant Dixit

National Institute of Malaria Research (NIMR), New Delhi, India

Dr. Rajnikant Dixit, a Scientist E at the National Institute of Malaria Research (NIMR), India, brings 23 years of expertise to malaria research. He heads the Department of Vector Genomics, where his team focuses on decoding the functional genomics of Indian malarial vectors. His work centers on identifying mosquito and microbe-derived biological factors to develop molecular strategies for vector control, aiming to alleviate malaria in endemic regions. Dr. Dixit earned his Ph.D. in Vector Biology from Maharishi Dayanand University, India, and completed postdoctoral training at the NIH, USA, where he researched mosquito immunity and vector competence. With over 40 publications in leading journals, his work has advanced the understanding of mosquito behavior, physiology, and vector-parasite interactions. Beyond research, he mentors emerging scientists, guiding several Ph.D. and M.Sc. students. Integrating his scientific work with Vedic knowledge, particularly insights from the "Shrimad Bhagwat Geeta," Dr. Dixit envisions a path of "Research for Peace," linking scientific inquiry with philosophical principles.

Prof. Javed N Agrewala

Indian Institute of Technology (IIT) Ropar, Punjab, India

Dr. Javed N Agrewala is a distinguished Professor at the Indian Institute of Technology (IIT) Ropar, with 38 years of research experience. His expertise spans various fields, including gut microbiota and disease susceptibility, immunomodulation for drug efficacy, novel vaccination strategies against tuberculosis, and host-directed therapies. Over his career, he has held prestigious positions, including Chief Scientist at CSIR-Institute of Microbial Technology and Visiting Scientist roles at the Trudeau Institute (USA) and the MRC-TB Unit in London. Dr. Agrewala's contributions have been recognized with numerous awards, including the Shanti Swarup Bhatnagar Award (2005), UP Science Award (2018), JC Bose Fellowship (2018), and National Bioscience Award for Career Development (2006). He is a Fellow of several prestigious academies, including the Indian National Science Academy and the National Academy of Sciences, India. His research has been widely published, with 128 publications in leading journals. Some of his notable works include studies on immunosuppressive effects of morphine, aging-related gut microbiota dysbiosis, and innovative strategies for tuberculosis vaccination using dendritic cells. His groundbreaking research continues to influence the fields of immunology and microbiology.

Dr. Sinosh S Kariyachan

St. Pius X College Rajapuram, Kasaragod, Kerala, India

Dr. Sinosh S Kariyachan is working as Assistant Professor in Microbiology, St. Pius X College Rajapuram, Kasaragod, Kerala. He specialized in Microbiology (M.Sc.) & Bioinformatics (M.Sc.) and Ph.D. He has a decade of experience in teaching and research. His current research thrusts are antimicrobial resistance, screening of novel natural lead molecules by chemo-informatics and computer-aided drug discovery and study of plastic degradation by novel microbial consortia and screening of novel metabolites from bacterial symbiotic associated with marine sponges. He is a life member of several scientific societies. He published 79 International papers and presented more than 89 scientific papers in conferences. He has received several awards. He has authored a text book and many book chapters as invited articles for reputed publishers.

Dr. Urmi Bajpai

Acharya Narendra Dev College, University of Delhi, India

Dr. Urmi Bajpai, Ph.D., is the founding faculty member and teacher-in-charge of the Department of Biomedical Science at Acharya Narendra Dev College, University of Delhi, where she established the B.Sc. (Hons) Biomedical Science program in 1999. She holds a Ph.D. in Microbiology from the University of Delhi and has pioneered undergraduate research, training over 150 students since 2007. Dr. Bajpai has secured ₹7.7 million in government funding for four major research projects, establishing a modern molecular biology laboratory and developing extensive resources, including 75 gene clones and 21 recombinant proteins of *Mycobacterium tuberculosis*. Her research efforts focus on multi-target therapies for tuberculosis, specifically targeting Mur pathway enzymes, and the exploration of Mycobacteriophages for diagnostic and therapeutic applications. As a recognized Ph.D. guide and national coordinator for Tata CSIR OSDD Fellowships, Dr. Bajpai contributes to advancing life sciences education across Indian colleges. She is a sought-after speaker on innovative educational models and was honored with the 2014 Meritorious Teacher Award from the Delhi Government. Through her initiatives, Dr. Bajpai not only fosters hands-on training for students but also builds valuable research repositories that serve the broader scientific community.

Prof. (Dr.) Sheetal Bhasin

Maharaja Ranjit Singh College of Professional Sciences, Indore, Madhya Pradesh, India

Dr. Sheetal Bhasin is the Professor and Head of the Department of Biosciences and IQAC Coordinator at Maharaja Ranjit Singh College of Professional Sciences, Indore, M.P., India. She holds a Master's in Microbiology from DAVV, Indore, and a Ph.D. in Microbiology from Gujarat University. Her research focuses on the production and application of bioactive compounds and enzymes from Actinobacteria, resulting in over 20 national and international publications and numerous microbial sequence submissions to NCBI. With 27 years of experience in teaching and training, she supervises Ph.D. students at DAVV and participates in examination panels across various universities. Prof. Bhasin has delivered over 55 conference presentations and guided around 80 postgraduate research projects. She has developed 15 e-content modules for Swayam online courses and coordinated MOOCs on Biochemistry, Molecular Biology, and Microbiology. Actively involved in research and industrial consultation, she collaborates with various industries and educational institutes while organizing skill development workshops and educational tours for students.

Prof. Bishwajit Kundu

Indian Institute of Technology, Delhi (IIT Delhi), New Delhi, India

Prof. Bishwajit Kundu holds a BSc in Agriculture from Bidhan Chandra Krishi Viswavidyalaya, an MSc in Biotechnology from Madurai Kamaraj University, and a Ph.D. from the Institute of Microbial Technology, JNU. After postdoctoral research at Case Western Reserve University, he joined IIT Delhi's Department of Biochemical Engineering and Biotechnology in 2004, and became a Professor at the Kusuma School of Biological Sciences in 2018. Specializing in protein science, enzyme engineering, and protein aggregation, he has 65 publications, commercialized two patents including In-house developed, cost-effective, COVID-detection kit and authored a book on protein engineering. He has supervised 6 postdocs, 22 Ph.D., and 4 MSR students.

Prof. Sarman Singh

AV Medical College (AVMC), Pondicherry, India

Prof. Sarman Singh has over 30 years of service at the All India Institute of Medical Sciences (AIIMS), retiring as Director and CEO of AIIMS Bhopal in November 2021. He also served as the founding Director in-charge of AIIMS Bibi Nagar (Hyderabad). After retirement, he mentored the Medical Sciences and Engineering Research (MEDSER) center at IISER Bhopal and currently directs Medical Research and Institutional Collaborations at AV Medical College, Pondicherry. As Editor-in-Chief of the Journal of Laboratory Physicians and an Academic Editor for several journals, Prof. Singh is involved in over 40 editorial boards. He has received more than 30 awards for his contributions to science and holds 7 patents, along with two technology transfers. He has led over 50 research projects and supervised 30 PhD/DM scholars, 36 MD residents, and over 40 MSc students. With 6 books, 46 book chapters, and over 366 research papers cited more than 15,000 times, he has an i10 index of 234 and an H-index of 64. Prof. Singh has been recognized among the world's top 2% scientists for four consecutive years.

Dr. Mahesh Dhar

Surya Corporation Pvt. Ltd., 63, DSIDC complex, Okhla-I, New Delhi, India

A trained microbiologist with 15 years of R&D and teaching experience, this professional has significant expertise in diagnostic lab setup and validation of testing tools. Currently, he is Vice President (Research) in Surya Corporation Pvt. Ltd., New Delhi. He established the NGS facility at NCDC and drafted INSACoG for identifying and surveilling SARS-CoV-2 variants in India. They also set up the first COVID-19 testing lab in North India, achieving 100% conformity in qualifying for WHO's Global EQAP. He developed and licensed recombinant bacterial superoxide dismutase with funding from the DBT-BIRAC Biotechnology Ignition Grant and received a DST-SERB Young Investigator startup grant for evaluating probiotic products in India. In 2019, he won the AMI Young Scientist Award in Medical and Veterinary Microbiology and have published as Lead Author in prestigious journals like Nature, Science, and NAR.

Prof. Bhabatosh Das

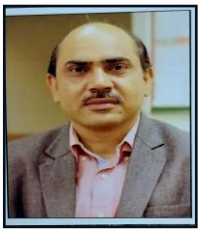
NCR Biotech Science Cluster, Faridabad, India

Dr. Bhabatosh Das held position of Professor & Coordinator, Centre for Microbial Research, Translational Health Science and Technology Institute, NCR Biotech Science Cluster, Faridabad. He is a trained microbiologist with an M.Tech. from IIT Kharagpur (2003) and a Ph.D. from the Indian Institute of Chemical Biology, Kolkata (2008). He completed postdoctoral research at the Institute of Integrative Biology of the Cell, France (2011), and was a JSPS Fellow at Osaka University, Japan (2017). He has received multiple international and national fellowships, including from the Japan Society for the Promotion of Science and the Centre National de la Recherche Scientifique. With over 126 research articles published in prestigious journals, Bhabatosh has garnered over 4,000 citations. He currently serves as a professor at THSTI and coordinates the Centre for Microbial Research. He also holds adjunct faculty positions at several institutions and is involved with organizations like the Global Task Force for Cholera Control. His research focuses on microbial community ecology, the emergence of multidrug-resistant pathogens, and genomic surveillance of infectious agents.

Dr. Sanjay Kumar

Indian Institute of Technology Delhi (IIT Delhi), India

Dr. Sanjay obtained his Ph.D. in Biotechnology from the Indian Institute of Technology (IIT) Delhi and Jiwaji University Gwalior in 2011. As a postdoctoral fellow at Ohio State University Columbus, USA, from 2012-2017 and at University of Arizona, USA, from 2017-2018. His study was focused on understanding the regulation of mitochondrial dynamics. Dr. Sanjay joined the Indian Institute of Science Education & Research in Tirupati, India, as a Ramalingaswami Fellow and Assistant Professor in 2018. Research in Kumar's laboratory is focused on studying how alteration in mitochondrial dynamics contributes to disease progression. Dr. Sanjay has established a multidisciplinary program engaged at the interface of cell biology, molecular biology, biochemistry, bioinformatics, proteomics, and genomics. Dr. Kumar received the SERB Young Scientist Award in 2015, the Ramalingaswami re-entry fellowship in 2017, and the SERB Core research grant in 2020. Dr. Kumar has published 28 research papers in internationally reputed journals, including Molecular Cell, Nature Communications, Oncogenes, Journal of Biological Chemistry, and Neoplasia.



Prof. Baljeet Singh Saharan

Chaudhary Charan Singh Haryana Agricultural University (CCS HAU), Hisar, Haryana, India

Prof. (Dr.) Baljeet Singh Saharan is the Principal Scientist and In-Charge of the Centre of Biofertilizer Production and Technology, as well as the Professor and Head of the Department of Microbiology at Chaudhary Charan Singh Haryana Agricultural University (CCS HAU), Hisar. He holds a Ph.D. in Microbiology from CCS HAU and has served as a Senior Scientist, Associate Professor, and Postdoctoral Fellow at USDA and UFZ in Germany. His research focuses on natural farming, sustainable agriculture, and food microbiology, with over 200 publications, including four books and twenty book chapters. Prof. Saharan is a member of several professional organizations, including AMI and ASM, and has been awarded the Singh-Obama Fellowship (2013-14), Louis Pasteur National Academic Excellence Award (2021), and Best Agricultural Scientist Award (2023). He has secured research funding from UGC and DST and is multilingual, fluent in five languages. Prof. Saharan has guided 30 Ph.D. students, 500 M.Sc. students, and 4 B.Tech. students, and has contributed significantly to curriculum development in natural farming. His work in Zero Budget Natural Farming (ZBNF) is widely recognized, and he is a prominent speaker on sustainable agriculture at national forums.

Dr. G. Velmurugan

KMCH Research Foundation, Coimbatore, Tamil Nadu, India

Dr. G. Velmurugan is a Scientist at KMCH Research Foundation in Coimbatore, Tamil Nadu. He holds a Ph.D. from Madurai Kamaraj University and completed his post-doctoral training at Cologne University (Germany), IIT Madras, and University of Florida (USA). His research focuses on the interactions between various chemicals (such as phytochemicals, pharmaceuticals, and pollutants) and microbes (including bacteria, viruses, and fungi) across different environments, examining their implications for ecosystem and human health. Dr. Velmurugan's team leverages microbiota to address global challenges like pollution, climate change, and human diseases, exploring microbiomes in soil, water, plants, cattle, and humans to establish their role in One Health. His research on pesticide metabolization by gut microbiota was included in the UN-FAO Technical document on food safety and quality. He has received several prestigious fellowships and the Young Scientist Award from the Association of Microbiologists of India.

Dr. Mukesh Kumar Yadav

Central University of Punjab (CUP), Bathinda, Punjab, India

Dr. Mukesh Kumar Yadav is an Associate Professor in the Department of Microbiology at the Central University of Punjab, Bathinda, India. Prior to joining CUP, he worked at Biosewoom Inc. and several universities in South Korea, as well as Mizoram University in India. With over 16 years of research experience, Dr. Yadav specializes in microbial biofilms, host-pathogen interactions, and endophytes. He has completed seven major research projects funded by various organizations, including the Korean Research Foundation, DBT, ICMR, DST, and UGC, and has published more than 85 research articles, along with three patents and five books. His research focuses on understanding microbial colonization and biofilm growth modes, particularly the pathogenicity of bacteria in biofilms, which are resistant to antibiotics. He aims to identify novel pathways for developing new antimicrobial and antibiofilm compounds and investigates the host response during bacterial colonization. Additionally, his group studies commensal bacteria colonization in the gut and the effects of gut microbiota biofilm formation on human health.

Dr. Khem Raj

Panjab University, Chandigarh, India

Dr Khem Raj is Assistant Professor in the Department of Microbiology, Panjab University, Chandigarh, India. His research expertise includes the Microbial Genomics, Microbial Transcriptomics, and Human Microbiomics. He has been conferred as a "DHR Long Term Fellow" by Department of Health and Family Welfare for advanced training in Genomics. Over the last 8 years, his lab has been funded by Government of India and Industries as a PI or CO-PI for more than 11 Million INR. His lab is also providing academic consultancy to Holistic Himalayas Pvt. Ltd. for Microbiological services. His lab has published 15 Research articles and 3 Book Chapter in high impact journals.

Dr. Belle Damodara Shenoy

CSIR-NIO Regional Centre in Visakhapatnam, Andhra Pradesh, India

Dr. Belle Damodara Shenoy is a renowned fungal taxonomist. He earned his Bachelor's and Master's degrees in India before completing a Ph.D. in fungal taxonomy at the University of Hong Kong, focusing on the evolutionary relationships of asexual genera.
After a post-doctoral fellowship at Agriculture and Agri-Food Canada, he joined the Microbial Type Culture Collection at CSIR-IMTECH in Chandigarh in 2008, where he supervised Ph.D. students and published extensively on fungal taxonomy and phylogeny. In 2013, he moved to CSIR-National Institute of Oceanography (CSIR-NIO) in Goa, researching microbes associated with tarballs. Currently based at the CSIR-NIO Regional Centre in Visakhapatnam, Dr. Shenoy has published 50 papers and is the founding Editor-in-Chief of MycoAsia. He has served on International Sub-commission on Colletotrichum Taxonomy and Advisory Board of Amity Institute of Oceanography. Outside of academia, he enjoys traveling and writing poetry.

Dr. Dinesh A. Nagegowda

CSIR-CIMAP, Research Centre, Bengaluru, Karnataka, India

Dr. Dinesh A. Nagegowda, an accomplished plant molecular biologist, completed his M.Sc. in Biotechnology from the University of Agricultural Sciences, Bengaluru, and earned a Ph.D. in Plant Molecular Biology from the University of Hong Kong. After postdoctoral research at Purdue University, USA, he returned to India under the Ramalingaswami Re-Entry Fellowship, briefly serving as Assistant Professor at IIAR Gandhinagar. In 2009, he joined CSIR-CIMAP, Lucknow, and he is presently serving as Chief Scientist and Scientist-In-Charge at CSIR-CIMAP's Bengaluru Research Centre. His research focuses on the biosynthetic pathways of specialized metabolites in medicinal and aromatic plants, applying findings to metabolic engineering and synthetic biology to enhance valuable compound production. With over 55 publications, 7 book chapters, and 4900+ citations, Dr. Dinesh is a respected figure in plant biotechnology. He has guided numerous postdoctoral, Ph.D., and M.Sc. students and presented extensively at international conferences. An honorary professor and Ph.D. guide, he also serves on editorial boards and reviews for over 20 journals. His accolades include the Indo-US GETin Fellowship, CSIR's Raman Research Fellowship, and Karnataka's Sir CV Raman Young Scientist State Award. Elected as a Fellow of both National Academy of Sciences and Indian National Science Academy, he has significantly contributed to advancing agricultural biotechnology in India.

Prof. Sivakumar Uthandi

Tamil Nadu Agricultural University (TNAU), Coimbatore, Tamil Nadu, India

Prof. Sivakumar Uthandi has 34 years of experience, including 4 years with the Tamil Nadu State Government and 30 years at Tamil Nadu Agricultural University (TNAU), where he served from Assistant Professor to Dean of Post Graduate Studies. He earned his degrees from TNAU and completed post-doctoral training at institutions including the University of Florida and Wageningen University. Recognized as a Visiting Associate Professor in the USA, he has also engaged in academic activities in Sri Lanka, Laos PDR, and Thailand, and has held an adjunct professorship at the University of Tokyo since 2019. Prof. Uthandi is noted for his pioneering research, including the first report of archaeal laccase and innovations in biomass conversion technology. His work includes bacterial cellulose synthesis and biodiesel production from sago wastewater. He focuses on plant microbiomes, biocatalysts, and lignin biotransformation, with 171 peer-reviewed publications and 4 patents to his name. As an editor for Springer Nature's Indian Journal of Microbiology, he has secured INR 1,271 lakhs in funding, offering 35 fellowships. He is a Fellow of Royal Society of Biology and has received multiple international and national awards.

Dr. Gitanjali Yadav

National Institute of Plant Genome research (NIPGR), New Delhi, India

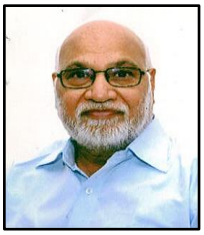
Dr. Gitanjali Yadav is a senior scientist at NIPGR and co-founder of semantic Climate, a global citizen science initiative for climate action. She serves as an adjunct professor of Data Science at IISER Bhopal and a visiting lecturer at the University of Cambridge. An expert in genomics and machine intelligence, her work focuses on food security and conservation. Dr. Yadav holds a Ph.D. in Immuno-Informatics from NII, a Master's in Biomedical Research, and a Bachelor's in Botany from the University of Delhi. She has received numerous accolades, including the Hamied Fellowship from Cambridge and the Exceptional Talent Award from the Royal Society. As co-chair of the International Data Policy Committee at CODATA, she advocates for FAIR principles and Open Access for data. Additionally, she coordinates the DBT's iBRIC+ Zero Waste Life Program and promotes science in education.

Dr. Hukukm Singh Gehlot

Professor, Centre for Advance Study Jai Narain Vyas Univetsity, Jodhpur, India

Dr. Hukam Singh Gehlot is a Professor in the Department of Botany at Jai Narain Vyas University, Jodhpur, India. With over 28 years of research experience post-Ph.D. and extensive teaching experience at both undergraduate and postgraduate levels, Dr. Gehlot has made significant contributions to the fields of biological nitrogen fixation, stress physiology, and molecular ecology. His current research focuses on nitrogen fixation in native legumes of arid regions and the antioxidant properties of desert plants. Dr. Gehlot has also held various prestigious positions, including Head of the Department and Coordinator for advanced research programs, and has collaborated with international scientists in the U.S., U.K., Hungary, and Australia.

Dr. Gehlot's research is widely recognized, with publications in leading journals, numerous conference presentations worldwide, and several awards, including a DBT-Visiting Research Professorship and the Crawford Fund Training Award. His projects are funded by national and international agencies, covering topics such as symbiotic relationships in arid legume species, the genomic characterization of rhizobia, and plant-microbe interactions. Additionally, Dr. Gehlot has supervised multiple Ph.D. students and contributed to collaborative research efforts in microbial culture characterization and genetic sequencing, enriching scientific knowledge in arid ecosystem resilience and plant microbiology.



Dr. Gaya Prasad

Former Director cum Vice Chancellor, IVRI, Baraellei, Uttar Pradesh, India; Former ADG (AH), Krishi Bhawan, New Delhi, India

Dr. Gaya Prasad, completed their B.V.Sc. & A.H. in 1977, M.V.Sc. in 1980, and Ph.D. in 1984 at G.B. Pant University of Agriculture & Technology, Pantnagar. They further advanced their expertise with a postdoctoral fellowship at M.D. Anderson Cancer Institute, University of Texas, USA (1986-88). Dr. Prasad has held various academic and administrative roles, including Teaching Associate, Assistant Scientist, and Professor in the Department of Animal Biotechnology at Chaudhary Charan Singh Haryana Agricultural University (CCS HAU), Hisar. Notably, he served as Acting Director of Indian Veterinary Research Institute (2012-14), Assistant Director General (Animal Health) at ICAR, New Delhi (2010-16), and later, as Vice-Chancellor of Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, in 2016. Throughout his career, Dr. Gaya Prasad**,** has received numerous accolades, including Rafi Ahmad Kidwai Award (2007-08), Prof. S.R. Vyas Memorial Award, and Dr. Richard Masillamony Oration Award. They have held prominent editorial roles, such as Volume Editor of *Progress in Vaccinology*, Editor of the *Indian Journal of Microbiology*, and Managing Editor of the *Indian Journal of Virology*. Further, he has also served as the President of Association of Microbiologists of India and Secretary General of National Academy of Veterinary Sciences. Recognized as a Fellow by multiple prestigious organizations, including National Academy of Veterinary Sciences and the Indian Virological Society, their research has significantly contributed to the fields of animal biotechnology, molecular virology, and molecular diagnostics.

Dr. Rahul Taneja

Haryana State Science and Technology (HSST), Panchkula, Haryana, India

Successfully delivered more than 300 talks on Intellectual Property Rights across India in various Institutions, Universities and Government Organization such as All India Institute of Medical Science (AIIMS) (New Delhi), CII, PHD-CII, MSME-DI (Ludhiana), MSME-DI (Haryana), MSME-DI (Himachal Pradesh), Government of India. Dr. Taneja facilitated Research, Scholars, Scientists, Doctors and Professors for Patent filing. Dr. Taneja also facilitated more than 250 Enterprises of India for Intellectual Property Issues (Such as Patent Infringement, Trademark Filing, Copyright Filing, Trademark Infringement and Industrial Design issues etc).

Dr. Anju Manuja

ICAR-National Research Centre on Equines, Hisar, Haryana, India

Dr. Anju Manuja is a Principal Scientist at ICAR-National Research Centre on Equines in Hisar, Haryana, with a Ph.D. in Veterinary Medicine from CCS HAU, Hisar. Her Ph.D. research included work at the Roslin Institute in Edinburgh, UK, followed by a postdoctoral fellowship in molecular epidemiology at Canada's Vaccine and Infectious Disease Organization. Dr. Manuja is a recipient of numerous prestigious awards, including ICAR's Panjabrao Deshmukh Outstanding Woman Scientist Award, Elsevier Emerging Investigator Award, GADVASU

Women Scientist Award, and ICAR Junior Research Fellowship. She has also been awarded fellowships by National Academy of Agricultural Sciences and National Academy of Veterinary Science, recognizing her contributions to veterinary and animal sciences. Dr. Manuja's expertise in nanomedicine has led to three granted Indian patents and six other national and international patents as a principal inventor. She has published over 100 research articles in high-impact journals and has more than 390 publications, including books, chapters, and conference proceedings. She has also served as an editor for special issues in esteemed journals like *Current Topics in Medicinal Chemistry* and *Frontiers in Nanotechnology*. Dr. Manuja is a member of various national and international scientific societies, such as the International Veterinary Vaccine Network, UK.

Dr. Jaskaran Singh

Geeta University, Panipat, Haryana, India

Dr. Jaskaran Singh, Ph.D., is the Dean (Research) and Head of the Forensic Science Department at Geeta University, Panipat. An accomplished academic, he completed his Ph.D. at Amity University under the INSPIRE fellowship from India's Ministry of Science and Technology. Dr. Singh holds an M.Sc. in Forensic Science (Gold Medalist) and a B.Sc. (H) in Forensic Sciences (Silver Medalist). His research spans emerging areas in forensic science and medicine, integrating theory with practical applications. His collaboration with experts in allied health sciences, advocating a multidisciplinary approach that has resulted in numerous patents, copyrights, and books. Dr. Singh is frequently invited as a keynote speaker at national and international conferences and has trained police officers globally in forensic investigations. Recognized for his contributions, he was awarded an Honorary Professorship from ISPTEC, Angola, and the prestigious FSIESRP fellowship from the Society of Innovative Educationalists and Scientific Research Professionals, Malaysia.

Prof. Neeraj Dilbaghi

Guru Jambheshwar University of Science and Technology, Hisar, Haryana, India

Dr. Neeraj Dilbaghi is a Professor of Biotechnology at Guru Jambheshwar University of Science and Technology, Hisar, where he also serves as Dean of Research and Development, Institutional Coordinator of RUSA, Director of Horticulture, and Nodal Officer for several national initiatives. With over 28 years in research and 25 years in postgraduate teaching, he has mentored a wide range of scholars, including Ph.D., M.Tech, and M.Sc. students. His research interests focus on microbial biotechnology, bionanotechnology, nanosensors, nano-medicine, and the toxicological evaluation of nanomaterials. To date, he has published over 210 research papers with more than 11,140 citations, and holds an H-index of 56. Prof. Dilbaghi has managed numerous research projects funded by prestigious national and international agencies, including DBT-GOI, DRDO, and an Indo-German collaborative project. He has also contributed three MOOCs for SWAYAM and actively participates in academic governance as a committee member in Haryana and Punjab. His achievements have been widely recognized, including his ranking in Stanford University's "Top 2% Scientists of the World" in 2022 and 2023 and Research.com's Materials Science Scientists list.

Dr. Minakshi Prasad

ICAR-National Research Centre on Equines, Hisar, Haryana, India

Dr. Minakshi Prasad holds a BVSc & AH from the College of Veterinary Sciences, Hisar (1979-83), an M.V.Sc. (1986), and a Ph.D. (1999). She further advanced her expertise through a postdoctoral fellowship at the University of Minnesota, USA, in 2003-04. Currently, Dr. Prasad is Professor and Head of the Department of Animal Biotechnology at the College of Veterinary and Animal Sciences, Hisar, a role she has held since 2013. Her professional journey began as a Senior Research Fellow in Veterinary Microbiology at CCS HAU, Hisar (1986-88), followed by a position as a Reserved Veterinary Surgeon with Government of Haryana in 1988. She then progressed through roles as Assistant Scientist, Associate Professor, and eventually Principal Scientist in the Department of Animal Biotechnology at CCS Haryana Agricultural University (CCS HAU). Throughout her career, Dr. Prasad has received numerous prestigious awards, including Prof. R.M. Sharma Memorial Award, AMI Best Research Paper Presentation Award, Jawaharlal Nehru Award, and ISVIB Scientist Award, among others. Her accomplishments have been recognized through the Commonwealth Academic Staff Fellowship, Shiksha Rattan Puraskar, and a fellowship from the National Academy of Veterinary Sciences, India. Dr. Prasad's research focuses on animal biotechnology, with an emphasis on molecular virology, diagnostics, and vaccine development. Her contributions to these fields have significantly advanced veterinary science in India and made a meaningful impact internationally.

THEME CODE ABBREVIATIONS

AWA	Awardee Abstracts
IS	International Speaker
NS	National Speaker
OP	Oral Presentation
PP	Poster Presentation
PR	Participation only
AMDT	Advanced Microbial Diagnostics/Detection Tools
AIMA	AI in Microbiological Applications
CASD	Climate Change and Agroecosystem: Effect on soil microbial diversity
EIPR	Entrepreneurship and IPR
ENVM	Environmental Microbiology
FIM	Food and Industrial Microbiology
MN	Microbial Nanotechnology
MTAMR	Microbial Therapeutics and Anti-Microbial Resistance
MM	Microbiology for Mankind
MSD	Microbiology for Sustainable Development
PMI	Plant Microbe Interactions
VDL	Vaccine Development for Life
PCW & SCL	Pre-Conference Workshop and School Conclave
LS	Late Submission

CONTENTS

156.	ENVM23(PP)	Bioremediation and Detoxification of Xenobiotic Compounds (Heavy Metals and Pesticides) using Novel Bacteria **Phogat A** Kumari S, Singh T, Gohel S, Prasad R and Banerjee A	97
157.	ENVM24(PP)	Effect of Increasing Sulfate Concentration on Fe^{2+} Ion Oxidation Kinetics by *Leptospirillum ferriphilum* Dominated Chemostat Culture **Shatakshi Tiwari**, Sugandha Aachhera, Pradeep Verma and Chandra Sekhar Gahan	97
158.	ENVM25(PP)	Nitrite Transformation using Potential Microbial Consortium **Anne Bhambri,** Santosh Kumar Karn and Arun Kumar	98
159.	ENVM26(PP)	Development of a Chemical Optode for the Detection of *Escherichia coli O157:H7* from Drinking Water **Bandita Panda** and Sandip Kumar Dash	99
160.	ENVM27(PP)	Eco-Friendly Co-Composting of Chicken Feathers with Cow Dung Using Keratinolytic Bacteria for Nitrogen-Rich Organic Fertilizer Production **Subhash Chand,** Sunita Devi, Kumari Manorma, Megha Sharma, Puneet and Parul Sharma	99
161.	ENVM28(PP)	Antioxidant Activity of Phenolic Compounds Extracted from Rice Straw **Sujeeta**, Kamla Malik, Shikha Mehta and Pushpa Dhillon	100
162.	ENVM29(PP)	Isolation and Screening of Heavy Metal Resistant Bacteria from Different Industrial Sites **Swati,** Vinod Goyal and Jagdish Parshad Jangra	100
163.	ENVM30(PP)	Isolation and Characterization of Halophilic Microorganisms from Salt Affected Soil of Cauvery Command Area **Sushma N N,** Suman Jayakumar Kankanwadi and Asha N N	101
164.	ENVM31(PP)	Enhancing Salt Stress Tolerance in *Oryza sativa* (Var. Swarna) through the application of *Streptomyces griseoincarnatus* RB7AG **Subhransu Sekhar Behera,** Suchismita Nivedita, Pratyush Kumar Behera, Zahra Parwez, Seemon Giri, Sourav Ranjan Parida, Lopamudra Ray	101
165.	ENVM32(PP)	Evaluating chromium-resistant bacteria for mitigating heavy metal pollution: Insights into their potential for sustainable remediation and phytoremediation **Simranpreet Kaur Natt,** Priya Katyal, Sumita Chandel and Pooja Manchanda	102
166.	ENVM33(PP)	Extremophiles and Extremozymes- Their Unique Biocatalyst Applications for Sustainable Development **Divya Mori** and Nikita Sinh Gohil	102
167.	ENVM34(PP)	Assessing the Impact of IHBT-VHH4 PGPR on Heavy Metal Bioremediation and Plant Growth for Sustainable Agriculture **Priya Kaushal** and Aparna Maitra Pati	103
168.	ENVM35(PP)	Batch Bioleaching of Zinc From Zinc Sulfide Concentrate using Adapted Microbial Culture of Iron Oxidising Microorganism **Sugandha Aachhera,** Shatakshi Tiwari, Pradeep Verma and Chandra Sekhar Gahan	103
169.	ENVM36(PP)	*Gibbago trianthemae*: A potential plant fungal pathogen for management of hazardous weed *Trianthema portulacastrum* **Monika Chopra,** Madhu Choudhary, Vikas Kumar and Manoj Singh	104
170.	ENVM37(PP)	Novel Biosynthetic Secondary Metabolites from *Streptomyces sp.* LKIT: Potential Antimicrobial Agents for Healthcare Management **Sudhansu K Gouda,** Khushbu Kumari, Ananta N. Panda, Lopamudra Ray, Dinabandhu Sahu and Vishakha Raina	104
171.	ENVM38(PP)	Metagenomic Profiling Reveals Unprecedented Microbial Diversity in Extreme Hypersaline-Alkaline Lakes of Rajasthan **Lekh Raj** and Shiv Swaroop	105
172.	ENVM39(PP)	Polyhydroxyalkanoate production by Sambhar Salt Lake haloalkaliphiles **Mamta,** Vishalakshi Bhanot, Shobham, Abhimanyu Kumar and Jitendra Panwar	105

192.	ENVM59(PP)	Toxicity of Pollutant-Adsorped Polyethylene Microplastics on Zooplanktons with Artemia as a Model Organism **Aiswarya, K. P., R.** Karthika and S. Rajakumar	116
193.	ENVM60(PP)	Characterization of the Lipid and Fatty Acid Composition in Marine Cyanobacteria **Selvapriya, S.,** G. Muralitharan and S. Rajakumar	117
194.	ENVM61(PP)	Biofermentation of Human Serum Albumin using E. coli as Host and its Biotechnological Applications **Priya Payla** and Ashima Sharma	117
195.	ENVM62(PP)	Microbial Utilization of Fish Scales for Protease Production and Chitin Extraction **Neha Kumari** and Shashwati Ghosh Sachan	118
196.	ENVM63(PP)	Unravelling Fipronil Biodegradation using *Pseudomonas* sp. FIP_A4: Multiomics Approaches **Anjali Jaiswal** and Suresh Kumar Dubey	118
197.	ENVM64(PP)	Isolation and Identification of Polyhydroxybutyrate (PHB) Producing Bacterial Species Isolated from Soil Samples of Ujjain **Sheeba Khan** and Rekha Khanna	119
198.	ENVM65(PP)	Production of BHETase Hydrolases for Depolymerization of PET **Nishu Yadav,** Prashant Kumar and Deepansh Sharma	119
199.	ENVM66(PP)	Phenotypic and Genetic Insights into ESBLs, Carbapenemase-Producing, and Biofilm-Forming Gram-negative Bacteria in the Hospital and Domestic Wastewater of Aligarh City **Nikita Chaudhary** and Iqbal Ahmad	120
200.	ENVM67(PP)	Computational Screening of Photoprotective Compounds from Polar Psychrophilic Cyanobacteria **Vinotha K,** Rajakumar S, Muralitharan G and D. Prabaharan	121
201.	ENVM68(PP)	Isolation and Characterization of Cadmium Tolerant Plant Growth Promoting Rhizobacteria **Shreya Verma** and Manishi Tripathi	121
202.	ENVM69(PP)	Phycoremediation and Lipid Synthesis Using Marine Microalgae: Exploring Mixotrophic Growth with Diverse Carbon Sources and Effluent Waters **Vivek, N**, K. Nitharsan, D. Prabaharan, L. Uma, G. Muralitharan and T. Sivasudha	122
203.	ENVM70(PP)	A Study on Prevalence of Resistance Genes and Pathogenicity Markers among ESBL Producing *Enterobacteriaceae* Focusing *Klebsiella pneumoniae* **Vikar Ahmed,** Syed Ahmed Rizvi and Qazi Mohd Rizwanul Haq	122
204.	ENVM71(PP)	Sample Preparation Strategies for Extraction of Microbial Protein from Diverse Environmental and Clinical Matrices for Downstream Proteomic Analysis **Veer Vikram Prakash** and Syed Imteyaz Alam	123
205.	ENVM72(PP)	Indigenous Microbial Isolation for Chlorpyrifos Remediation of Contaminated Field Soils of Parbhani, Maharashtra **Sandeep Kumar Singh,** Livleen Shukla, Suaad Khadeeja, Brijesh Kumar Mishra, Aravindharajan S.T.M, Vijayashree D, Dolamani Amat and Ajay Kumar	124
206.	ENVM73(PP)	*Streptomyces* Mediated Synthesis of Silver Chitosan Nanocomposite for Antibiofilm Applications Subhransu Sekhar Behera**, Smaranika Pradhan,** Seemon Giri, Pratyush Kumar Behera, Zahra Parwez and Lopamudra Ray	124
207.	ENVM74(PP)	Chitosan as a Dietary Supplement: Evaluating its Effects on Zebrafish Physiology and Development **Zahra Parwez**, Subhransu Sekhar Behera, Seemon Giri, Pratyush Kumar Behera, Smaranika Pradhan and Lopamudra Ray	125
208.	ENVM75(PP)	Evaluating Biogas Production Potential of Cattle Dung Supplemented with Tea Waste under Batch Digestion **Mansi Phogat,** Shikha Mehta, Kamla Malik, Pragati and Raj Bala	125

226.	FIM4(OP)	Biomimetic Nanoparticles Influence *Listeria monocytogenes* Communication to Reduce Virulence and Biofilm forming Properties **Vaibhav Bharat Rokade**, Abhishek Kumar, Lalit Pratap Singh, Raghu HV and Shilpa Vij	135
227.	FIM5(OP)	Physicochemical Properties of Honey from Different Agro-Climatic Zones of Haryana **Manoj Kumar Jat**, Sunita Yadav and Harish Kumar	136
228.	FIM6(OP)	Characterization of a Novel Thermo-Acidophilic L-Asparaginase of *Pseudomonas aeruginosa* CSPS4 And its Applicability in Acrylamide Degradation in Starch-Based Food Products **Digvijay Verma**	136
229.	FIM7(OP)	Isolation of Probiotic Microorganisms with Antimicrobial and Bacteriocin Activity from Fermented Pearl Millet Porridge **Jamuna Elumalai,** Srividhya Srinivasan, V. Vijayageetha, Shibi Sebastian, R.Neelavathi, Arul Selvi and S. Thiruvarassan	137
230.	FIM8(OP)	Bioprospecting Sourdough Fermentation for the Alleviation of Irritable Bowel Syndrome (IBS) **Richa Arora** and Kritika Jain	137
231.	FIM9(OP)	Metabolome analysis of traditional Kombucha and its nutraceutical properties **Katyal P**	138
232.	FIM10(OP)	Saccharification and Isomerization Studies using Actinobacteria **Tannu Kushwah**[1*] and Sheetal Bhasin[2]	138
233.	FIM11(OP)	Thermal Inactivation of *Salmonella* during Manufacturing of High Milk Protein Cookie Baking Process Arshdeep Singh, Conor Hunt, Drushya Ramesh and **Lakshmikantha H. Channaiah**	139
234.	FIM12(PP)	Isolation and Characterization of Glucose Oxidase Enzyme from Fungal Source: Towards Enhanced Production **Pinakin Dhandhukia**, Heena Asfak Khan and Janki N Thakker	139
235.	FIM13(PP)	Fructosyltransferase Production by *Bacillus stercoris* S1 Isolated from *Stevia rebaudiana* for the Biocatalytic Conversion of Sucrose into Oligosaccharides Puneet and **Neha Gautam**	140
236.	FIM14(PP)	Rheological Study of Modified Guar Gum Cross-Linked with Nano Material for Gelling Agent Fracturing Fluid Application **Shishram Chahar,** Banwari Lal, Sivakumar Pandian, C Paul Jeyaseelan, K Nanthakumar, Veeranna Channashettar, Sunil Kumar and Mukesh Yadav	140
237.	FIM15(PP)	Modulating Permeability and Metabolic Efficiency: Unlocking the Industrial Potential of Bacterial Microcompartments **Komal Timane** and Chiranjit Chowdhury*	141
238.	FIM16(PP)	Functional Potential of *Toddy*, a Traditional Fermented Palm Beverage of India: an *in-silico* Metagenomics Study **Souvik Das** and Jyoti Prakash Tamang	142
239.	FIM17(PP)	Optimization of Xylanase Enzyme Activity using Response Surface Methodology **Monika sri S,** Vinuthana V H and Sivakumar Uthandi	142
240.	FIM18(PP)	Incidence and Virulence Characterization of the Emerging Pathogen *Cronobacter* Spp. in Seafood Sold in Fish Markets of Mumbai **Deeksha Bharti,** B.B. Nayak, Sanath Kumar H. and Manjusha L.	143
241.	FIM19(PP)	*Lactiplantibacillus plantarum* Mediated Millet-Rice Fermentation for Folate Fortification Antipathogenic and Anti-Inflammatory Effects **Priyadarshini Pratikshya Nayak** and Sandeep Kumar Panda	143
242.	FIM20(PP)	Evaluation of Microbial Quality of Masmin from Lakshadweep, India **Mohammed Ihzan M.P.,** Sanath Kumar H., Layana P., Fathima Salam and Nayak B.B	144
243.	FIM21(PP)	Statistical Optimization of Cellulase Production by *Aspergillus fumigatus* PSF1 under Submerged Fermentation (SmF) **Vinuthana V H,** Santhoshkumar Subramaniam and Sivakumar Uthandi	144

299.	MN14(PP)	Hydrogel Based Encapsulation and Antimicrobial Properties of *Bacillus cereus* NSD MTCC 10072 Derived Bioactive Compound **Renuka Sharma,** Bharti Sharma and Namita Singh	175
300.	MN15(PP)	Advancing Organic Farming: The Scope and Application of Nano-Biofertilizers **Ravi Kumar** and Tanvi Bhatia	175
301.	MN16(PP)	The Utilization of Bacterial Exopolysaccharides (EPS) for Nanoparticle Synthesis and Their Role in Human Health **Shikha Rana,** Swati Panchal, Roshan Mohiddin, Rashi Rastogi, Suman Kapila and Rajeev Kapila	176
302.	MN17(PP)	Unraveling the Mechanisms of Nanoparticles in Antimicrobial Therapeutics: Pathways to Enhanced Efficacy against Resistant Pathogens **Priyanka** and Tanvi Bhatia	176
303.	MN18(PP)	Antagonistic Activity of Silver Nanopaticles against Microbial Phytopathogens in Tomato Crop **Preeti Kaleramana,** Seema Sangwan, Pooja Swami, Mukesh Kumar and Kuldeep Kumar	177
304.	MN19(PP)	Multifunctional smart micronutrient nanomaterial for controlling phytopathogenic fungus **Monika,** Sumistha Das and Nitai Debnath	177
305.	MN20(PP)	Fabrication, Characterization and Anti-Rhizobial Activity of Green Synthesized Zinc Oxide Nanoparticles using *Trifolium alexandrinum* Leaves Extract Oshin Verma, Tejveer Singh, Radhakrishna Auji and **Ramesh Kumar**	178
306.	MN21(PR)	Production of Nanobiochar using Agro-Industrial Waste by Alliance of Nanotechnology **Ajay Kamboj,** Pardeep Kumar Sadh, Babli Yadav, Inderjeet Singh, Prabhat Kumar and Joginder Singh Duhan	179
307.	MTAMR1(OP)	Antibiofilm Potential of Farnesol against *S.aureus* MRSA **Nitika Bhasin,** Mohd Murtaza, Poonam Choudhary, Priya Kumari and Sundeep Jaglan	179
308.	MTAMR2(OP)	Detection of Carbapenem Resistant Genes among Carbapenem resistant *Pseudomonas aeruginosa* Clinical Isolates **Gaurav Verma,** Nipa Singh, Subhra Snigdha Panda, A Raj Kumar Patro, Dipti Pattnaik, Ashok K. Praharaj and Sukanta Tripathy	180
309.	MTAMR3(OP)	Investigation of G-Quadruplex DNA Motifs in the *Helicobacter Pylori* Genome and their Potential as a Target for Pharmacological Intervention Monika Kumari, Priyanka Payal, Neha R Sahu, Uma Shankar, Amit Kumar, Debasis Nayak, Sharad Gupta, Vikas Yadav and **Puja Yadav**	180
310.	MTAMR4(OP)	In Silico and In-vitro Analysis for Determining the Antibacterial Potential of Aztreonam against *Pasteurella multocida* Sialic Acid Protein Subodh Soni, Manjeet Chahar, Pooja Chugh, **Hari Mohan**	181
311.	MTAMR5(OP)	Impact of Food Based Antimicrobial Peptides against the Biofilm of ESKAPE Pathogens and Oral Bacteria through Invitro and In Silico Approaches **Indranil Chattopadhyay**	181
312.	MTAMR6(OP)	The Rational Approach to Multikinase Inhibitor Discovery for the Development of Resistance Immune Antimalarial Drugs **Dhaneswar Prusty**	182
313.	MTAMR7(OP)	Biosynthesis, Characterization and Anti-Biofilm Activity of Silver nanoparticles on *Staphylococcus aures* (MRSA) Prayrna Kulkarni, Rujula Deoghare and **Kedar Ahire**	182
314.	MTAMR8(OP)	Echinomycin, a Peptide Antibiotic from New Bacterial Source and its Potential to Tackle Drug Resistance in Methicillin-Resistant *Staphylococcus aureus* **Mohd Murtaza,** Nitika Bhasin, Priya Kumari, Avleen Kour, Poonam Choudhary, Manoj Kushwaha, Sandeep Sharma and Sundeep Jaglan	183

385.	MTAMR79(PP)	Biocontrol of *Salmonella Typhimurium* using predatory bacteria *Bdellovibrio*: *In vitro* predation and *in vivo* non toxicity tests in Zebrafish Dhanyashree Rai, Andrea Emilia Lobo, Anirban Chakraborty and **Divyashree M**	221
386.	MTAMR80(PP)	Cloning and Expression of Sserratiopeptidase Gene from *S. marcescens* AD-W2 in *E. coli* **Devtulya Chander** and Asha Chaubey	222
387.	MTAMR81(PP)	Identification of Potential Therapeutic Target of *Salmonella enterica* **Minal Bhalerao,** Aishwarya Davkhar, Sachin Agawane and Chiranjit Chowdhury	222
388.	MTAMR82(PP)	Antimicrobial Resistance: An Emerging Health Concern **Shreya Maheshwari, Kanika,** Raj Shayama, Shashwat Kumar and Shagun Chaudhary	223
389.	MTAMR83(PP)	Phage therapy: A Solution to AMR **Menal Jain and Vanshika Agrawal**	224
390.	MTAMR84(PP)	Comprehensive Analysis of Etiological Agents and Drug Resistance Patterns in Ventilator-Associated Pneumonia **Harendra K. Thakur,** Bansidhar Tarai and Manoj Kumar Jena	224
391.	MTAMR85(PP)	Repurposing of Anti-Fungal Drug -Nystatin- against Multi-Drug Resistant Bacterial Pathogens **Manya,** Neena Capalash and Prince Sharma	225
392.	MTAMR86(PP)	Harnessing Lactic Acid Bacteria for Bioactive Peptide Production: Enhancing Antioxidative Properties in Fermented Sheep and Goat Milk **Pudke Payal Udelal,** Maitri Goel, Harsh Panwar, Manvesh Kumar Sihag and Vikas Sangwan	225
393.	MTAMR87(PP)	Optimization of Submerged Fermentation Process for Enhancement of Lignocellulolytic Enzymes Production and Red Gram Stalk Degradation **Pratima S B,** Nagaraj M. Naik, Saroja N. Rao, Veeresh H, Pampanagouda, and Yallappa M	226
394.	MTAMR88(PP)	Anti-Diabetic Potential of Microbial Hydrolysis Derived Goat Milk Protein Hydrolysates **Maitri Goel,** Payal Pudke Udelal, Vikas Sangwan, Manvesh Kumar Sihag and Harsh Panwar	227
395.	MTAMR89(PP)	Isolation and Comparison Between Poultry Litter Isolated Bacteria in Terms of Antibiotic Sensitivity **Madhushree Ghorui,** K Rajendra R Roy and Rajib Bandopadhyay	227
396.	MTAMR90(PP)	Exploring Wheatgrass Phenolic Compounds as Promising Antimicrobial Agents in Understanding the Microbial Therapeutic Solutions **Manju Rani**, Jayanti Tokas, Shivangi and Sujeeta	228
397.	MTAMR91(PP)	Preclinical Evaluation of Encapsulated Bile Salt Hydrolase Consortium in Reducing Serum Cholesterol and Managing Weight Using in vitro and in-vivo Models **Pratisha P. Nair** and Uday S. Annapure	228
398.	MTAMR92(PP)	Emerging Challenges in Treating Neonatal Sepsis: Antimicrobial Activity and Pathogen Resistance **Vijay Laxmi,** Sheetal Verma, Vimala Venkatesh, Amita Jain, Shalini Tripathi, and Manoj Kumar	229
399.	MTAMR93(PP)	Bacteriophage and Antibiotic Combinations Effectively Inhibit *Escherichia coli* Biofilms **Damini Thakur,** Sushant Kumar Pal, Juhi Prasad and Lokender Kumar	230
400.	MTAMR94(PP)	Endophytic bacterial diversity associated with the roots of endemic *Viola odorata* **Richa Salwan** and Vivek Sharma	230
401.	MTAMR95(PP)	Structural Differences in Superoxide Dismutase Enzyme of Chilling Tolerant & Chilling Sensitive Isolates of Arthrospira using in-silico Approach **Kanu Priya** and Namita Singh	231

402.	MTAMR96(PP)	Optimization of Bacteriophage Dosing against Multidrug-Resistant *Klebsiella pneumoniae*: Insights from MOI and Time-Kill Curve Assays for Therapeutic and Prophylactic Applications **Prexha Kapoor**, Bhupendra Kumawat, Karan Bhutani, Rinku Chaudhary, Priya Sharma, Ruma Rani, B.C. Bera, R. K. Vaid, Nitin Virmani and Taruna Anand	231
403.	MTAMR97(PP)	Production, Purification, and Application of Bacteriophage Endolysin Proteins against Drug-Resistant Bacteria **Ruma Rani,** Prexha Kapoor, Karan Bhutani, Rinku Chaudhary, Priya Sharma, B.C. Bera, R. K. Vaid, Nitin Virmani and Taruna Anand	232
404.	MTAMR98(PP)	Targeting Integrase to Improve Phage Therapy Against MDR *E.coli* : A Step Toward CRISPR-Mediated Lysogeny Control **Priya Sharma,** Rinku Chaudhary, Prexha Kapoor, Ruma Rani, Karan Bhutani, Jyoti Gupta, B.C. Bera, R.K. Vaid, Nitin Virmani and Taruna Anand	232
405.	MTAMR99(PP)	Comparative genomic characterisation of multidrug-resistant (MDR) *Escherichia coli* bacteriophages for phage therapy, research and prophylaxis" **Karan Bhutani,** Prexha Kapoor, Rinku Chaudhary, Ruma Rani, Priya Sharma, Nitin Virmani, B.C. Bera, .K. Vaid, Taruna Anand	233
406.	MTAMR100(PR)	Effect of Lactic Acid and Peroxyacetic Acid on Biofilm Formation Ekta Sehgal**, Anju Kumari,** Anil Panghal, Rakesh Kumar and Ritu Sindhu	234
407.	MM1(OP)	Waste to Wealth: A Novel Approach to Sustainable *Catla catla* Aquaculture using Probiotics Consortium from Fruit and Vegetable Peels **Nikita Goyat** and Baljeet Singh Saharan	234
408.	MM2(OP)	The multi subunit Cascade Protein of CRISPR-Cas System in *Escherichia coli*: The Expendables **Neha Pandey**, Chitra S Misra, and Devashish Rath	235
409.	MM3(OP)	Microbiology Applications in Forensic Sciences: A New Paradigm in Investigation **Neetu Sharma** and Jaskaran Singh	235
410.	MM4(OP)	High-risk HPV testing vs Liquid-Based Cytology for Cervical Cancer Screening among Adult Women in Vadodara Region, Gujarat **Gunjan Shrivastava**	236
411.	MM5(OP)	Impact of Mode of Delivery on the Quality and Quantity of Microbial Population Present in Human Colostrum **Riteshkumar Arya** and Komalben Hirani	236
412.	MM6(OP)	Mycochemistry, Antioxidant, Anticancer activity and Molecular Docking of Compounds of F12 of Ethyl Acetate Extract of *Astraeus asiaticus* with BcL2 and Caspase 3 **Koushik Pandey** and Swapan Kumar Ghosh	237
413.	MM7(OP)	Anti-oxidative Activity of Bioactive Peptides Produced from Pearl Millet Fermentation using *Lactobacillus* sp. **Meena Sindhu,** Anil Panghal, Sushil Nagar and Ajay Kumar	237
414.	MM8(OP)	Lytic-Lysogenic Switches Cross-Regulation in *Listeria monocytogenes* 10403S **Avijit Das** and Anat A. Herskovits[1]	238
415.	MM9(OP)	Assessment of Biofortified Compost from Agricultural Residue on Growth of Mungbean (*Vigna radiata* L.) **Kamla Malik** and Shikha Mehta	238
416.	MM10(PP)	Microplastics in Human Urine Sample: Detection and Implications using Raman Spectroscopy Suresh Subramanium, Sai Karthik, and **Nandhini Babu**	239
417.	MM11(PP)	Public Health Implications of Bacterial Zoonotic Infections from Pigeons in and Around the Nilgiris, Tamil Nadu, India Nandhini. B, Susmitha S. and **Suresh. B**	239

475.	MSD29(PP)	Potato Waste Valorization for Gluconic Acid Production Using Microbial Consortium: A Step towards Waste to Wealth **D. Vijaysri,** Livleen Shukla, S. T. M. Aravindharajan, S. H. Manoj and Sandeep Kumar Singh	271
476.	MSD30(PP)	Isolation and Screening of Lignocellulolytic Enzyme Producing Bacteria from Hydrilla Compost **Sunaina Kumari,** Monika Kayasth and Jagdish Parshad	271
477.	MSD31(PP)	Harnessing Phragmites Biomass: A Sustainable Strategy for Chilika Wetland Ecosystem Management and Conservation **Deepsikha Panigrahi** and Vishakha Raina	272
478.	MSD32(PP)	Unravelling Methanogens Evolution: A Comparative Study of Phylogenetic Methods **Rashmi Dhanwar,** Ujjwala Wagmare, Dimple Davray and Om Prakash	272
479.	MSD33(PP)	Exploration of Pigmented Endophytic Fungi from Medicinal Plants for Sustainable Production of Bioactive Red Chromes and Testing of their Potential as Cosmetic Colourants **Mehak Kaur** and Dr Mayurika Goel	273
480.	MSD34(PP)	Physiological Characterization of Fish Scale Degrading Bacteria from the Marine Environment **Pragati Shetty**, Manjusha L, Amjad K. Balange, B.B. Nayak and Sanath Kumar H	273
481.	MSD35(PP)	Optimisation of the Production Parameters of a Novel Heteropolysaccharide Obtained from *Periconia* sp., RA1 an Endophyte of Native Rice Variety **Hiran Kanti Santra** and Debdulal Banerjee	274
482.	MSD36(PP)	Acid-Tetrahydrofuran-Organosolv Sequential Two-step Microwave-Assisted Pretreatment for Lignocellulosic Biomass Fractionation to Valuable Platform Chemicals: A Circular and Sustainable Approach **Lakshana G Nair** and Pradeep Verma	275
483.	MSD37(PP)	Enrichment-Based Isolation and Identification of 4-Chlorophenol Degrading Bacteria from Industrial Polluted Soil **Ritu Rani** and Dharmender Kumar	275
484.	MSD38(PP)	Ammonia Oxidation by Ammonia-Oxidizing Bacteria (AOB), *Staphylococcus* Sp. **Arti Chamoli** and Santosh Kumar Karn	276
485.	MSD39(PP)	Bacterial Pigment: Sustainable alternative to Synthetic Dyes **Shruti. B. Mhaske** and Rohini.P. Kulkarni	276
486.	MSD40(PP)	Optimization of Cultivation Conditions and Upstream Bioprocess Development for Higher Production of Recombinant Clostridial Cellulolytic Chimeric Enzyme (*Ct*GH1-*Ct*GH5-F194A) **Vishwanath Yadav** and Arun Goyal	277
487.	MSD41(PP)	Molecular Characterization and Bioremediation Potential of Isolated Cadmium-Resistant *Pseudomonas* Strains from Industrial Sludge **Sachin Malik** and Dharmender Kumar	277
488.	MSD42(PP)	Adaptive Laboratory Evolution to Enhance Tolerance of *Saccharomyces cerevisiae* against Furfural **Sukhwinder Singh**, Sukesh Chander Sharma and Tanzeer Kaur	278
489.	MSD43(PP)	Process Development for Converting Rice Straw into Biofertilizer Formulation for Sustainable Agricultural Practices **Jyoti Yadav,** Sanjiv Kumar Soni, Raman Soni and Deepak Kumar Rahi	278
490.	MSD44(PP)	Extraction of Renewable Biochemicals from Enzolv Pretreated Cotton Stalk Using Column Chromatography **Santhoshkumar Subramaniam,** Kumutha Karunanandham and Sivakumar Uthandi	279
491.	MSD45(PP)	Bioinformatics Analysis Reveals Pathways Involved in Ethanol Tolerance in *Saccharomyces cerevisiae* during Ethanol Fermentation **Amandeep Kaur,** Sukesh Chander Sharma and Sonia Bhonchal Bhardwaj	280

510.	MSD64(PP)	Optimization of Cellulase Production Using Response Surface Methodology from *Bacillus pumilus* Strain FZM Isolated from Fecal Sample of Spotted Deer (*Axis axis*) Shaikh Mohammedfaizan, Maaz Ahmed and **Krishan Kumar**	290
511.	MSD65(PR)	Valorising Agro-Waste into High-Value Nutraceuticals: A Pathway to Sustainable Nutrition Babli Yadav, Pardeep Kumar, Prince Chawla, Ajay Kamboj and **Joginder Singh Duhan**	290
512.	PMI1(OP)	Effect of *Priestia flexa* IIRRPSB14 Phosphate Solubilizer on the Growth and Development of ISM rice cultivar **Bandeppa S,** P.C. Latha, Amol S Phule, V. Manasa, R. Gobinath, K. Surekha, G. Rajani, M.B. Kalyani, M.B.B Prasad Babu and R. M. Sundaram	291
513.	PMI2(OP)	Synergistic Interactions and Metabolic Activities of Bacterial Isolates in Rhizoremediation of Heavy Metals **Jagdish Parshad,** Monika Kayasth and Baljeet Singh Saharan	292
514.	PMI3(OP)	Shift in Tree Species Leads to Dramatic Changes in the Belowground Fungal Communities in Boreal Forests **Sunil Mundra**	292
515.	PMI4(OP)	Optimizing *Bacopa monnieri* Micropropagation: the Role of Plant Growth Regulators as Catalysts for Enhanced Development **Avni Dahiya,** Namita Singh, Subhash Kajla, Madhu Choudhary and Adhisha	293
516.	PMI5(OP)	Role of Rhizosphere Methylotrophic Bacteria in Rice Plant Growth Promotion and Improvement of Soil Health **Kavya T,** Geeta Singh and Venkadasamy Govindasamy	293
517.	PMI6(OP)	Biotechnological Potential of Bifunctional *Pantoea* sp. for Developing Sustainable Agriculture System in Arunachal Pradesh **Bhagyashree Bora,** Takam Akash, Refad Ahmed and Natarajan Velmurugan	294
518.	PMI7(OP)	Rhizospheric Soil Micobiome of Landrace and Domesticated Wheat Variety of North-Western India Cultivated Under Phosphate Stress **Garcha S,** Garg S, Srivastava P and Mavi GS	295
519.	PMI8(PP)	Assessment of Drought Tolerant Bacteria for Sustainable Production of Mustard in Alkaline Soils of South- West Haryana **Tanvi Bhatia,** Abhinav Saini, Ankush Sharma, Ashwani Sharma, Pinki and Simran Alimer	295
520.	PMI9(PP)	Investigating the Biocontrol activity of Marine Actinobacteria against Fungal Pathogen *Fusarium Oxysporum Pallidoroseum* in Saline Conditions **Parth Ahir,** Hazel Mendes, Kushboo Rathod, Pinakin Dhandhukia and Janki N. Thakker	296
521.	PMI10(PP)	Prospecting the Role of Non-Rhizobial Bacterial Endophytes in Enhancing Soybean Growth and Nodulation Efficiency **Kirti Suman,** Hirudhaya Ravi, Pushpendra Sharma, Meena Rathore and Rajeev Kaushik	296
522.	PMI11(PP)	Enhancing Wheat Resilience: The Role of Halotolerant Exopolysaccharide Producing Bacteria under Salt Stress **Suman Jayakumar Kankanwadi,** Sushma N N and Leela Wati	297
523.	PMI12(PP)	Relationship between Electrical Conductivity, pH and Microbial Soil Enzyme Activity in Salt Affected Agricultural Fields of Lentil **Deepak Sharma,** Madhu Choudhary, Rakesh Kumar, Vijayata Singh and Awtar Singh	298
524.	PMI13(PP)	Synergistic Impact of Multi-trait *Kosakonia* sp. and *Serratiamarcescens* in Improving Maize (*Zea mays*) Germination and Root Morphology under Drought Stress **Ashish Kumar** and Ajay Veer Singh	298

525.	PMI14(PP)	Salicylic Acid Pretreatment Elevates the Endogenous Concentration of Salicylic Acid to Protect against *Fusarium oxysporum*-Led Biotic Stress in *Vigna Mungo*: Transcriptomics and Molecular Insights of Defense Pathways **Lucky Duhan,** Ritu Pasrija, Deepak Kumar and Raman Manoharlal	299
526.	PMI15(PP)	Identification and Characterization of Cyanobacterial Isolates from the Himalayan Region for Plant Growth Promotion **Srishti Yaduvanshi,** Shobit Thapa and Smriti Mall	299
527.	PMI16(PP)	Exploring Biocontrol and Plant Growth Promoting Potential of Multifaceted PGPR against the Causal Agent of Alternaria Blight for Agricultural Sustainability **Sheetal Alchoni** and Ajay Veer Singh	300
528.	PMI17(PP)	Assessing the Drought-Tolerance, Growth-Promoting Potential of Strawberry (*Fragaria Ananassa* Duch.) Rhizobacteria for Consortium Bioformulation **Vinay Kumar Dhiman** and Neerja Rana	301
529.	PMI18(PP)	Comparative Analysis for Plant Growth Promoting and Biocontrol Traits in *Bacillus carbialesii* strains Isolated from Rhizosphere Soil of Chickpea **Prajwal S.K.,** Sushil K. Sharma and S.K. Jain	301
530.	PMI19(PP)	Examining *Microcella putealis* for its Biotic and Abiotic Defense Mechanisms in Conjunction with the Promotion of Plant Growth **Meetkunwar Dahiya,** Pinakin Dhandhukia and Janki N. Thakker	302
531.	PMI20(PP)	Plant Growth Promoting Traits of Marine Bacteria with Bio-Control Capability against *Fusarium sp.* in Cowpea Plant **Bhasha Choksi,** Archita Patel, Pinakin Dhandhukia and Janki Thakkar	303
532.	PMI21(PP)	Rhizobial and Passenger Nodule Endophytic Bacteria in Combination with Acyl Homoserine Lactones Enhances the Groundnut Growth and Yield **Madhan S,** Yuvasri E A, Anandham R, Balachandar D, Johnson I, Vincent S and Senthil Kumar M	303
533.	PMI22(PP)	Exploring the Root Microbiome of Wheat and Barley in Hot and Cold Desert Ecosystems of India: Potential for Enhancing Drought Tolerance **Udita Pushpad,** Pushpendra Sharma, Riwika Das, Minakshi Grover and Rajeev Kaushik	304
534.	PMI23(PP)	Root Iron Plaques as Potential Inducers of Plant-Microbe Interaction and Fe-Biogeochemistry in Paddy Soil **Subhra Satahrada,** Ritesh Pattnaik	305
535.	PMI24(PP)	Nano Bioremediation of Arsenic in Rice: Combining Arsenic-Resistant Bacteria and Zinc Oxide Nanoparticles for Rice Improvement under Arsenic Stress **Rahul Beniwal,** and Ramakrishna Wusirika	305
536.	PMI25(PP)	Impact of Rice Cultivation Systems on Bacterial Abundance, Microbial Metabolic Activity and Growth of Succeeding Chickpea Crop: A Comparative Study under Transplanted and Direct-Seeded Rice **Koj Haniya,** Vijay Pooniya and Karivaradharajan Swarnalakshmi	306
537.	PMI26(PP)	Endophytic Fungal Community of *Rosa damascena* Mill. as a Promising Source of Indigenous Biostimulants: Elucidating its Spatial Distribution, Chemical Diversity and Ecological Functions **Abid Bashir, Farha Bhatii,** Maryam Banoo, Syed Riyaz-Ul-Hassan	306
538.	PMI27(PP)	Mesorhizobial Inoculation and Fertilizer Application Influence Microbial Community Structure and Function in Chickpea Rhizosphere **N.S. Nysanth,** Koj Haniya, M. Senthil Kumar, Vijay Pooniya, C. Viswanathan and K. Swarnalakshhmi	307
539.	PMI28(PP)	Exploring the Role of *Nepenthes Khasiana* Endophytes in Organic Phosphate Mineralization and Plant Growth Promotion **Kiran Dhiman**, Shiv Shanker Pandey and Jeremy Dkhar	308
540.	PMI29(PP)	Ecosystem Services of PGPR in sustainable production of Fenugreek (*Trigonella foenum -graecum* L.) Ravinder and **Mohd Kashif Kidwai**	308

559.	PMI48(PP)	Plant-Soil-Microbe Interactions in Sustaining Ecosystem Stability and Coordinated Biogeochemical Turnover amidst Environmental Change **Rohit Nain** and Shweta Laura	318
560.	PMI49(PP)	Screening of Chilli Rhizosphere Bacterial Isolates for their Beneficial Traits and Volatile Bioactive Compounds **Mohankumar Udagi,** Nagaraj M. Naik, Mahadevaswamy, Pampangouda and Prabhuraj A	319
561.	PMI50(PP)	Metagenomic Profiling of Soil Bacterial Communities to Study the Impact of Nitrification Inhibitors on Functional Gene Diversity and Nitrogen Cycling **Sriram Lakshmanan**, Devi Priya Arumugam and Sivakumar Uthandi	320
562.	PMI51(PP)	Studies on the Physicochemical Parameter's Optimization of Indole-3-Acetic Acid Using Cost-Effective Medium by Pantoea Agglomerans CPHN2 One Factor at a Time Approach **Chetna Rathi,** Simran Rani, Priyanka Dahiya and Pooja Suneja	320
563.	PMI52(PP)	Enhanced Nutrient Uptake in Saline Conditions with Mycorrhizal Soil Application in Wheat (*Triticum aestivum*) **Sujata Yadav**, Anita Mann, Priyanka Chandra, Ashwani Kumar and Parvender Sheoran	321
564.	PMI53(PP)	Deciphering Plant Growth-Promoting Traits in Rhizobial Endophytes across Diverse Soybean Genotypes (*Glycine max*) Cultivated in Central India **Hirudhaya Ravi,** Kirti Suman, Pushpendra Sharma, Meena Rathore and Rajeev Kaushik	321
565.	PMI54(PP)	Diversity of Arbuscular Mycorrhiza (AM) fungi and their Application for Sustainable Cultivation of Some Endangered Medicinal Plants of Meghalaya **Nilufa Afruza** and Dhritiman Chanda	322
566.	PMI55(PP)	Exploring the Structural Diversity of Root-Colonizing and Soil-Inhabiting Arbuscular Mycorrhizal Fungi in Acidic Soils of North-East India **Priya M,** Subrata Nath Bhowmik and Rajeev Kaushik	323
567.	PMI56(PP)	A Comparative Transcriptomic Approach to Unravel the Molecular Basis of Cotton's Response to CLCuD **Ramandeep Kaur,** Satish Kumar Sain and and Priyanka Siwach	323
568.	PMI57(PP)	Understanding Microbial Contributions to GABA Dynamics in Tomato Rhizosphere **Ejeoghene Rita Ogbimi,** Tanushri Kaul and Rashmi Kaul	323
569.	PMI58(PR)	Thermal Stress Adaptability Study in Whiteflies in Relation to Climate Resilience-A Review Prabhat Kumar, Rishi Kumar, Debashis Paul, **Priyanka Siwach,** Sunita and Rahul Kumar	324
570.	VDL1(OP)	Web-based Predictions and328 Experimental Validations of T cell and Antibody Epitopes In *Mycobac329terium tuberculosis*-Specific Proteins330 **Abu Salim Mustafa**	235
571.	VDL2(OP)	F gene Based Genetic Characterisation of Newcastle Disease Virus Isolated from *Pavo cristatus* **Anubha Sharma,** Aman Kumar, Sushila Maan and Namita Singh	325
572.	VDL3(PP)	Evaluating Inflammation in In Vivo Zebrafish Model: A Promising Therapeutic Approach **H Thamarai Kannan** and Ieshita Pan	326
573.	VDL4(PP)	The Therapeutic Vaccine Potential of Live Recombinant *Lactococcus Lactis* Secreting Murine Ifnλ3 against Influenza Type A Virus (IAV) Infection **Sandeep Yadav** and Amirul Islam Mallick	327
574.	VDL5(PP)	Reverse Vaccinology-Machine Learning (RV-ML) Based Discovery of a Highly Protective Protein-Based Vaccine Antigen against Methicillin Resistant *Staphylococcus aureus* (MRSA) **Pranaya M. Mishra,** Suman Chaudhary, Ravi S. Manhas, Diksha Sharma, Manoj K.Baranwal and Ravi P.N. Mishra*	327

575.	VDL6(PP)	Immunoinformatics Approach for Designing a Multi-Epitope Peptide Vaccine against Drug-Resistant *Acinetobacter Baumannii* **Shiv Nandan Sah,** Neha Bhardwaj, Neena Capalash and Prince Sharma	328
576.	VDL7(PP)	Investigating the Role of Protein Phosphate 5 Catalytic Subunit PPP5C Gene in Vesicular Stomatitis Virus (VSV) Lifecycle Using Short Hairpin RNA (Shrna)- Mediated Knockdown **Himanshi Bilwal**	328
577.	VDL8(PP)	From COVID to Cancer: The Role of mRNA Technology in Oncology **Ayushi Malik, Annu**	329
578.	LS-1	Screening and Assessment of Rhizospheric PGPR Strain of *Chakhao*, With Different PGP Characteristics **Sushma Khaidem** and Menaka Devi Salam	330
579.	LS-2	Effect of Adenine Sulphate on Growth and Secondary Metabolites Profile of Callus Cultures of *Ficus Religiosa* L. **Anita Rani Gill1** and Priyanka Siwach	330
580.	LS-3	Isolation of Endophytic Fungi from Cichorium Intybus and Determination of Their Phosphate Solubilization Ability Abdusamatov Sokhibjon**,** Numonjon Sultanov, **Jabborova Dilfuza**	331
581.	LS-4	Immunohistochemical Detection of *Pasteurella Multocida* in Ruminants with Respiratory Illness Rakshita Sharma, Gulshan Narang, **Paras Saini**, Babu Lal Jangir, Deepika Lather and Vikas Nehra	331
582.	LS-5	Isolation and Characterization of Endophytic Bacteria from Capparis Spinosa L. **Jabborova Dilfuza**, Namita Singh, Baljeet Singh Saharan	332
583.	LS-6	Isolation of Endophytic Fungi from Different Organs of *Rosa Canina L.* and Determination of their Some Extracellular Enzyme Activities Abdusamatov Sokhibjon,Numonjon Sultanov, **Jabborova Dilfuza**	332
584.	LS-7	Therapeutic potential of gut microbiota-derived p-Cresyl Sulfate for the treatment of colorectal cancer **Manish Kushwaha**, Akhilesh Kumar Singh,JyotiJaiswal, Anil Kumar	333
585.	**LS-8**	Targeting Dephospho Coenzyme A Kinase (DPCK) in *Leishmania donovani*: Discovery and Validation of steroidal alkaloids as Potent anti-leishmanial drugs **NaveenaMenpadi,** Pranjal Chandra, Vikash Kumar Dubey	334
586.	**LS-9**	Potential plant growth-promoting rhizobacteria 35ccumula the Cadmium stress tolerance in Tomato (*Solanum lycopersicum* L.) **Rajganesh Marappa**, Rahul Krishnappa, Renuga Selvakumar, Srinivas Chowdappa	334
587.	**LS-10**	Green Synthesis of Zinc Oxide Nanoparticles from Clitoriaternatea and its Bioactive Potential Rahul Krishnappa, Rajganesh Marappa, Renuga Selvakumar, **Srinivas Chowdappa**	335
588.	**LS-11**	Isolation and Identification of *Stenotrophomonas maltophilia* from Upper Respiratory Tract of Equines **Sumanshu**, Ritu Rani, Jyoti Bakshi, Taruna Anand, R.K. Vaid	335
589.	**LS-12**	Influence of Chemicals and Bioagents on Physiological Parameters under Drought Stress in Upland Cotton (*Gossypium hirsutum L.*) **Ande Aravind Reddy**, Shiwani Mandhania, Vikram Singh, Rashi Datten, and Arman Khan	336
590.	**LS-13**	*Monas cuspurpureus*: A Potential Source for Natural Pigment Nikita**, Aastha Dewan**	336
591.	**LS-14**	*In silico* bio-prospecting and Chemoinformatics Screening of Potential Inhibitors Against Drug Resistant *Acinetobacter baumanii* And *Pseudomonas Aeruginosa* **Sinosh Skariyachan**	337
592.	**LS-15**	Development of Whey-Kodo Millet Based Probiotic Product and Its Bioactivities **Nikita Yadav*,** Aayushi Rohilla, Savi Khurana, Navnidhi Chhikara	337

593.	AWA14	A promising approach for food safety and food pathogen control **Namita Singh**, Madhavi Chahar, Vinay Gupta	74

INVITED TALK

NS-AMDT-1

Smart Sensing Platforms for SARS-CoV-2

Sonu Gandhi
gandhi@niab.org.in

National Institute of Animal Biotechnology, Department of Biotechnology
Ministry of Science & Technology, Gachibowli, Hyderabad, Telangana, India

Abstract: COVID-19 pandemic has emphasized the need for the development of a rapid diagnostic device for the effective treatment of COVID-19 for its mitigation. Diagnostic devices which has the benefit of providing quick results, easy to handle, low cost, and on-site detection. So far, several techniques have been developed for the detection of infectious SARS-CoV-2, however, only few of them are antigen-based. Here, I will be discussing mainly the biosensors which we have developed in our laboratory. We have developed in-house RBD protein via molecular biology tools, in-house RBD antibodies, high-affinity aptamers to develop diagnostic platforms for biosensing of SARS-CoV-2 in clinical samples. The fabricated sensor platforms were optimized for different parameters for its efficient detection capabilities. The optimized sensors were validated in spiked buffer samples and the optimal limit of detection was calculated. Moreover, the developed platforms effectively detected RBD antigen (Ag) in clinical samples with high sensitivity and specificity in clinical samples when compared with gold standard (RT-PCR). The fabricated LFIA are reported to have storage stability of up to 21 days at 4˚C and room temperature (RT) and hence, can be used as a portable, cost-effective diagnostic device for rapid detection of SARS-CoV-2.

Keywords: COVID-19 pandemic; SARS-CoV-2; RBD protein; Molecular biology; Smart sensing platforms

IS-AIMA-1

Practical Bioinformatics: Case Studies of the Microbial World of Gas Production Wells

Bharat K. C. Patel
bharat.patel@qut.edu.au; bharatgu19@gmail.com

Centre for Agriculture and the Bioeconomy (CAB), School of Biology and Environmental Science,
Queensland University of Technology, Brisbane (4001), Australia

Abstract: The Great Artesian Basin (GAB) of Australia is one of the largest subsurface aquifers in the world occupying 1.7 million km² (22% of the Australian land mass). Distinctly different microbial communities have evolved and adapted to a variety of physiochemically heterogeneous ecosystems of the GAB which include temperatures (ambient to boiling), pH (neutral to alkaline), chemicals (iron, chlorides, carbonates, sulfates) and gasses (methane, carbon dioxide, carbon monoxide, hydrogen sulfide, hydrogen and oxygen). Over the past 30 years our lab has cultured a range of taxonomically new and standard microbes including extremophiles but their diversity, evolution and adaptation mechanisms and physiology has remained poorly understood. The introduction of high throughput Next Generation Sequencing (NGS) in 2010 has revolutionised the development of bioinformatics and computational infrastructure and has challenged our views on biological systems and life on earth. In the last 5 years, bioinformatics and computational infrastructure has developed rapidly. Bioinformatics programs are written as human readable scripts (python, R and perl) which are portable and can be easily cloned to many computers as opposed to the older versions of machine codes which had to be compiled with computer hardware making them non-portable. Separate environments to avoid conflicts can now be easily created with mamba and analysis processes initiated as workflows with snakemake, docker etc. The microbiology community should be able to add bioinformatics to the arsenal of tools that are already routinely available to them (e.g., visualization techniques with microscopes, measurement techniques with spectrophotometers, chromatography separation techniques for molecules etc) and not view them than as a separate, high-end science. This paper will focus on (a) the installation and workflow of bioinformatics tools used in our studies and (b) discuss the microbial habitat, ecology, taxonomy and metagenomics of metal-petroleum-methane-dominated gas fields and a gas industry waste-water settling pond of GAB in relation to the presence of overall gene families / metabolic pathways, and genomes of the most dominant microbes, their metabolic pathways and possible functions in this specific environment and how these studies could assist in the potential storage of carbon that is emitted from coal-fired power stations.

Keywords: Bioinformatics; Microbes; Gas production wells; Great Artesian Basin; Australia

IS-AIMA-2

Next Generation Sequencing and Bioinformatics Analysis for the Characterization of Pathogenic Bacterial Genomes

Abu Salim Mustafa
abu.mustafa@ku.edu.kw

Department of Microbiology, College of Medicine, Kuwait University,
PO Box 24923, Safat (13110), Kuwait

Abstract: The success in determining the nucleotide sequence of a pathogenic bacterial genome was first achieved in 1995 by sequencing the complete genome of *Haemophilus influenzae* strain Rd (genome size = 1.83 Mb) by Fleischmann et. al. The methodology used in these experiments was the first-generation DNA sequencing technology using chain-terminating dideoxy nucleotide analogs, which was established by Sanger et al. in 1977. However, the first-generation DNA sequencing technology is laborious, costly and time consuming. After 2000, next generation sequencing (NGS) technologies have been developed for whole genome sequencing (WGS) to provide efficient and cost-effective results. WGS provides the details of an organism's genetic makeup and includes all the coding and non-coding sequences and regulatory regions present in the genome. In the recent years, the technological advancements have drastically reduced the cost of WGS by using NGS. Furthermore, WGS coupled with the bioinformatics analysis (BA) of the sequenced genomes have been projected to revolutionize clinical microbiology practices. The WGS technologies can be used in identification of bacterial species from cultured specimens and directly from clinical specimens. Furthermore, WGS and appropriate bioinformatic tools are used for strain identification and genotyping of pathogenic bacteria. It can also help in detection of antimicrobial resistance mechanisms, identification of virulence factors, and epidemiologic tracking of organisms. In this conference, data will be presented from our lab related to pathogenic bacteria covering all of the above-mentioned applications of WGS and BA.

Keywords: Next generation sequencing; Bioinformatics analysis; Pathogenic bacterial genomes

NS-AIMA-1

A Fuzzy Based Artificial Intelligence based Decision Making Approach from Pixel Values to Detect Caries from Digital X- rays Data

Avnesh Verma
verma.avnesh@gmail.com

Department of Electrical Engineering, Kurukshetra University, Kurukshetra (KUK)
Haryana, India

Abstract: Dental caries are caused by bacterial invasion on the tooth surface. It involves dissolution and destruction of calcified tissues. Early detection is the only way out to control this disease. Most commonly it can either be investigated by visual inspection or through X-rays. X-rays investigation is more precise and accurate, but the chances of human error and accurate diagnosis are still not possible with naked eyes. To make it more precise image processing techniques are used. It has been investigated AI system based on fuzzy logic and final diagnoses can be derived. A comparative study of four edge detection techniques; Sobel, Prewitt, Roberts and Canny have been made for better outcomes. For caries detection Grayscale pixel values matrix were formed and results have been analysed through fuzzy. The fuzzy controller has proved to be an intelligent system in diagnosis and the results were much more precise. The pixels were accurately judged and outputs were as expected. The fuzzy controller has proved to be intelligent system in diagnosis and the results were much more precise. The pixels were accurately judged and outputs were as expected.

Keywords: Dental caries; Artificial Intelligence; Pixel values; X- rays; Fuzzy controller

IS-CASD-1

Shift in Tree Species leads to Dramatic Changes in the below Ground Fungal Communities in Boreal Forests

Sunil Mundra
sunilmundra@uaeu.ac.ae: sunilmundra@hotmail.com

Department of Biology, College of Science, United Arab Emirates University, Al-Ain, Abu-Dhabi, UAE

Abstract: Summary: Trees and understory vegetation are tightly connected with belowground microbiota and these interactions are susceptible to change in tree species. Replacements of native birch with exotic Norway spruce has been initiated in Norway to increase long-term carbon storage, with limited knowledge on belowground impacts. We examined the impact of the tree species shift (birch to spruce) on the belowground microbial communities, fungal biomass, and their relationship with vegetation biomass and soil organic C (SOC) along a soil depth gradient (up-to 30cm). Replacement of birch with spruce negatively influenced the bacterial and fungal richness and strongly altered compositional patterns in the forest floor layer, most strikingly for fungi. Tree species-mediated variation in soil properties was a major driver for bacterial communities. For fungi, both soil chemistry and understory vegetation were important structuring factors, even more pronounced for ectomycorrhizal (ECM) fungi compared to saprotrophs. The relative abundance of ECM and ECM: saprotrophic fungi ratio, were higher in spruce compared to birch stands, particularly in the deeper mineral soil layers, and vice versa for saprotrophs. The positive relationship between ergosterol and SOC stock in forest floor layer suggests higher C sequestration potential in this layer of spruce forests, which further affects ecosystem functioning.

Keywords: Boreal forest; Carbon and nitrogen stock; Downy birch (*Betulapubescens*); Fungal guild; Ectomycorrhiza; Norway spruce (*Piceaabies*); Tree species effects

IS-CASD-2

Thermophilic Microorganisms from the Geothermal Environments of Chile and Antarctica with a Potential Role in Food and Agriculture in a Climate Change Context

Aparna Banerjee[1*], Patricio Arce-Johnson[2]
*aparna.banerjee@uautonoma.cl

[1]*Universidad Autónoma de Chile, Instituto de CienciasAplicadas, Facultad de Ingeniería, sede Talca, Talca, Chile*
[2]*Instituto de CienciasAplicadas, Facultad de Ingeniería, Universidad Autónoma de Chile, Santiago, Chile*

Abstract: To adapt to the time of changing climate, one of the sustainable development goals of United Nation is to ensure food security, improved nutrition, and promoting sustainable agricultural practices. Microbes play a pivotal role in this goal not only via maintaining the world´s biogeochemical cycles, but also as a plant growth promoting bacteria (PGPB) endorsing sustainable agricultural practices and their bioproducts in food processing improving nutritional qualities. Geothermal environments, such as hot springs, hot soils, and fumaroles, host diverse thermotolerant bacteria that produce unique exopolysaccharides (EPS) as a part of their survival strategy under extreme environments with potential biotechnological applications. Our study focuses on the EPS-producing bacterial strains from geothermal sites in Chile and Antarctica, evaluating their potential as natural additives in the food industry. Bacterial strains were isolated from the different hot springs in Chile, Andean mountain-regions soils, as well as from the fumaroles and hot soils of Deception Island, Antarctica. The antioxidant, emulsifying, flocculating, and gel-forming properties of the EPS were assessed using standard techniques. Significant antioxidant and β-glucosidase inhibition activities, forming viscoelastic gels at acidic pH, indicated potential applications of the EPSs as a natural food additive. Good thermal stability and emulsification properties of the EPSs suggested their utility as bio-based emulsifiers and stabilizers in food products. Whereas, Deception Island, Antarctica-origin bacteria demonstrated notable antioxidant and emulsifying activities. The EPS produced by thermotolerant bacteria from Chilean and Antarctic geothermal environments was also used for encapsulating PGPB strains and their consortium and was observed for

improved growth and yield in Chilean local common bean varieties under increased temperature, drought, and salinity. Common beans contain significant amounts of plant proteins, fibres, vitamins; improved yield under climate change context using biostimulants ensure food security and foster sustainable agriculture. The findings promote bioprospection of geothermal ecosystem-origin microbes with broad industrial applications in food and agriculture.

Acknowledgement: Fondecyt Regular 1231917, INACH Regular RT_24-21
Funding: Proyecto Anillos de Investigación ANID-2024. Code: ATE230007
Keywords: Thermophiles; Geothermal environments; Chile; Antarctica; Climate change

IS-CASD-3

Revitalizing Contaminated Soils: Harnessing Fly Ashes to Enhance Soil Microbiota and Ecosystem Health

Łukasz Drewniak*, Szymon Rzuczkowski, Monika Dang, Dawid Gmitter, MikołajIwan
*drewniak2@uw.edu.pl

Department of Environmental Microbiology and Biotechnology, Institute of Microbiology, Faculty of Biology, University of Warsaw, ul. Miecznikowa 1, 02-096 Warsaw

Abstract: Coal fly ash (CFA), a byproduct of coal combustion, constitutes 65–95% of the total waste generated during coal-fired power production. With an annual global output of approximately 800 million tons, CFA is predominantly produced in China (500 million tons), India (140 million tons), and the United States and European Union combined (115 million tons). While around a quarter of this global production finds economic applications in industries such as metallurgy, construction, and agriculture, the remainder is typically stored long-term in industrial heaps or landfills. One significant barrier to the broader industrial utilization of CFA is its residual unburned carbon content, often in the form of polycyclic aromatic hydrocarbons (PAHs) like naphthalene, fluoranthene, anthracene, and phenanthrene. These PAHs contribute to the toxicity of CFA, with established carcinogenic and toxic effects on living organisms. In addition to organic contaminants, stored CFA also contains heavy metals (Pb, As, Hg, Cd, Se, Cu, Cr, Ni) and valuable rare earth elements (REEs) such as Nd, Y, La, and Gd. The unique composition and alkaline nature of CFA suggest its potential as a soil amendment for the reclamation of agricultural and industrial lands.
This presentation will explore the potential benefits, limitations, and risks associated with the use of CFA in soil improvement. Key topics include the impact of CFA on soil structure, permeability, and aeration, particularly in heavy soils such as clay. Additionally, the enrichment of soil with essential trace elements and the regulation of soil pH through the alkaline properties of CFA will be discussed. The presentation will also address the implications of CFA application on soil microbiota structure and activity, and the broader consequences for soil ecosystem functioning.

Funding: The National Science Centre under the OPUS grant no. 2022/45/B/NZ9/02018 entitled Fly ash management - microbiological degradation of unburned coal.
Keywords: Contaminated Soils; Coal Fly Ash; Soil Microbiota; Ecosystem Health

NS-CASD-1

Nanobiofertilizer for Next Generation Agriculture for Enhancement of Wheat and Rice Growth and Soil Health

Ramakrishna Wusirika*, Anagha Karunakaran, Yaraa Fathima, Pallavi Singh, Rahul Beniwal, Jyoti Singh
*rk.wusirika@cup.edu.in

Department of Biochemistry, Dean Incharge Academics, Central University of Punjab, Ghudda, Bathinda, Punjab, India

Abstract: The excessive use of chemical fertilizers by farmers is harmful for soil, plant and human health and environment. Organic farming, biofertilizers and nanofertilizers are viable alternatives. Here, we employed an

innovative approach of employing nanobiofertilizer which is a combination of Plant Growth Promoting Bacteria (PGPB) belonging to *Bacillus* sp. CP4 and mesoporous silica, zinc oxide and copper oxide nanoparticles to enhance HD3086 wheat variety and black wheat growth, biofortification and soil health in a greenhouse study.Various morphological parameters, chlorophyll, proline, protein, nitrogen, and phosphorus, along with the nutrients Mg, Ca, Mn, Fe, Cu, Zn, and Se content of leaves, soil organic carbon, invertase, and dehydrogenase showed significant increase in treated plants. The ZnO NP based nanobiofertilizer showed the best results followed by mesoporous NP based nanobiofertilizer. The same bacterial isolate in combination with ZnO showed similar enhancement in rice growth. Rice tends to accumulate arsenic about ten time higher than other crop plants. A *Bacillus infestans* isolate when used in combination with ZnO counteracted the effects of arsenic thereby improving plant growth parameters. The development of a nanobiofertilizer as a biotechnological advancement is a step towards next generation agriculture.

Keywords: Agriculture; Plant Growth Promoting Bacteria (PGPB); Nanobiofertilizer; *Bacillus* sp. CP4

NS-CASD-2

Cold Deserts of NW Himalayas: Gold Mines for Microbial Cell Factories

Asha Chaubey
achaubey@iiim.res.in

Fermentation and Microbial Biotechnology Division, CSIR-Indian Institute of Integrative Medicine, Jammu (180001), Jammu & Kashmir, India
India Academy of Scientific and Innovative Research, CSIR-Human Resource Development Centre, (CSIR-HRDC) Campus Ghaziabad (201002), India

Abstract: Himalayas are recognized as a highly diverse region in terms of geographical as well as biological aspects. These include evergreen forests, lakes, hot springs, cold deserts, glaciers, grass lands etc. NW Himalayas thus provide unique terrestrial habitats in its sub-zero temperature, ice caped mountain peaks, oligotrophic nutrients and limited vegetation. These conditions create competitive environment for the isolation of novel microbial species and/or novel biochemical scaffolds to be used as new antimicrobials. The need to find novel, crucially significant molecules for pharmacology has consequently dramatically increased. Due to the high rediscovery rate of known compounds from microbes inhabiting conventional environments, there has been a renewed interest in the exploration of untapped regions of the Himalayas, more specifically the Northwestern Himalayas, for the production of new secondary metabolites for rare and novel actinobacteria about the urgent need to combat the increasing number of multidrug-resistant human pathogens. The presentation will include the strategies and highlights of the institute for exploration of microorganisms from the under-explored cold desert regions of NW Himalayas of India.

Keywords: NW Himalayas; Cold deserts; Bioactives; Antimicrobials

NS-CASD-3

Antagonist Bacteria against Phytopathogens and Nematodes: A Boon for Organic Farming

Surender Singh
surendersingh@cuh.ac.in

Department of Microbiology, Central University of Haryana, Mahendergarh, Haryana (123031), India

Abstract: Indiscriminate use of pesticides in the agriculture led to severe environment contamination. These agro-chemicals enters into the food chain causing many diseases and also reduces export potential of many crops. Recent emphasis on natural and organic farming have renewed the interest in biocontrol agents for controlling the plant diseases and nematodes. The antagonistic bacteria have the potential to control many soil-borne pathogens like *Macrophomina* and *Fusarium* in different crops. The antagonistic bacteria against the

devastating pests like root knot nematodes have also been explored. The antagonistic bacteria employ different strategies like production of enzymes, organic compounds, antibiotics, cyclic peptides etc. to effectively control the proliferation of fungi and nematodes. Use of the selected antagonistic agents demonstrated their efficacy against soil-borne pathogens in cotton and root know nematode in tomato. Furthermore, the bacteria also showed PGP activities like siderophore production and P solubilization. The liquid formulation of these agents can be stored at room temperature without losing viability. The use of the selected antagonistic bacteria will help in reducing pesticide consumption and improving the crop yield of selected crops.

Keywords: Antagonistic Bacteria; Phytopathogens; Nematodes; Organic farming

NS-CASD-4

Potential of Native AM Fungi in Enhanced Crop Production and Soil Carbon Sequestration Assessed under Soybean-Based Cropping System

Mahaveer P. Sharma
mahaveer620@gmail.com, Mahaveer.Sharma@icar.gov.in

ICAR-Indian Institute of Soybean Research, Khandwa Road, Indore, Madhya Pradesh (452001), India

Abstract: Global change, partly mediated by the agricultural intensification is the foremost challenge to sustain the agricultural production in the long run. The atmospheric CO_2 concentration has crossed 400 ppm which is much above the upper safety limit of 350 ppm. Agricultural farms have been ranked second when it comes to global GHG emissions. Adoption of suitable agricultural practices coupled with biological interventions could help in reduction of ever-growing atmospheric CO_2 concentration by sequestering soil carbon and enhance productivity of agricultural lands. One such important mechanism counts the role of arbuscular mycorrhizal fungi (AMF) which is a ubiquitous group of fungi that by forming symbiotic relationship with about 80% of land plant species benefits plants in terms of nutrient acquisition, disease resistance, drought tolerance etc. AMF hyphae grow deep down in soil to absorb nutrients beyond the reach of plant and make them available to plants. Apart from growth promoting attributes, AMF also produce copious amount of a sticky glycoprotein termed as 'glomalin' that stabilizes soil aggregates and acts as C sequester in the soil. However, the extent to which carbon is sequestered in soil by AMF is driven by many factors and depends on agricultural practices, soil type edaphic factors, climate, microbial flora etc. For example, when soybean intercropped with maize found to have higher AMF biomass and sustained the system productivity. The conservation tillage practices have also promoted the AMF biomass. It was observed that AM fungi inoculation in maize grown in intercropping with soybean particularly under organic practice enhances AMF biomass assessed microscopically and through the AM signature fatty acid biomarkers i.e., phospholipid and neutral lipid fatty acid 16:1ω5cis. Apart, from this the stocks of soil organic carbon and glomalin were also found to be the highest in the same system. Microbial biomass carbon and the activity of soil enzyme β-glucosidase were also found to be higher under AMF inoculated plots managed with organic practice. The system was also accompanied by lower CO_2 emissions. In another study, dealing with a long-term field experiment managed with organic, inorganic and integrated nutrient management practice having soybean-wheat (S-W) and soybean-chickpea (SC) rotation, we explored the role of native AMF species in SOC sequestration. It was observed that both integrated and organic practice of the SW system and the organic practice of the SC system harboured the highest SOC, glomalin stocks, AMF signature lipids biomass, microbial biomass carbon, and associated enzymes. Furthermore, the plots of organic practice were recorded with the lowest CO_2 emissions. These findings justify the functioning of glomalin which together with AMF hyphae works as a soil particle binding machinery and sequesters carbon therein without compromising soil quality. Thus, it is concluded that AMF by producing glomalin sequesters excess soil carbon in the root zone remain stable enough to prevent its release into the atmosphere and sustain the productivity of soybean-based cropping systems.

Keywords: Soybean-based cropping system; Native AM fungi; Glomalin; AM signature fatty acids; Soil carbon sequestration

NS-EIPR-1

Patents in Microbial Research

Indrani Ghosh
indrani.ipu@niscair.res.in

Guru Gobind Singh Indraprastha University, New Delhi, India

Abstract: Patent protection gives the researcher an impetus to work progressively and contribute towards Nation's scientific upliftment. The objective of patent law is to encourage inventions by promoting their protection and utilization for the development of industries and to foster an environment to flourish creativity and innovation. It stimulates new inventions of commercial utility and gives credit to its innovator. The patent gives inventor monopoly on its invention for a period of twenty years. Patent right is territorial in nature and therefore it needs to be protected in each country separately where the invention finds commercial potential and use. Patent obtained in one country cannot be enforced in another country. In order to meet the legal requirement of sufficiency of disclosure, patent applications and patents must disclose in their description the subject-matter of the invention in a manner sufficiently clear and complete to be carried out by the person skilled in the art. Many researchers are so much involved in their innovation that they fail to realise that their invention can reap multi-fold benefits, both academically and industrially. Most of the Academic researchers have a primary goal of getting their work published in scientific journals and fail to understand the interplay between publishing and patenting. With the advancement of Microbiological research and IPR regime it is very important for all the researchers to understand the Patenting system and its requirements.

Keywords: Patents; Microbial research; Academic researcher; Invention

NS-EIPR-2

From Lab to Market: Opportunities for Microbio-Entrepreneurs and StartUps

Prince Sharma
prineesah@gmail.com

Department of Microbiology, Panjab University, Chandigarh, India

Abstract: StartUps and Bio-Entrepreneurship are the initiatives that GoI is pushing for young generation. Microbiology has a lot to contribute in this initiative. Enzymes, Vaccines, Eco- and Health- friendly Cosmetics, Repurposed drugs, Antimicrobial Peptides, PoC Biosensor based diagnostic kits, Biosensors in food industry are some examples of microbiological products which have a huge market and whose CAGR is growing rapidly. A big opportunity is waiting for budding microbiologists to enter this market and be the microbio-entrepreneurs. This talk is on the journey of my lab for the patenting and successful transfer of technologies to industry; current collaborations with industry to develop vaccines, PoC biosensor kits, cosmetic products and Antimicrobial Peptides. The market is wide open for microbiologists/researchers to take a leap for StartUps.

Keywords: StartUps; Bio-Entrepreneurship; Microbiological products; Microbio-entrepreneurs

NS-EIPR-3

Role of DBT, Govt. of India in Human Resource Development in India and Writing Good Research Proposals: An Overview"

Sanjay Mishra
sanjaykr.mishra@nic.in

Department of Biotechnology, Government of India

Abstract: The Department of Biotechnology (DBT), under the Government of India, has played a transformative role in human resource development within the fields of biotechnology and life sciences.

Established with the aim to foster research and innovation in biotechnology, DBT has implemented numerous initiatives to support, train, and encourage scientists, researchers, and students across India. Through strategic programs and funding, DBT has been pivotal in addressing skill gaps, promoting interdisciplinary research, and enhancing India's capacity in biotechnology research and development.

DBT's initiatives for human resource development focus on fostering talent at various educational and professional stages. These include fellowship programs, research scholarships, and hands-on training schemes for students, young scientists, and established researchers. For instance, DBT's STAR College Scheme, Junior Research Fellowships (JRF), and the Biotechnology Industry Research Assistance Council (BIRAC) offer financial and technical support to nurture scientific skills and innovation. Such programs aim to create a skilled workforce that can address complex scientific challenges and contribute to India's socio-economic development. Through its partnerships with academic institutions, DBT facilitates infrastructure development and knowledge-sharing, creating an ecosystem conducive to advanced research and development.

An essential component of DBT's strategy for human resource development is the emphasis on research proposal writing. DBT recognizes that effective proposals are key to obtaining funding and driving impactful research. As such, Ding sessions, workshops, and mentorship programs are regularly conducted to enhance research offers guidance and resources to researchers on developing high-quality research proposals. Trainchers' skills in articulating clear research objectives, methodologies, and potential outcomes. These initiatives not only improve the quality of proposals submitted to DBT and other funding agencies but also increase the chances of securing financial support for promising projects. DBT's focus on proposal writing has led to an increase in research quality, encouraging scientists to address key issues with innovative and practical solutions.

In summary, DBT's role in human resource development and research proposal training has had a profound impact on India's biotechnology sector. By investing in talent, supporting infrastructure, and promoting high-quality research proposals, DBT has contributed to positioning India as a global leader in biotechnology research and innovation. Looking forward, DBT aims to continue enhancing India's research landscape by fostering a new generation of skilled professionals who can leverage biotechnology to address critical challenges in health, agriculture, and environmental sustainability.

Keywords: BIRAC, DBT, JRF, Human Resource Development, Schemes

IS-ENVM-1

Agnihotra and Microorganisms - Effects on Environment, Agriculture and Climate Change

Ulrich Berk
dr.ulrich.berk@homatherapie.de

President, German Association of Homa Therapy, 78357 Mühlingen, Germany

Abstract: Environmental Pollution and Climate Change are two of the biggest problems of our time, and all of us are affected in several ways. A method coming from Ancient Vedic Knowledge called Agnihotra offers an answer to this challenge in many areas, especially in the fields of environmental sciences, in agriculture, and medicine.

Our objective is to examine these statements from Ancient Vedic Knowledge using methods of Modern Science.

What is Agnihotra?

Agnihotra is a method of purification through the agency of fire which is prepared in a copper pyramid of fixed size and shape. Only cow dung, cow's ghee and rice are burnt. The process has to be done exactly at the time of sunrise and sunset, and specific vibrations (mantras) are part of it.

Both the process of Agnihotra and the resulting Agnihotra Ash are said to have beneficial effects on the environment.

The presentation will show results we got so far in these areas:

Air

Agnihotra reduces bacteria in indoor environment. Using Settle Plate Method and blood agar as medium it was shown that pathogenic micro-organisms and total microbial load of indoor air were reduced.

Water

Water gets purified by Agnihotra and Agnihotra Ash.

Coliform bacteria in water got considerably reduced both by keeping the water next to Agnihotra as well as adding Agnihotra Ash.

Soil

Harmful fungi in soil are controlled whereas beneficial bacteria multiply if Agnihotra Ash is added to the soil. Adding Agnihotra Ash resulted in increase in the overall bacterial flora, including the effective bacteria i.e nitrogen fixers and phosphate solubilisers while reduction in the fungal flora was seen.

Microflora and microfauna in soil helps to sequester carbon from the atmosphere, thus helping to combat Climate Change and to bringing Nature back to Harmony.

Human Health

Also, some preliminary studies show that multi drug-resistant strains of *E. coli* are reduced by Agnihotra Ash, and the virulence of harmful bacteria is decreasing.

A pilote study revealed that even in case of HIV infected children there was a considerable improvement. Their general health became much better, and also the viral load could be reduced.

A recent study done in Germany with organ-specific cell cultures shows that Agnihotra Ash

- Reduces the effect of free radicals from our environment
- Improves the defence function of neutrophil granulocytes in the blood against foreign germs
- Leads to an improvement of cell vitality

All these findings are preliminary results; more research is required and will be suggested.

Keywords: Agnihotra; Ancient Vedic knowledge; Purification; Environment

IS-ENVM-2

Persistent Organic Pollutants in the Environment: Insights into Impact and Sustainable Remediation Strategies

Sonam Paliya
sonampaliya140@gmail.com

Institute for Organic Biogeochemistry in Geo-Systems, RWTH Aachen University, Germany

Abstract: Persistent Organic Pollutants (POPs) are a class of toxic chemicals that persist in the environment, bioaccumulate in living organisms, and pose significant risks to human health and ecosystems. Their widespread distribution, long-range transport, and resistance to degradation have made them a global concern. This talk delves into the environmental behavior of POPs, emphasizing their sources, pathways, and the multifaceted impacts they exert on natural systems. Drawing on recent advancements, we will discuss the intricate mechanisms through which these pollutants interact with abiotic and biotic components, causing long-term ecological disruption. In light of the urgency to mitigate POP contamination, this talk also provides a comprehensive overview of current and emerging remediation strategies. These include chemical, physical, and biological approaches, with a particular focus on sustainable techniques such as bioremediation. We will discuss the efficacy, feasibility, and scalability of these solutions, highlighting innovative methods that minimize secondary pollution and energy consumption. By integrating scientific insights with practical applications, this talk aims to inform about the path forward in addressing the persistent threat posed by POPs, ultimately fostering a more resilient and sustainable environmental management framework.

Keywords: Persistent Organic Pollutants (POPs); Emerging contaminants; Toxicity; Sustainable; Remediation

IS-ENVM-3

Navigating the Landscape of Fuels and Chemicals from Solid Waste

Sunita Varjani
drsvs18@gmail.com; sunita.varjani@ddn.upes.ac.in

School of Engineering, UPES, Dehradun, Uttarakhand (248 007), India
School of Health Sciences and Technology, UPES, Dehradun, Uttarakhand (248 007), India
Korea University, 145 Anam-ro, Seongbuk-gu, Seoul 02481, Republic of Korea
Institute of Chartered Waste Managers, Gopalpura Bypass, Jaipur, Rajasthan (302019), India

Abstract: The escalating generation of municipal solid waste (MSW) presents both a challenge and an opportunity within the framework of a circular bioeconomy. As environmental concerns mount, there is a

growing imperative to repurpose waste into renewable energy sources. Modern waste management has transformed from a focus on mere disposal to innovative approaches that emphasize energy recovery and recycling. The integration of Waste-to-Energy (WtE) technologies not only mitigates reliance on imported fossil fuels but also promotes the generation of clean, sustainable energy in an economically viable manner. This talk will explore the landscape of fuels and chemicals derived from MSW, highlighting the importance of a biorefinery model that effectively recycles materials while considering the environmental implications of various energy recovery technologies. Key challenges in identifying the most efficient WtE methods will be addressed, alongside insights from simulations conducted using ASPEN Plus, which investigated the gasification process of MSW to produce syngas. Preliminary findings indicate that optimal syngas yields occur at temperatures exceeding 800°C. A detailed discussion of these results will shed light on the potential pathways toward a sustainable bioeconomy through effective waste management strategies.

Keywords: Biorefinery; Circular Bioeconomy; Waste-to-Energy (WtE); Syngas; ASPEN Plus

IS-ENVM-4

Application of Bacterial Technologies in Environmental Processes

Zainul Akmar Bin Zakaria
zainulakmar@utm.my

NS-ENVM-1

Biotreatment of Extreme Ecological Niche by Diversified Native Microbial Consortia

Ragini Gothalwal
ragini_gothalwal@yahoo.com

Professor & Head, Coordinator
Department of Biotechnology, Barkatullah University, Bhopal, Madhya Pradesh, India

Abstract: As the global population grows, so too do the demands for water for drinking, sanitation, farming and energy production among many other users. At the same time human activity and climate change are disrupting natural water cycles putting fresh water ecosystem under pressure pollution, infrastructure development and reserve extraction pose additional challenges (Davidsen, 2014). In India, lots of idols are worshiped with all rituals in different time in a year. Afterwards these are immersed into water bodies. The material used for making idols have led to use of non-biodegradable material like POP, plastic, thermacol synthetic colour, synthetic fiber etc., which deteriorates the water quality (Kishor et. al., 2014). Moreover, the chemical dyes used to paint these idols contains heavy metals which are potentially hazardous.

The current agricultural practices are heavily dependent on the application of synthetic fertilizer and pesticide. Intensive tillage and over irrigation which have helped to meet the food requirement of the peoples. In spite of that increased environmental & health problem, which includes deterioration of soil fertility, executive use of pesticides and also increased cost of agricultural production (Vanessa et. al. 2009). These soils are unproductive, impermeable and hard due the presence of undesirable pollutants on the soil surface and called extreme soil. Pesticide contaminated soil has high pH and high electrical conductivity and are deficient in organic carbon, Na, K, and Phosphors. Nostoc 00246 strain is very useful in agricultural applications and because of their N2 fixation activity, extracellular polysaccharides, photosynthesis system and particularly desiccation tolerance ability and their property help to improve the quality of nutrient poor soils Cynoformulation can enhance the N2, phosphors and potassium content in soil and they play a very important role in plant metabolism such as cell division, growth and development, breakdown of sugar and nutrient transport within the plants.

Quorum sensing bacteria produces and release chemical signal modules termed auto inducer whose external concentration increases as a function of cell density. Quorum sensing thus enable bacteria to coordinate and respond quickly to environmental changes, such as the availability of nutrients other microbes or toxins in the environment. The mix consortium of *Micrococus* sp. GS2-22, *Corynebacterium* sp. GS5-66, *Flavobacterium* sp. DS5-73, *Bacillius* sp. DS6-86 and *Pseudonomonas* sp. degraded maximum 78% of BH crude oil of 1% crude oil concentration at 33^0C and pH 7.5 (Rahman et. al. 2002). On the comparative study on the biodegradation of 2,6-dichlolorophenol indophenol of bacterium consortium and individual bacteria, the consortium showed the fastest utilization of 2,6-dichlolorophenol than the individual isolate (Varjani and Upasani, 2013). The study involves

biodegradation of benzene, diesel, hexane, petrol, toluene and xylene. This approach could be a milestone between labs and field trial as a bioremediation technology in term of biofilm and biosplling in future.
Most contaminated sites are generally contaminated with multiple pollutants rather than a single type and harbour a variety of different environmental condition for biological activity, Therefore, bioremediation using a single type of microorganism after results in failure due to low biodegradability adaptively and viability of the applied microorganism in a contaminated site with diverse environment condition. However, there limitation may be easily overcome by the application of a native microbial consortium containing of multiple sps. with diverse biodegradation ability for different types of pollutants. A native-consortia was tried which can serve as promising for remediation of plastic and heavy metal degradation, dye decolourisation as no microorganism has been reported that can bioremediate all these together. The major advantage is low cost, low technology technique which generally has a high public acceptance and can often be operated on site.

Keywords: Bioremediation; Extreme ecological niche; Native microbial consortia; Biodegradation

NS-ENVM-2

Greenhouse Gases to Biomolecules: Key Role of Methanotrophs

Sanjay Kumar Singh Patel
sanjaykspatel@gmail.com; sanjaykspatel@hnbgu.ac.in

Department of Biotechnology, Chauras Campus, Hemvati Nandan Bahuguna Garhwal University (A Central University) Srinagar, Uttarakhand (246174), India

Abstract: Greenhouse gas (GHG) emissions, particularly methane (CH_4) and carbon dioxide have been a significant environmental concern in recent years due to their contribution to global warming and climate change. However, one potential solution to mitigate these emissions is the production of methanol by methanotrophs. Methanotrophs, a unique group of bacteria, can convert greenhouse gases, specifically methane, into valuable biomolecules such as methanol. These microorganisms thrive in anaerobic environments, playing a crucial role in the biogas upgrading process through the anaerobic digestion of biowastes. Biogas, a product of anaerobic digestion, is primarily composed of CH_4 and carbon dioxide. This renewable energy source can be further upgraded to value-added biomolecules. The microbial communities responsible for this upgrading process have been the subject of extensive research, revealing the presence of diverse metabolic pathways and potential syntrophic interactions. The advancement in synthetic microbial designing, protein engineering, and immobilization strategy can be helpful for the up-scaling of CH_4-based biomolecules. Further, the engineered *Escherichia coli* strains have also demonstrated the potential to utilize methanol, a byproduct of methanotroph activity, to produce various metabolites. The intriguing interplay between methanotrophs, methanogens, and engineered microbial platforms holds promise for the development of sustainable biogas upgrading systems and the production of valuable diverse types of biomolecules from GHGs.

Keywords: Greenhouse gas (GHG) emissions; Methanotrophs; Anaerobic digestion; Biomolecules

NS-ENVM-3

Boost the Production of Biogenic Methane in Coalbed Methane Wells

Banwari Lal* and Meeta Lavania
*banwaril@teri.res.in

Environmental and Industrial Biotechnology, The Energy and Resources Institute, Darbari Seth Block, IHC Complex, Lodhi Road, New Delhi (110 003), India

Abstract: Coalbed methane (CBM) represents a significant portion of the world's natural gas reserves, and it has been suggested that up to 20% of the world's natural gas, including CBM, is microbial in origin. Little is understood regarding microbial processes of upstream of methanogenesis, especially which microorganisms are responsible to hydrolyse the coal. This process can also be stimulated by injecting only nutrient recipe into CBM wells to stimulate the microbial community responsible for hydrolysis to produce volatile fatty acids and methanogens to produced methane. Studies were conducted to determine the function of microorganisms found in association with methanogens in CBM reservoirs.

In view of the benefits of microbial process for conversion of coal to methane in the CBM wells, with a specific objective of isolating and developing native microbes to generate methane from coal seams. The studies were conducted with ONGC CBM Asset Bokaro for isolation and development of the thermophillic anaerobic microorganism for enhanced methane production. Two consortia (CBM50-03 and CBM50-08) were developed after numerous enrichment cycles at 50°C with coal as sole carbon sources and one consortium at 65°C were developed for detailed studies to test their ability for methane production by coal as carbon source. Two set of processes were developed and optimized in the laboratory and subsequently taken up for field trials in Jharia CBM block:

1. Bio-stimulation: Injection of nutrient solutions to stimulate the indigenous microbial consortia for enhanced methane production.
2. Bio-augmentation: Injection of theromophillic anaerobic microbial consortium with nutrient for enhanced methane production.

Bio-stimulation job was carried out in 12 CBM wells in ONGC Jharia and Bokaro and cumulative methane production from CBM wells were reported significant increase. Another CBM process used was "Bio augmentation" which implemented in one ONGC CBM well at Jharia and reported more production from its pre job production. These developed processes have great potential and could provide a gaseous fuel which is clean and less carbon intensive.

Keywords: Biogenic methane; Coalbed methane wells; Bio-stimulation; Theromophillic anaerobic microbial consortium; Bio-augmentation

NS-ENVM-4

Harnessing the Potential of Hydrogenotrophic Methanogens in Carbon Sequestration and Climate Risk Mitigation

Om Prakash
prakas1974@gmail.com

Symbiosis Centre for Climate Change and Sustainability, Symbiosis International (Deemed University), Gram: Lavale, Tal: Mulshi, Pune, Maharashtra (412115), India

Abstract: Methanogens belong to the third domain of life known as Archaea. Similar to bacteria, they are prokaryotes but different in several respects from bacteria. Methanogenesis or biomethanation are the unique features of this group of organisms, which are generally lacking in other microorganisms. Based on the substrate utilization for energy generation they are classified as Acetoclastic, Methylotrophic or Hydrogenotrophic. Excess release of carbon in the form of greenhouse gases is the major culprit for global warming and climate change. The impacts of climate change are visible in the form of ocean acidification, increasing sea levels, changing patterns and intensity of rain, strong storms, biodiversity loss and hampered ecosystem functionality. Methane is a potent greenhouse gas with several fold higher greenhouse potential than carbon dioxide. Hydrogenotrophic methanogens have special significance in climate risk mitigation due to carbon sequestration with simultaneous methane generation. In the present talk, I will discuss the cultivation and characterization methods along with an assessment of the carbon sequestration and methane generation ability of hydrogenotrophic methanogens. Finally, I will discuss how to harness the carbon sequestration ability of this group of methanogens for climate risk mitigation with high-quality biogas generation.

Keywords: Hydrogenotrophic Methanogens, Carbon Sequestration, Mitigation

NS-ENVM-5

अभाव से समाधान तक: Microbial Magic for Sustainable Industry and Environment

Naveen Gupta
ng.puchd@gmail.com

Chairperson, Department of Microbiology Panjab University, Chandigarh, India

Abstract: "Imagination and creativity are more important than knowledge, for knowledge is limited to what we already know and understand, while imagination embraces the entire world and all there is yet to discover." By

approaching science creatively, we can extend its reach from the classroom to the laboratory and, ultimately, to society.

Through collaboration with the Chandigarh Administration and industry, several societal challenges were addressed economically using simple microbiological techniques.

In modern cities, most sewage water is treated in sewage treatment plants (STPs). However, even after treatment, much of this water is discharged into natural water bodies. Tertiary-treated sewage water (TT water) holds the potential for alternative uses such as irrigation, construction, service stations, and recreational activities like lake replenishment. However, several issues arise when using treated water for these purposes:

1. Improper treatment and irregular monitoring of STP efficiency
2. Excess nutrients such as phosphates and nitrates, leading to eutrophication
3. The growth of sulfate-reducing bacteria (SRB), which causes foul odors

These problems were addressed using microbiological knowledge. Over the course of one year, the STPs of Chandigarh were regularly monitored, and it was concluded that management, rather than technology type, determines the quality of treated water. With specific recommendations, the quality of the treated water improved significantly.

In exploring the possibility of using TT water for the management of Sukhna Lake in Chandigarh, a comparison was made between the quality of TT water and the lake water. The TT water was found to be suitable in all respects except for an excess of nutrients. A technology was developed using denitrifying and phosphate-solubilizing bacteria, which completely removed these nutrients from the TT water. The Chandigarh administration has taken note of this work and is exploring the potential of using treated sewage water to help preserve Sukhna Lake.

While TT water is already being used for irrigation in Chandigarh, foul odor remains a significant issue. A process was developed to reduce the growth of SRBs through aeration and the addition of safe chemicals, which led to the complete removal of odor from the TT water. The Municipal Corporation has adopted this process and plans to implement it to eliminate the foul smell.

Additionally, an enzyme consortium was developed in the laboratory to manage solid waste from the Sabzi Mandi (vegetable market) of Chandigarh.

Further work has led to the development of environmentally friendly industrial processes through the isolation of novel microorganisms and enzymes. These innovations are being applied in biobleaching of pulp, bioremediation of industrial effluents, dehairing of animal skin and for developing chemical-free hair dyes. Pilot-scale trials are being conducted in collaboration with various industries.

These applications highlight how microorganisms and knowledge of Microbiology can be harnessed to solve issues directly impacting society.

Keywords: Microbes; Sustainable development**;** Sewage Treatment Plants (STPs); Chandigarh

NS-ENVM-6

Bacterial Assisted Heavy Metals Phytoextraction Potential of Native Plants and their Histological Observation Growing on Distillery Sludge: A Novel Green Technology Tool for in-situ Phytoremediation of Hazardous Industrial Waste Management for Eco-restoration

Ram Chandra
prof.chandrabbau@gmail.com

Department of Environmental Microbiology, School of Earth and Environmental Sciences, Babasaheb Bhimrao Ambedkar University (A Central University), Lucknow, Uttar Pradesh (226 025), India

Abstract: The pollutants discharged from sugar mills and distilleries are a major threat to the environment due to their complex organo-metallic waste. The study revealed that distillery sludge contains not only mixture of complex organic pollutants but also retains a high quantity of Fe (5264.49), Zn (43.47), Cu (847.46), Mn (238.47), Ni (15.60), and Pb (31.22 mg kg−1) which aggravate the toxicity of sludge to the environment. The major identified organic pollutants were benzene, 1-ethyl-2-methyl, benzene, 1-ethyl-4-methyl benzoic acid, 3,4,5-tris(TMS oxy), TMS ester; hexanedioic acid, dioctyl ester; stigmasterol TMS ether; 5α-cholestane,4-methylene; campesterol TMS; β-sitosterol and lanosterol. These compounds are listed under EDCs as emerging pollutants by U.S. Environmental Protection Agency. The phytoextraction potential of growing native weeds and grasses i.e. *Argemone mexicana, Saccharum munja, Saccharum arundinaceuym, Cynodon dactylon, Pennisetum purpureum, Chenopodium album, Cannabis sativa, Parthenium hysterophorus, Ricinus communis, Rumex dentatus, Tinospora cordifolia, Calotropis procera* and *Basella alba* revealed the high accumulation of Fe, Zn,

Cu, Mn, Ni, and Pb in their root and leaves compared to shoot. The rhizosphere of these plants were dominated by *Bacillus albus (MN793207), Bacillus cereus (MW793498), Bacillus paranthracis (CP045777),* and plant growth promoting activities i.e. IAA production, HCN production, organic acid production, phosphate-zinc-potassium solubilizing, Nitrogen fixing ability, were noted positive. Further, metagenomics analysis revealed *Proteobacteria* (50%), *Bacteriodetes* (33%), *Firmicutes* (5%) *Gemmatimonadetes* (2%), *Chlorofexi* (2%), and *Tenericutes* (2%). The dominant three genera were detected as *Rheinheimera* (21%), *Sphingobacterium* (17%), and *Idiomarina* (8%). In addition, other minor genera such as *uncultured Bacillus* (4%), *Acidothermus* (4%), *Bacillus* (3%), *Pseudomonas* (2%), *Flavobacterium* (2%), *uncultured bacterium* (2%), *Parapedobacter* (2%), *Alcanivorax* (2%), *Acholeplasma* (2%), *Hyphomonas* (1%), and *Aquamicrobium.* This indicated high accumulation and translocation capabilities of these plants due to bacterial communities growing in the rhizospheric of the tested plant. Further, the bioaccumulation coefficient factor (BCF) and translocation factor (TF) were found >1 for the majority of plants for various metals. Furthermore, the ultrastructural observations of root tissues also revealed the deposition of heavy metals at various cellular components without any apparent toxic effects. This indicated the variable adaptive characteristics of these plants growing at a hazardous waste polluted site. Thus, the study gives strong evidence for the application of these weeds and grasses as a green technology for the eco-restoration of polluted sites.

Keywords: Heavy Metals; Phytoextraction potential; Distillery sludge; Eco-restoration

NS-ENVM-7

Sustainable Pathways to Address Stubble Burning: Environmental Impacts, Policy Interventions, and Alternative Solutions

Rajesh Dhankhar* and Rahul Langyan
*rajeshdhankar.EVS@mdurohtak.ac.in

Department of Environmental Science, Maharshi Dayanand University, Rohtak, Haryana (124001), India

Abstract: Stubble burning is a significant contributor to air pollution in South Asia, releasing substantial amounts of carbon dioxide (CO_2), carbon monoxide (CO), nitrogen oxides (NO_x), sulfur oxides (SO_x), methane (CH_4), and particulate matter (PM2.5 and PM10). This practice, particularly prevalent in India's intensive rice-wheat rotation systems, has escalated air quality concerns, with an estimated 84 million tons of crop residue burned annually. The resulting severe haze, especially during October and November, elevates pollution levels in the National Capital Region (NCR), causing Air Quality Index (AQI) values to spike to hazardous levels. Health impacts linked to this pollution are extensive, ranging from respiratory and cardiovascular diseases to increased mortality rates. Additionally, stubble burning negatively affects soil quality, reducing its nutrient content and undermining agricultural sustainability. While alternative uses for crop residue such as biofuel, compost, and industrial applications offer sustainable options, low awareness among farmers in North India leads many to continue burning.
The study explores the origins of stubble burning, its environmental and health impacts, and the sociopolitical challenges farmers face in managing crop residue. It also examines government initiatives aimed at curbing this practice, including policies, incentives, and penalties, alongside recommendations for awareness campaigns to promote viable alternatives. Through a comprehensive synthesis of existing literature, this paper aims to provide a pathway toward sustainable residue management and enhanced public health outcomes.

Keywords: Air pollution, Air quality Index, Crop residue, Stubble burning, Sustainable residue management

IS-FIM-1

Food Safety Management System: Challenges and Opportunities

Manju Balhara[1*] and Inderdeep Kaur[2]
*manjubalhara007@gmail.com

[1] International Flavors& Fragrances Inc., Edwin Rahrsvej 38, DK-8220 Brabrand, Denmark
[2]Sri Guru TeghBahadurKhalsa College, University of Delhi, Delhi (110 007), India

Abstract: In the food industry microorganisms play a crucial role where they contribute to the production, spoilage, and preservation of various food products. Since ages microorganisms have been used to produce food,

antibiotics, preservatives, and several other products for mankind. Their use in enhancing the antioxidant and probiotic properties has made them popular in all health-associated food items.
However, while microorganisms are an important component of food industry with significant role in welfare of mankind, they also play a key role in food spoilage, rendering it unfit for consumption by human. Several foodborne diseases are caused by the ingestion of microbial-contaminated harmful food products. In the times when information and technology are just a click away, food safety has become an important concern of the consumers, food industries and the regulatory authorities. The production of 'safe' food is responsibility of everyone in the food chain that functions "from farm to folk" involving various stakeholders, including farmers, manufacturers, distributors, and retailers. The Food Supply Chain Management (FSCM) is dynamic and complex since it deals with perishable items or products where transit time plays a vital role. Coordination, therefore, in the food supply chain from production to consumption is a necessity with FSCM playing a major role in ensuring high quality food.
As the consequences of unsafe food may be serious, Food Safety Management System (FSMS) has a pivotal role in providing safe food to the consumers and reducing food wastage. Through programs such as Hazard Analysis and Critical Control Points (HACCP), Good Manufacturing Practices (GMPs) and International Organization for Standardization (ISO), countries have regulated standards at the national and international levels.
Though India is the world's largest food producer and exporter, but active adaption of food safety culture is an enormous challenge in the whole food supply chain. The food safety regulation system which came into being in 2006 in India, acts through measures governed by the Food Safety and Standards Authority of India (FSSAI).
The government's more stringent vigilance and enforcement policies have come a long way since the inception of FSSAI. Food safety demands comprehensive information regarding the how, why, and what next through regular participation of the research institutes, experts, and scientists.

Keywords: Microbes; Food Safety Management System; Challenges; FSSAI; FSMS

IS-FIM-2

Microbial Biorefinery System for Valorising Agri-food Biomass into Single Cell Proteins for Food and Feed

Luu Hoang An[a], Ishita Sanjay Telang[b], Rochak Mittal[c] and Gaurav Rajauria[a,b,c*]
*grajauria@ucc.ie

[a] *School of Microbiology, University College Cork, Cork, Ireland*
[b] *School of Food and Nutritional Sciences, University College Cork, Cork, Ireland*
[c] *SUSFERM Centre for Sustainable Fermentation and Bioprocessing Systems for Food and the Bioeconomy, University College Cork, Cork, Ireland*

Abstract: The global food security landscape has become increasingly precarious/alarming. With a 2023 report on global food crises by the Food Security Information Network (FSIN) reveals a 25% surge in the population on global scale, facing severe acute food insecurity. The issue of food insecurity is further compounded due to the generation of the food waste in agri-food sector, posing environmental degradation and health risks. Globally, an estimated 1.3 billion tons of food is wasted each year, accounting to approximately one-third of the world's food supply, and generating about 8-10% of total greenhouse gas emissions, annually. Therefore, there is an urgent need of sustainable solutions to overcome contemporary food shortage challenges. The pressing questions, such as, how a growing world population can be fed when agricultural land per capita is decreasing? How to transform biological resources into value-added products to make agriculture more circular and sustainable? How to produce more protein in a sustainable way without destroying the planet? The SC-Protein project proposes a potential solution of these challenges by developing an integrated microbial biorefinery system that utilises agri-food biomass for producing alternative single cell proteins (SCPs). SC-Protein project is built on the prior state-of-the art and aims to advance pre-treatment technologies/processes and cost-effective bioreactor designs for SCP production. SC-Protein project is envisaged to utilise locally available agri-food industry waste/side streams (from dairy processing, brewery, mushroom and food processing industry) and transform it into cost-effective alternative growth substrates. Employing microbial fermentation, these alternative growth substrates are then being used as sole carbon source for cultivating high protein containing microorganisms (bacteria, yeast and fungi), in a bioreactor. By decoupling protein production from fishing and

farming, SC-proteins provides sufficient feed-grade proteins for pig, poultry and aquaculture, without using arable land and water.

Keywords: Microbial biorefinery system; Valorisation; Single cell proteins; Food; Feed; Agriculture

NS-FIM-1

Valorization of Avocado (*Persea americana*) by-products for Extraction of Bioactive Compounds and its Incorporation in Vegan Mayonnaise

R. V. Maruthi Prasad and Bhim Pratap Singh*
*bhimpratap@gmail.com

Department of Agriculture and Environmental Sciences, National Institute of Food Technology Entrepreneurship and Management, Sonipat, Haryana, India

Abstract: This study investigates the proximate composition, phenolic content, and antioxidant activity of avocado (*Persea americana*) by-products. The findings reveal that the seeds contain higher carbohydrate (66.20%) and protein (5.02%) contents, while the peels exhibit higher ash (6.15%) and crude fiber (12.50%) contents. Total phenolic content (TPC), total flavonoid content (TFC), and total anthocyanin content (TAC) were assessed, demonstrating enhanced extraction yields with the application of pulsed electric field (PEF) technology. The antioxidant activities, measured using DPPH and ABTS assays, show that PEF-extracted samples exhibit significantly higher radical scavenging activities compared to conventional ethanol-extracted samples, indicating the potential of PEF in maximizing the bioactive compound extraction from avocado by-products. Fourier Transform Infrared (FTIR) spectroscopy and High-Resolution Mass Spectrometry (HRAMS) were employed to analyze the chemical profiles of avocado seed extracts obtained through solvent extraction and pulsed electric field (PEF) extraction. FTIR spectra revealed changes in functional groups with notable peaks corresponding to O-H, C-H, and polysaccharides, indicating the presence of various organic substances in the extracts. HRAMS analysis demonstrated that PEF extraction yielded a more diverse and abundant range of compounds, including unique antioxidants and lipid derivatives, than solvent extraction. The distinct chemical profiles obtained from each extraction method highlight their potential applications in the food, pharmaceutical, and cosmetic industries, with PEF extraction offering enhanced bioactive properties. The study investigates the effects of incorporating avocado seed extract into vegan mayonnaise, focusing on sensory, nutritional, and rheological properties. Sensory analysis reveals that a 1% concentration of avocado seed extract enhances overall acceptability, closely approaching the control's performance. Phyto-chemical analysis indicates significant nutritional improvements, including increased fat, dietary fiber, and antioxidant activity, without drastically altering the product's core properties. Rheological and textural analyses demonstrate enhanced firmness, consistency, and cohesiveness, suggesting that the 1% avocado seed extract improves the product's physical properties, making it a promising additive for vegan mayonnaise.

Keywords: Valorization; Avocado (*Persea americana*); By-Products; Bioactive compounds; Vegan mayonnaise

NS-FIM-2

Paradigm Shifts in Microbiome Research from Probiotics to Postbiotics towards Development of Functional Foods

Gunjan Goel
gunjanmicro@gmail.com

Department of Microbiology, Central University of Haryana, Mahendergarh, Haryana (123031), India

Abstract: The human intestinal microbiota, a population of microorganisms that reside in the gastrointestinal system, is recognised for its significant role in regulating metabolic pathways and influencing immunological and neurological responses in the host. Nevertheless, it has been widely acknowledged that non-viable microorganisms, together with their cellular constituents and metabolic byproducts, can also have an effect on health. Postbiotics are compounds that are produced by the metabolism of microbiota and have a positive impact

on both the microbiota and the host. The effects of postbiotics appear to be mediated by an interaction between the host and microbial products at the molecular level. Consequently, it leads to stimulation of immune system to various anti-inflammatory responses. These postbiotic components include various metabolic products such as vitamins, short-chain fatty acids and enzymes and structural components like plasmalogens, teichoic acids and peptides. Various studies have reported antimicrobial and antioxidative activities of Cell-free supernatants from probiotic bacterial. Research has emphasised the beneficial impacts of postbiotics through antimicrobial, antioxidative, maintaining integrity of intestinal barrier and regulating the immune system. Postbiotics offer many advantages over live probiotic strains as these do not need strict storage conditions, and their activity is not affected by processing or storage. Their stability renders them very suitable for incorporation into a diverse array of food matrices. Although various health benefits have been attributed to postbiotic components, still there is a need for validated clinical trials for these health claims.

Keywords: Human intestinal microbiota; Microbiome research; Probiotics; Postbiotics; Functional foods

NS-FIM-3

Revealing the Metagenomes and their Biomarker Genes Related to Human Health in some Indian Fermented Foods

Jyoti Prakash Tamang
FNA, FNASc, FNAAS, FIAMS, FBRS
jyoti_tamang@hotmail.com

Department of Microbiology, School of Life Sciences, Sikkim University (Central University), Tadong, Gangtok, Sikkim (737102), India

Abstract: The food culture and gastronomy of India's diverse ethnic and racial communities are unique and unmatched compared to other nations. The use of multi-omics has provided scientific validation for the domestication of beneficial microbial communities, highlighting their functions, health benefits, and disease-fighting mechanisms in various Indian fermented foods and alcoholic beverages. Sequence-based metataxonomic research utilizing shotgun sequencing has uncovered extensive microbial community structures in ethnic fermented soybean products and dairy items. Given the complex microbial composition of naturally fermented foods, the classification and recovery of genomes from metagenome-assembled genomes (MAGs) are crucial for understanding genetic and evolutionary processes, as well as identifying known or new species and their roles in the fermented food ecosystem. MAGs have revealed the presence of numerous genes with potential functions related to various probiotic and prebiotic effects, production of short-chain fatty acids, immune modulation, antitumor activity, and the synthesis of essential amino acids and vitamins in certain ethnic fermented foods. Gene clusters for antimicrobial peptides and CRISPR-Cas systems were also found in MAGs. The metabolomes of some Indian fermented foods indicate a wealth of metabolites, particularly secondary or untargeted metabolites like immunomodulators, bioactive compounds, biopeptides, and vitamins, which are associated with health benefits and disease-fighting properties. Therefore, employing integrated multi-omics approaches may support the recognition of traditional fermented foods as "foods as medicine."

Keywords: Metagenomes; Biomarker genes; Human health; Indian fermented foods

NS-FIM-4

Microalgae: An Emerging Sustainable Source with Multiple Applications

Veena Pande
veena.biotech@gmail.com

Department of Biotechnology, Kumaun University, Sir J. C. Bose Technical Campus, Bhimtal, Nainital, Uttarakhand (263136), India

Abstract: Microalgae, a renewable source, are photosynthetic microbes that have recently gained attention due to their extensive applications in the transportation sector, food and feed, pharmaceuticals and nutraceuticals

industries. They have photosynthetic and metabolic capabilities enabling them to produce pigments, lipids, carbohydrates, proteins, vitamins and antioxidants. Carbohydrates and lipids extracted from microalgae are used to produce different types of bioenergy like biohydrogen, biodiesel, bioethanol and biogas. Photosynthetic pigments such as chlorophyll and carotenoids are used in nutraceuticals and cosmeceutical products. Other high-value-added compounds derived from microalgae include astaxanthin, beta-carotene, phycocyanin and polyunsaturated omega-3 fatty acids, which have notable medicinal properties such as antibacterial, antioxidation, and anticancer effects. They can grow in a wide range of habitats and tolerate a broad range of abiotic factors such as salinity, pH, temperature, and light intensity, thus, contributing to carbon dioxide mitigation, wastewater treatment and contaminant removal. Recently they have also been used in making bioplastics.

While microalgae have great potential, some various challenges and limitations need to be addressed before they can be used on an industrial scale. These challenges include improving the growth rate and synthesis of biochemical compounds, pre-treating biomass, and dewatering microalgae for biomass production. Therefore, optimizing growth conditions is necessary to enhance the production of these beneficial compounds.

Keywords: Microalgae; Bioactive compounds; Bioenergy; Pharmaceuticals; Bioremediation

NS-FIM-5

GRAS Microbes: Silent Carriers of Antimicrobial Resistance Genes and their Challenges to Ensuring Food Safety

Neetu Kumra Taneja
drneetu.niftem@gmail.com

National Institute of Food Technology, Entrepreneurship and Management, Kundli (NIFTEM-K), Sonipat, Haryana, India

Abstract: While significant research has focused on pathogenic bacteria in the transmission of antimicrobial resistance (AMR), emerging evidence highlights the pivotal role of Generally Recognized as Safe (GRAS) microorganisms in disseminating AMR genes throughout the food chain. AMR represents a pressing global health crisis, with the World Health Organization (WHO) warning that by 2050, drug-resistant infections could result in over 10 million deaths annually, surpassing cancer as a leading cause of mortality. Beyond health implications, the economic burden of AMR is projected to reach $100 trillion, affecting productivity and increasing healthcare costs. This talk aims to elucidate the mechanisms through which GRAS microorganisms like lactic acid bacteria (LAB) acquire, carry, and transfer AMR genes, thereby jeopardizing food safety. Furthermore, gaps in current regulatory frameworks addressing AMR surveillance and management of GRAS microorganisms shall be discussed and effort shall be made to explore innovative strategies to mitigate AMR transmission. Special focus shall be given on emerging resistance in lactic acid bacteria from traditional Indian fermented foods. The data discussed during the talk shall provide a unique platform to address the complexities of AMR transmission through GRAS microorganisms and collectively chart a path toward enhanced food safety and responsible practices in food production.

Keywords: GRAS Microbes; Antimicrobial resistance genes; Food safety; Lactic acid bacteria (LAB)

NS-FIM-6

Bacterial Keratinases: Optimized production, Characterization and Applications

Naveen Kango*, Isha Sharma and Pranshi Gupta
*nkango@gmail.com

Department of Microbiology, Dr. Harisingh Gour Vishwavidyalaya (A Central University), Sagar, Madhya Pradesh, India

Abstract: Feather keratin waste from the poultry industry presents a formidable environmental challenge due to its recalcitrant nature. This study investigates the biotechnological potential of keratinase producing bacteria

Ochrobactrum intermedium, *Bacillus velezensis* NCIM 5802, and *Brevibacillus borstelensis* isolated from soil for efficient keratin waste degradation. The optimum pH and temperature for keratinase activity were noticed to be 9.0-10.0 and 60°C, respectively. Presence of multiple keratinases (Mr ~ 100, 62.5, 36.5 and 25 kDa) was revealed in case of *B. velezensis* indicating its multiple forms, while in case of *O. intermedium* three active bands were detected (Mr ~ 250, 100, and 50 kDa) signifying the polymeric nature of the enzymes. As keratin being a complex, recalcitrant molecule may require endoprotease, exoprotease, and oligopeptidase activities to work synergistically. Analyses confirmed 18 free amino acids from feather degradation, with structural changes validated by X-ray diffraction (XRD) and spectroscopic techniques (FTIR, Raman), reducing the crystallinity index from 1.00 to 0.63. Scanning electron microscopy (SEM) illustrated progressive feather keratin degradation. The findings from this study suggest the feasibility of converting feather keratin into valuable products such as feather meal, amino acids, or protein concentrates using keratinases derived from the newly isolated bacteria. Feather hydrolysate generated by these bacteria contained soluble peptides and free amino acids displayed significant antioxidant and free-radical scavenging activity (90.46%, 80.0%, respectively). *B. borstelensis* keratinase exhibited compatibility with various commercial detergent suggesting its possible use as an additive to detergent. Additionally, *B. velezensis* keratinase immobilized on silver nanoparticles enhance antibacterial activity, antioxidant and biofilm degradation capacity of nanoparticles. The presentation will discuss isolation of keratinolytic bacteria from soil, their characteristics and applications in poultry waste management.

Keywords: Feather keratin waste, Bacterial Keratinases, SEM, XRD, FTIR, Raman

NS-FIM-7

Cyanobacteria as Nutri-fertigation and Priming Options to Invigorate Growth, Yields and Quality of Produce

Radha Prasanna*, Akanksha Bhardwaj[a], Nivedha RM[a], Deepti Varsha[a], Aditi Tayade[a], Awani Kumar Singh[b] and Yashbir Singh Shivay[c]
*radhapr@gmail.com

[a]*Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi (110 012), India*
[b]*Centre for Protected Cultivation Technology (CPCT), ICAR-Indian Agricultural Research Institute (IARI), New Delhi (110 012), India*
[d]*Division of Agronomy, ICAR-Indian Agricultural Research Institute, New Delhi (110 012), India*

Abstract: Cyanobacteria, a diverse group of photosynthetic microorganisms, possess a remarkable ability to release numerous extracellular compounds consisting of various nitrogenous and non-nitrogenous substances at different stages of their growth. Although these organisms have been consistently reported to have several positive effects on soil health and crop yields based on numerous studies because of their C-and N-fixing abilities, scanty information is documented on the nature of signalling in the plant-soil interactions which stimulated research into the nature of metabolites produced by them. Cyanobacteria being highly cosmopolitan, ubiquitous and adaptive, they establish well in several types of niche, and in recent years, GC-MS and use of their spectrometric analyses revealed that these compounds primarily comprised mainly of sugars, their conjugates, besides metabolites belonging to amino acid metabolism pathways, which are important players in plant–microbe interactions.

Traditionally, used as dry flakes which can be broadcast over standing water in rice fields, or mixed in soil before sowing/transplanting, they are being explored as a group of bioactive biostimulants. With the growing significance of precision agriculture, vertical farming, protected cultivation and the growing market for biostimulants, a need was felt to explore different modes of application, which are targeted, in terms of crop, relevant stage of growth and attribute (s).

During the last five years, optimization and development of cyanobacterial formulations., with multifarious modes of application- as seed priming or seedling dip or as foliar sprays or soil drenches were developed, evaluated and optimized.PCA and multivariate analyses revealed a significant role for cyanobacteria-based application in establishing positive correlations among quality traits with plant, soil and yield attributes. Future research is directed towards gaining a better understanding of the underlying metabolic fluxes involved in the modulation of growth-related attributes, yield, and quality, using omic tools.

Keywords: Cyanobacteria; Nutri-fertigation; Priming options; Biostimulants; Growth; Yield

NS-FIM-8

Solution NMR Studies of Penicillin Binding Protein PBP5

G Senthil Kumar
gskumar@nii.ac.in

Integrative Structural Biology Laboratory, National Institute of Immunology, Aruna Asaf Ali Marg, New Delhi (110067), India

Abstract: Enterococci infections are the major cause of nosocomial and community-acquired infections. The major hurdle in the treatment of enterococci infections is their increased resistance to many classes of β-lactam antibiotics. The primary reason for such increased resistance is the expression of low-affinity penicillin-binding proteins PBP4 (*E. faecalis*) and PBP5 (*E. faecium*). Hence, it is crucial to characterize how low-affinity PBPs bind and catalyze transpeptidation and the role of sequence changes in these PBPs that reduce their affinity for β-lactam antibiotics. To overcome the PBP- mediated resistance, it is important to identify the role of structure and dynamics of these amino acid variations. Although PBP5 (>70 kDa) is a challenging NMR target we were able to employ NMR spectroscopy to investigate its solution state interaction with penicillin and ceftaroline. Here, the results of interactions between the PBP5 variants with antibiotics and the changes in their structure and dynamics using the combination of solution NMR spectroscopy and X-ray crystallography will be presented.

Keywords: Enterococci infections**;** NMR; X-ray crystallography; Penicillin Binding Protein

NS-FIM-9

Overcoming Tuberculosis Resistance: *Amycolatopsis mediterranei* Rifamycin B Biosynthetic Gene cCuster as a Key Source for the Production of Rifamycin B Derivatives

Rup Lal
ruplal@gmail.com

INSA Senior Scientist, Acharya Narendra Dev College, University of Delhi New Delhi (110019), India

Abstract: *Amycolatopsis mediterranei,* an actinobacterium, produces rifamycin B. Semisynthetic derivatives of rifamycin B have been widely used for treating tuberculosis caused by *Mycobacterium tuberculosis*. *A. mediterranei* was first isolated in 1957 from French pine soils, and its ability to produce rifamycin B was recognized in the same year. In 1968, rifampicin, a semisynthetic derivative of rifamycin B, was introduced to combat *M. tuberculosis* infections. However, over the years, several strains of *M. tuberculosis* resistant to rifampicin have emerged, rendering rifampicin ineffective against these strains. We have been working on *A. mediterranei* for more than 40 years, focusing on overcoming the problem of resistance. Our research centers on genetic manipulation of *A. mediterranei* to produce rifamycin B analogues that are effective against rifampicin-resistant strains of *Mycobacterium*. Specifically, we have altered the rifamycin biosynthetic gene cluster and rifamycin B-producing regulatory genes to create analogues whose semisynthetic derivatives may prove effective against rifampicin-resistant strains of *Mycobacterium tuberculosis.* Our work on the production of rifamycin B analogues, through the manipulation of the rifamycin polyketide synthase gene cluster and regulatory elements, will be presented.

Keywords: Tuberculosis Resistance; *Amycolatopsis* mediterranei; Rifamycin B; Gene Custer

IS-MN-1

Exploring the Antimicrobial Potential of Silver Nanoparticles Synthesised from Marine Polychaetes

Mohd UlulIlmie Bin Ahmad Nazri
ululilmie@umt.edu.my

STEM Foundation Centre, Universiti Malaysia Terengganu, Malaysia

Abstract: Silver nanoparticles (AgNPs) are well-known for their ability to kill bacteria, viruses, and fungi, making them useful in medical and environmental applications. However, current AgNP productions using chemical and physical approaches are costly, complex and toxic to the environment. Thus, biosynthesis of AgNPs from biological samples is green alternative to be explored. In our recent study, the AgNPs synthesised from *Marphysamoribidii* (Annelida, Polychaeta) were evaluated for their physicochemical properties. We further tested the antibacterial efficacy and their actions against the wild-type and antibiotic resistance bacteria. The analyses using UV-Vis and dynamic light scattering confirmed the formation of stable spherical AgNPs with a surface plasmon resonance peak at 397 nm and a zeta potential of -36.48 mV. The antimicrobial efficacy of these AgNPs was assessed using disk diffusion, minimum inhibitory concentration (MIC), minimum bactericidal concentration (MBC), and time kill assays. Results demonstrated that AgNPs effectively inhibited the growth of both wild-type and antibiotic-resistant bacteria, with effective concentrations ranging from 0.05 µg/mL to 0.40 µg/mL for wild-type strains and 0.10 µg/mL to 0.40 µg/mL for antibiotic-resistant strains. Our study reveals that AgNPs exhibit bactericidal effects against wild-type bacteria and bacteriostatic effects against antibiotic-resistant strains. Detailed imaging with scanning electron microscopy (SEM) and transmission electron microscopy (TEM) highlighted significant membrane damage in bacteria exposed to AgNPs. Leakage assays further demonstrated cellular leakage resulting from AgNPs' interaction with bacterial membranes. Additionally, reactive oxygen species (ROS) detection assays confirmed that AgNPs induce oxidative stress within bacterial cells that later caused the damage. Our investigation for antibiotic resistance bacteria signifies that several physiological pathways such as nicotinate and nicotinamide metabolism, aminoacyl-tRNA and glutathione metabolism were impacted from the action by AgNPs. Nuclear magnetic resonance data also revealed significant alterations in vital bacterial metabolic pathways, leading to detrimental effects on bacterial growth.

Keywords: Antimicrobial potential; Silver nanoparticles; Marine polychaetes; *Marphysa moribidii*

NS-MN-1

Biogenic Copper Oxide @ rGO Nanocoatings for Decontamination of a Food Threat *B. cereus* in Packaged Cooked Rice Bowls

Shruti Shukla[1*], Yuvraj Haldorai[2], Mercyland Pamshnong[1] and Ibansaralang Kharthangmaw[1]
*shrutishukla1983@gmail.com

[1]*Department of Nanotechnology, North-Eastern Hill University (NEHU), East Khasi Hills, Shillong, Meghalaya (793022), India*
[2] *Department of Nanoscience and Technology, Bharathiar University, Coimbatore, Tamil Nadu (641046), India*

Abstract: Infectious diseases resulting from pathogenic microorganisms are one of the most important menaces to health all over the world. This issue of increased microbial resistance to antibiotics and other antimicrobial agents seems to be critical day-by-day. Among all the nanoparticles (NPs), copper oxide (CuO/Cu_2O) NPs are one of the most popular ones because they are inexpensive and abundant compared to other antibacterial NPs, such as silver or gold NPs. Furthermore, CuO/Cu_2O NPs are chemically stable, and have a long shelf life. In this study, we have synthesized graphene oxide (GO) *via*Hummers' method followed by the synthesis of copper NPs using copper benzoate dihydrazinate precursor for developing a CuO/rGO composite. The developed composite was characterized for its structure, morphology and compositions *via* TEM, Raman, XRD etc. We report a facile one-step synthesis of biocompatible, copper oxide @ rGO nanocomposite coating as a multifunctional agent for the food matrix decontamination. The developed copper oxide @ rGO coating exhibited high toxicity towards *B.*

cereus, as confirmed by the means of fluorescent live-dead cell counting, disruption of membrane permeability/potential, changes in the levels of cellular ions, genetic materials, and proteins, as well as intracellular production of reactive oxygen species. Moreover, the copper oxide @ rGO coating was used as a rinse solution (5, 10, and 20%) for rice bowl packages. Interestingly, a 20% rinsing solution applied for 40-60 min inhibited the *B. cereus* counts significantly on cooked rice packaged bowl. This research highlights the effectiveness of copper oxide @ rGO coating against food menace *B. cereus*, suggesting that the developed copper Oxide @ rGO coating can be used as an effective antimicrobial rinse for packaged cooked rice preservation.

Keywords: Copper oxide @ rGO nanocomposite; *B. cereus*; Packaged cooked rice; Food test model

NS-MN-2

Prospective Antimicrobial Applications of Plant-based Biogenic Matal and Metal Oxide Nanomaterials

Sandip Kumar Dash
dashsandipkumar@gmail.com

Department of Zoology, Berhampur University, Berhampur, Odisha (760007), India

Abstract: Gold, silver oxide, and silver oxide-manganese dioxide composite nanomaterials (NMs) were synthesised *in vitro* using different plant or plant parts as bio-reducing as well as capping agents. The chemical composition of the NMs were detected, using Fourier transform infrared (FTIR) spectroscopy (500-4000 cm^{-1}), in a FTIR (Spectrum 3 MIR/NIR/FIR Spectrometer, PerkinElmer, USA) under ATR mode. The crystalline nature, grain size, and alignment of the NMs were detected through X-ray diffraction study at step width, scan rate, and 2θ of 0.02°, 0.025°/s, and 10-80°, respectively, using AXRD benchtop powder diffraction system (30 kV and 20 mA), PROTO Manufacturing, USA. The shape and size of the NMs were determined using scanning electron microscope-energy dispersive X-ray analysis, GeminiSEM 300, ZEISS, USA 5.00 kV and 55.00 kX and transmission electron microscopy. Subsequently, the thermal stability, catalytic properties against hydrogen peroxide, glucose oxidase activity, adsorption assay for the synthesized NMs against methylene blue was done. The antibacterial properties of the NMs were also evaluated against some of the common waterborne disease causing pathogenic bacterial strains. The NMs showed broad antibacterial properties with the composite NMs being superior than the mono metallic or metal oxide NMs.

Keywords: Biogenic, Biosynthesis, Plant-based synthesis, Antimicrobial, Antibacterial, Water treatment

NS-MN-3

Mycosynthesis of Magnetic Nanoparticles using a Thermophilic Mould *Myceliophthora thermophila* Exhibiting Novel Biotechnological Applications

Bijender Singh* and Vinod Kumar
*ohlanbs@gmail.com

Department of Biotechnology, Central University of Haryana, Jant-Pali Mahendergarh, Haryana (123031), India

Abstract: Among the metallic nanoparticles, iron nanoparticles (FeNPs) have attracted researchers due to their magnetic property. Biological method has advantages over chemical and physical routes due to economical and non-toxic in nature. Culture filtrate of thermophilic fungus *Myceliophthora thermophila* BJTLRMDU7 showed biogenic synthesis of iron nanoparticles. The mould showed both extra- and intra-cellular routes of synthesis using ferrous sulphate as precursor salt. The change in colour was primary indication of the formation of FeNPs. Green FeNPs were synthesized at 50 ^{o}C and pH 5.0 after 24 h using 2 mM ferrous sulphate and one ml culture filtrate. Biogenic FeNPs synthesis was significantly improved by light. Biogenic FeNPs showed absorption peak in the range of 250-350 nm in UV–vis spectral data. The absorption peaks of Fourier-transform infrared spectroscopy (FTIR) at different wavelengths, indicated the presence of different metabolites/biomolecules and

functional groups, which are involved in the formation and stabilization of biogenic FeNPs. Atomic force microscopy analysis indicated the average size of FeNPs as 80 nm, while X-ray diffraction (0XRD) data showed their crystalline nature. Iron nanoparticles efficiently decolorized bromophenol blue up to 96% alone, whereas, malachite green and crystal violet decolorized up to 96% and 90% respectively, in the presence of H_2O_2. Biogenic iron nanoparticles exhibited catalytic conversion of 4-nitrophenol and the same was also confirmed by thin layer chromatography. Biogenic iron nanoparticles inhibited the growth of bacteria anf fungi in a concentration dependent manner. Biogenic FeNPs did not show hemolysis and cytotoxicity in cell cultures. Growth of *Plasmodium falciparum* was also inhibited by green FeNPs during parasite cultures. Phosphatase was immobilized on iron nanoparticles with an immobilization efficiency of more than 56%. The characterization of phosphatase-immobilized iron nanoparticles was carried out using FTIR, AFM and SEM analysis. The immobilized-phosphatase resulted in time dependent release of inorganic phosphate from wheat, rice and gram flours at 37 and 60 ^{o}C. Therefore, biogenic FeNPs synthesized using culture filtrate of *Myceliophthora thermophila* showed potential as therapeutics and as matrix for enzyme immobilization. Furthermore, biogenic iron nanoparticles also showed ability in environmental remediation.

Keywords: Magnetic nanoparticles; Mycosynthesis; *Myceliophthora thermophila*; Novel biotechnological applications

IS-MTAMR-1

Advanced Immunophenotyping through Flow Cytometry: Unlocking the Complexity of Immune Responses

Sushma Bharrhan[1,2*], Andrew D Yurochko[1,2] and Matthew Woolard[1,2]
*sushma.bharrhan@lsuhs.edu

[1] Department of Microbiology and Immunology,
Louisiana State University Health Sciences Center-Shreveport, Shreveport, LA, USA
[2] Center for Applied Immunology and Pathological Processes,
Louisiana State University Health Sciences Center Shreveport, Shreveport, LA, USA

Abstract: Flow cytometry stands at the forefront of immunophenotyping, offering unparalleled precision in identifying and characterizing diverse immune cell populations. This powerful technology employs fluorescently labeled antibodies to probe cell surface markers, enabling high throughput multiparametric analysis critical for dissecting innate and adaptive immune responses. Its applications range from studying immune system dynamics to monitoring disease progression and evaluating therapeutic interventions. The Immunophenotyping Core at Louisiana State University Health-Shreveport provides cutting-edge flow cytometry platforms, including the Bigfoot Spectral Cell Sorter, to support high-dimensional immune profiling. Advanced techniques, such as UMAP clustering and Phenographs, facilitate a deep exploration of immune cell diversity. Pre-optimized antibody panels for mouse and human immune cells ensure streamlined workflows and reproducibility across studies. From cell viability and apoptosis assays to complex immune profiling, flow cytometry's versatility is pivotal for driving innovation in immunological research. The core's comprehensive services—experimental design, sample preparation, antibody optimization, and data analysis and interpretation—empower researchers to uncover critical insights into immune function. This robust infrastructure accelerates discoveries in immunology, paving the way for new therapeutic approaches and advancing our understanding of immune regulation and disease.

Keywords: Immunophenotyping; Flow cytometry; Immune responses; Advanced techniques

IS-MTAMR-2

Cross-regulation Between Phage Elements of *Listeria monocytogenes* 10403S

Avijit Das* and Anat A. Herskovits
*ovijit.logy@gmail.com

The Shmunis School of Biomedicine and Cancer Research, The George S. Wise Life Sciences Faculty, Tel Aviv University, Ramat Aviv, Tel Aviv (6997801), Israel

Abstract: *Listeria monocytogenes* (*Lm*) is an intracellular pathogen infecting mammalian cells. *Lm* 10403S harbors an active prophage in its genome integrated within the *comK* gene, which is induced during macrophage infection. Notably, this induction leads to prophage excision without virion production or bacterial lysis, suggesting a cooperative phage behavior termed active-lysogeny that supports host survival. Our lab recently identified a regulatory element, the monocin element, which produces phage tail-like bacteriocins, named the monocin element. This study investigates cross-regulatory interactions between the prophage and monocin elements by examining the binding of their respective regulators, CI- and Cro-like repressors, to operator sites. Bioinformatic analysis identified phage operator sites (*O*, *O*1, *O*2, *O*3, *O*4) and monocin operator sites (*O*1, *O*2, *O*3). Gel shift assays demonstrated that the Cro-like repressor binds all phage operators and one monocin site, while the CI-like repressor binds three phage operators. Interestingly, Cro-like repressors also interact with the monocin regulatory region. These findings reveal complex regulatory interactions that may sustain active-lysogeny, enhancing our understanding of temperate phage and host dynamics, which could inform phage therapy strategies.

Keywords: *Listeria monocytogenes; Lm* 10403S; Bioinformatic analysis; Phage operator; Regulator

IS-MTAMR-3

Emergence of *Candida auris* as a Major Bloodstream Pathogen

Suhail Ahmad
suhail.ahmad@ku.edu.kw; suhail_ah2000@yahoo.com

Department of Microbiology, Faculty of Medicine, Kuwait University, P. O. Box 24923, Safat (13110), Kuwait

Abstract: Invasive fungal infections (IFIs) are associated with high morbidity and very high mortality rates and mostly affect patients with compromised immunity. The incidence of IFIs is increasing worldwide with the expanding population of immunocompromised individuals and other susceptible patients and the spectrum of fungi causing IFIs is changing due to changes in clinical practice. *Candida* and other yeast infections represent a major component of IFIs and candidemia represents nearly 75% of all invasive *Candida* infections. Nearly 50% episodes of candidemia occur in intensive care units (ICUs). Also, nearly 30% of all invasive *Candidia* infections do not yield a positive blood culture. *Candida auris* is a recently emerged, often multidrug-resistant yeast pathogen that has caused major outbreaks in healthcare facilities in many countries which have been difficult to control and treat and so were associated with high mortality rates. Although described as a novel species only in 2009, this notorious yeast pathogen has spread globally and has recently been declared as an urgent antimicrobial resistance threat by the Centers for Disease Control and Prevention (CDC) of USA and placed in the critical group of the fungal priority pathogen list by the World Health Organization (WHO). *C. auris* easily colonizes and sheds from human skin and has demonstrated prolonged survival in the environment as it resists elimination by robust cleaning and other decontamination procedures by commonly used disinfectants. Susceptible hospitalized patients, particularly those with multiple comorbidities in ICU settings, acquire *C. auris* rather easily from close contact with *C. auris*-infected patients or their environment or the equipment used on colonized patients, often with fatal consequences. Whole genome sequencing-based studies have identified six genetically distinct clades, and the vast majority of clinical *C. auris* isolates from South Asia and the Middle East exhibit resistance to fluconazole and belong to clade I. Therapeutic options for invasive *C. auris* infections are limited as many isolates exhibit resistance to one or more drugs, and there are only four classes of antifungal drugs. Echinocandins are the first-line treatment for invasive *C. auris* infections; however, resistance can develop during treatment. Resistance to amphotericin B has also been increasing, particularly among patients candiduria and/or respiratory tract colonization/infection. Rapid diagnosis and accurate

antifungal susceptibility testing of *C. auris* isolates to commonly used antifungal drugs are crucial for proper management and improved outcomes of invasive infections. Rapid identification of hospitalized patients infected/colonized with *C. auris* and appropriate use of infection control measures can also help to contain the spread of this highly pathogenic yeast in healthcare settings and prevent/control outbreaks.

Keywords: Invasive fungal infections; Candidemia; *Candida auris*; Diagnosis; Antifungal susceptibility testing; Infection control

IS-MTAMR-4

Integrating Machine Learning and Receptor Binding Studies to Identify Reservoir Bat Species for Ebola Viruses

Rohit K. Jangra[1, 2, 3,*], Gorka Lasso [4,†], Michael Grodus[5,25,†], Estefania Valencia[4,26,†], Veronica DeJesus[4,27], Eliza Liang[5], Isabel Delwel[4,28] Rob H. Bortz III, [4,29] Dmitry Lupyan,[6] Hanna Ehrlich,[7] Adrian A. Castellanos,[8] Andrea Gazzo,[9] Heather L. Wells,[10] Supaporn Wacharapluesadee,[11] AlexandreTremeau-Bravard, [7] Janine F.R. Seetahal,[12] Tom Hughes,[13,14] Jimmy Lee,[13,14] Mei-Ho Lee,[13,14] Anna R. Sjodin,[15] Marike Geldenhuys,[16] Marinda Mortlock,[16] Isamara Navarrete-Macias,[10] Kirsten Gilardi,[7] Michael R. Willig,[15,17] Alessandra F.D. Nava,[18] Elisabeth H. Loh,[19] Makda Asrat,[10] Tierra Smiley-Evans,[7] Walter S. Magesa,[20] Zikankuba Sijali,[20] David Wolking,[7] Gerardo Suzán,[21] Rafael Ojeda-Flores,[21] Christine V.F. Carrington,[22] Ariful Islam,[14,23] Jonathan H. Esptein,[14] Wanda Markotter,[16] Christine K. Johnson,[7] Tracey Goldstein,[24] Barbara A. Han,[8] Jonna A.K. Mazet,[7] Kartik Chandran,[4] and Simon J. Anthony [10]

*rohit.jangra@lsuhs.edu

[1] *Department of Microbiology and Immunology,*
Louisiana State University Health Sciences Center-Shreveport, Shreveport, LA, USA
[2] *Center for Applied Immunology and Pathological Processes,*
Louisiana State University Health Sciences Center Shreveport, Shreveport, LA, USA
[3] *Center of Excellence for Emerging Viral Threats,*
Louisiana State University Health Sciences Center Shreveport, Shreveport, LA, USA
[4] *Department of Microbiology and Immunology, Albert Einstein College of Medicine, Bronx, NY, USA*
[5] *Center for Infection and Immunity, Mailman School of Public Health,*
Columbia University, New York, NY, USA
[6] *Schrödinger Inc., Cambridge, MA, USA*
[7] *One Health Institute, School of Veterinary Medicine, University of California, Davis, CA, USA*
[8] *Cary Institute of Ecosystem Studies, Millbrook, NY, USA*
[9] *Department of Pathology and Laboratory Medicine,*
Memorial Sloan Kettering Cancer Center, New York, NY, USA
[10] *Department of Pathology, Microbiology, and Immunology,*
School of Veterinary Medicine, University of California, Davis, CA, USA
[11] *Thai Red Cross Emerging Infectious Diseases Clinical Center,*
King Chulalongkorn Memorial Hospital, Faculty of Medicine,
Chulalongkorn University, Pathumwan, Bangkok, Thailand
[12] *Department of Diagnostic Medicine/Pathobiology,*
College of Veterinary Medicine, Kansas State University, Manhattan, KS, USA
[13] *Conservation Medicine, Selangor, Malaysia*
[14] *EcoHealth Alliance, New York, NY, USA*
[15] *Department of Ecology and Evolutionary Biology,*
University of Connecticut, Storrs, CT, USA
[16] *Centre for Viral Zoonoses, Department of Medical Virology,*
University of Pretoria, Pretoria, South Africa
[17] *Center for Environmental Sciences and Engineering, Institute of the Environment,*
University of Connecticut, Storrs, CT, USA
[18] *FundaçãoOswaldo Cruz-Fiocruz, InstitutoLeônidas& Maria Deane, Laboratório de Ecologia de DoençasTransmissíveisnaAmazônia – EDTA, Manaus, AM, Brazil*
[19] *Division of Natural Sciences and Mathematics, Transylvania University, Lexington, KY, United States*

[20] *Department of Veterinary Medicine and Public Health, Sokoine University of Agriculture, Morogoro, Tanzania*
[21] *Laboratorio de Ecología de Enfermedades y UnaSalud, Departamento de Etología, Fauna Silvestre y Animales de Laboratorio, Facultad de MedicinaVeterinaria y Zootecnia, Universidad Nacional Autónoma de México, Ciudad de México, Mexico*
[22] *Department of Preclinical Sciences, Faculty of Medical Sciences, The University of the West Indies, St. Augustine, Republic of Trinidad and Tobago*
[23] *One Health Epidemiology, Charles Sturt University, New South Wales, Australia*
[24] *One Health Institute, Colorado State University, Fort Collins, CO, USA*
[25] *Present address: Rockefeller University, New York, NY, USA*
[26] *Present address: Icahn School of Medicine at Mount Sinai, New York, NY, USA*
[27] *Present address: Cancer Research UK Beatson Institute, Glasgow, Scotland, UK*
[28] *Present address: Stanford University, Stanford, CA, USA*
[29] *Present address: University of Pittsburgh Medical Center, Pittsburgh, PA, USA*
† Equal contribution

Abstract: Evidence suggests that bats are important hosts of filoviruses, but the specific bats involved remainlargely unknown. The Niemann-Pick C1 protein (NPC1) serves as an essential entry receptor, withamino acid variations at the virus-receptor interface influencing viral susceptibility and species-specifictropism. We reasoned that variation in virus-receptor binding would aid in identifying potential hostspecies. We performed binding studies across seven filovirus glycoproteins (GPs) and NPC1 orthologsfrom 81 bat species, finding that GP-NPC1 binding agreed poorly with overall sequence identity orphylogeny. However, integrating binding assays with machine learning revealed genetic factors influencing virus-receptor binding. The implemented model predicts GP-NPC1 binding avidity (R^2 of0.69-0.75). Experimental and predicted binding avidities, combined with data on bat distribution andpast Ebola virus outbreaks, helped rank bat species' potential as Ebola virus hosts. This study provides amultidisciplinary approach for predicting susceptible species and guiding filovirus host surveillance.

Keywords: Machine Learning; Receptor binding; Bat species; Ebola virus

IS-MTAMR-5

Angicin, a Novel Bacteriocin of *Streptococcus anginosus*

Barbara Spellerberg*, Verena Vogel, Richard Bauer and Stefanie Mauerer
*barbara.spellerberg@uniklinik-ulm.de

Institute of Medical Microbiology and Hygiene, University Hospital Ulm, Germany

Abstact: The production of bacteriocins is a bacterial defense mechanism providing a colonization advantage in a multispecies environment. Angicin is the first characterized bacteriocin of *Streptococcus anginosus,* a commensal, which is however also a common cause of severe infections. We identified Angicin from *S. anginosus* strain BSU 1211 by genetic mutagenesis. As an unmodified peptide of 54 amino acids it belongs to the class IId bacteriocins. Synthetic Angicin shows high activity against closely related streptococci, listeriaand vancomycin resistant enterococci. It causes membrane disruption in bacteria by an interaction with the mannose phosphotransferase system (Man-PTS) of target cells. Due to its high stability in a temperature range from -70 to 90 °C and pH values from 2-10 it represents an interesting compound for applications in food preservation or clinical settings.

Keywords: Angicin; Bacteriocin; *Streptococcus anginosus*; Mannose phosphotransferase system (Man- PTS)

NS-MTAMR-1

Targeting of Transcription Anti-termination Protein RfaH for Novel Antimicrobial Development

Anam Ashraf and Md. Imtaiyaz Hassan
mihassan@jmi.ac.in

Centre for Interdisciplinary Research in Basic Sciences, Jamia Millia Islamia, Jamia Nagar New Delhi (110025), India

Abstract: Anti-termination protein RfaH plays a crucial role in promoting virulence across various Gram-negative pathogens, including *Klebsiella pneumoniae* (KP). RfaH directly interacts with RNA-polymerase and ribosomes, which in turn facilitates the activation of operons associated with capsule, cell wall, and pilus biosynthesis. This study aimed to investigate the repurposing potential of rifaximin, a well-established antibiotic, against KP by strategically targeting RfaH, a pivotal anti-terminator protein in transcription. Fluorescence studies observed an excellent binding affinity between rifaximin and RfaH (Ka= 7.38 x $10^6 M^{-1}$). Intriguingly, rifaximin treatment causes a significant reduction in capsule production in KP when compared to untreated controls, elucidating its inhibitory influence on RfaH activity. The minimum inhibitory concentration for Rifaximin was calculated as 100µM and a minimum bactericidal concentration of 200µM against KP (ATCC 700603 strain). Docking and MD simulation studies provided detailed atomic insights into the Rifaximin binding to RfaH and structural dynamics of the RfaH-Rifaximin complex. These multifaceted findings collectively investigated the potential of rifaximin as a repurposed antibiotic against KP. Finally, a strong interaction of RfaH with rifaximin and subsequent inhibition of the growth of KP provides a novel avenue for antimicrobial development for addressing the persistent global challenge of antibiotic-resistant infections.

Keywords: Rifaximin; Anti-termination Protein RfaH; MD simulation; Fluorescence studies; Anti-biotic resistance

NS-MTAMR-2

Novel β-lactam/β-lactamase Inhibitor Combinations show Limited Activity against Indian *Pseudomonas aeruginosa* Isolates due to Conundrum of Diverse Resistance Mechanisms

Arun S. Kharat
arunkharat2007@gmail.com

210 School of Life Science, Jawaharlal Nehru University, New Delhi, India

Abstract: Background: Infections caused by multidrug-resistant (MDR) *Pseudomonas aeruginosa* are making it difficult to develop effective antibiotics, causing substantial morbidity and mortality. Inability of antibiotics to comprehensively tackle MDR *P. aeruginosa,* results from the interplay of intrinsic resistance as well as from the increasing prevalence of metallo-beta-lactamases in certain regions. Though advancement over older antibiotics, the recently approved anti-pseudomonal β-lactam/ β-lactamase inhibitor (BL/BLI) combinations overcome limited spectrum of resistance mechanisms and therefore need to be assessed for their potential utility in regions known for high resistance rates.
Method: The *P. aeruginosa* isolates (n=419) were collected from 16 Indian hospitals, and susceptibility was assessed by employing reference broth microdilution method. The presence of metallo-beta lactamases in the clinical isolates was confirmed by PCR method. The selective isolates were subjected for whole genome sequencing in order to reveal the entire range of molecular determinants of antibiotic resistance.
Results: Overall, ceftazidime/avibactam, ceftolozane/tazobactam and imipenem/relebactam showed 55-62% susceptibility against *P. aeruginosa*. Among carbapenem resistant isolates, 68% harboured MBLs. The genome sequencing revealed variety of mutations in PBP3 (*ftsI*) as well as genes that regulate expression of *oprD* and efflux proteins. The resistance determinants to fosfomycin, polymyxins, quinolones and aminoglycosides were also encountered in these isolates.
Conclusion: Among carbapenem-resistant *P. aeruginosa* isolates collected in India, NDM was the most common carbapenemase. In non MBL-producing isolates, array of multiple resistance determinants also

adversely impacted the effectiveness of newer BL/BLIs. Treatment of infections caused by MDR *P. aeruginosa* would continue to pose significant challenges, especially, in high-resistance regions.

Keywords: Multidrug-resistant (MDR); Novel β-lactam/β-lactamase; Inhibitor combinations; *Pseudomonas aeruginosa;* Resistance mechanisms

NS-MTAMR-3

Gut Microbial Prospection for Improved Human Health and to Mitigate Disease Burden

Yogendra Padwad
yogendra@ihbt.res.in

CSIR-Institute of Himalayan Bioresource Technology, Palampur, Himachal Pradesh, India

Abstract: Contemporary research is elucidating the pivotal role of the gut-liver axis in the pathophysiology of metabolic dysfunction-associated fatty liver disease and colitis-associated colorectal cancer. However, further investigation is warranted to account for the inevitable alterations in gut microbiota that accompany disease progression. A more in-depth examination is necessary to consider the unavoidable shifts in gut microbiota that occur as these conditions worsen. To investigate this association, the temporal evolution of gut microbiota makeup in MAFLD and CAC was comprehensively assessed. The study assessed the implications of time-dependent alterations in gut microbiota for disease development and the efficacy of plant-based prebiotics in attenuating disease progression. A preclinical model was established in C57BL/6J mice to recapitulate both disease conditions. The etiologies of these conditions were subsequently verified. Fecal samples were collected and analyzed using 16S rRNA amplicon sequencing to characterize the gut microbiome. A significant elevation in the abundance of pathogenic taxa, including *Desulfovibrionaceae*, *Peptostreptococcus*, *Clostridium*, and *Terrisporobacter*, was observed. However, phloretin treatment effectively mitigated this dysbiosis and facilitated the restoration of beneficial taxa, such as *Ruminococcus*, *Lactobacillus*, and *Alloprevotella*, known to exert positive influences on the gut microenvironment. Synbiotics and other nutraceutical interventions are currently considered indispensable for promoting and maintaining optimal health, controlling disease, and mitigating disease risk in both animals and humans. Investigations into the interrelationship between the gut microbiota of animals and humans and their immune status have underscored the pivotal role of synbiotics in maintaining optimal health. Evidence substantiates that synbiotics exert a significant influence on the gut microbiome and play a pivotal role in mitigating various diseases, including immune dysfunctions.

Keywords: Gut microbiota, MFLD, CRC, Microbiome, Metagenome

NS-MTAMR-4

Multi-omics: Connect between MDR *Escherichia coli* and Disease Severity in Ulcerative Colitis

K. K. Sharma* and Asha Yadav
*kksharma.microbiology@mdurohtak.ac.in

Head and Associate Dean, R & D (Science)
Department of Microbiology, Maharshi Dayanand University, Rohtak, Haryana, India

Abstract: Ulcerative colitis (UC) is a chronic inflammatory condition that affects the inner lining of colon, where gut microbiota is the major contributor. *Escherichia coli* is a Gram-negative commensal of human gut. Surprisingly, the role of *E. coli* in the pathogenesis of ulcerative colitis (UC) has not been explored till date. In UC patients, meta-gut resistome was found to be dominated by AMR genes compared to healthy control (HC). Approximately, 40% of all *E. coli* isolates were multi-drug resistant with higher prevalence in UC (43.75%) compared to HC (33.33%). Metagenome study revealed higher prevalence of AMR genes in rural population compared to urban. Up-regulated expression of antimicrobial human proteins (lactotransferrin, azurocidin, cathepsin G, neutrophil elastase, and neutrophil defensin 3) and immune proteins suggest microbial infection in

UC gut. In addition to the conventional culturomics method, multi-omics strategy provides deeper insights into the disease etiology, emergence of pathobionts, and its role in the disruption of the healthy gut environment in UC patients.

Keywords: Metagenome; Ulcerative colitis; *Escherichia coli*; MDR

NS-MTAMR-5

Unlocking New Antibacterial Potential: A Case Study of Discovery and Impact

Becky M Thomas
beckythomas20@gmail.com

Director, Shriram Institute for Industrial Research, Gurugram, Haryana, India

Abstract: Bacterial infections remain a major health problem worldwide because of the emerging resistance to the existing antibiotics. Among these, Methicillin resistant *Staphylococcus aureus* (MRSA) is an important cause of nosocomial infections, especially surgical wound infections, bloodstream infections and nosocomial pneumonia. Another important pathogen responsible for serious infections are Vancomycin resistant enterococci (VRE) causing urinary tract infection, endocarditis, bacteremia and wound infection. It is a continuous endeavor of the scientific community to avidly pursue the discovery of novel antibiotics to treat such infections. Here we report the activity of a novel antibiotic PM181104 isolated from a marine sponge-associated microorganism *Kocuria* species (MTCC 5269) that has potent antibacterial activity against MRSA and VRE. PM181104 showed *in vitro* biological activity against a wide range of gram-positive bacteria, including those belonging to *Streptococcus, Staphylococcus, Enterococcus* and *Bacillus* genera. *In vivo* efficacy of an injectable formulation of PM181104 was tested against MRSA in general testing models as well as tissue & organ – specific infection models. In general – purpose efficacy testing model of systemic disseminated septicemia, the mice were challenged with a lethal dose of MRSA strain E710 or VRE strain 47077, intraperitoneally, and subsequently treated intravenously with different doses of PM181104. Treatment with PM181104 protected mice from a lethal systemic MRSA or VRE infection and also showed significant reduction in the bacterial count in specific organs infected with MRSA and VRE in different murine infection models. The overall efficacy was comparable to standard antibiotics such as linezolid or vancomycin. The presentation will discuss the results obtained with reference to the development of the PM181104 molecule as a potential antibiotic for MRSA and VRE infections.

Keywords: Antibacterial potential; Methicillin resistant *Staphylococcus aureus;* Vancomycin Resistant Enterococci (VRE); Antibiotics

NS-MTAMR-6

Recombinant Therapeutic Antibodies for the Treatment of Infectious diseases

Vijay K. Chaudhary[1,3 *], Surbhi Chauhan[2], Navneet Kaur[2] and Amita Gupta[1,2,3]
*vkchaudhary@south.du.ac.in

[1]*Centre for Innovation in Infectious Disease Research, Education and Training (CIIDRET), University of Delhi, New Delhi, India*
[2]Department of Biochemistry, *University of Delhi South Campus (UDSC), New Delhi, India*
[3]*Delhi School for Skill Enhancement & Entrepreneurship Development (DSSEED, University of Delhi, New Delhi, India*

Abstract: Antibiotics and antiviral compounds have been the mainstay of treatment for majority bacterial diseases and some viral infections. With the increase in antimicrobial resistance and emergence of newer infections, the lack of licensed therapeutics and vaccines advocates a need for alternate therapy. For viral infections, one of the potential treatments is the use of neutralizing antibodies to prevent the entry and infection by the virus.
Antibodies are naturally made glycoproteins that constitute one arm of our immune system. The antibody molecule was discovered more than a century ago, as protective molecules in plasma, the cell-free component of

blood. Following this discovery, whole plasma has been used successfully as a therapy for many disease conditions including Tetanus, Diphtheria, Rabies and Snake bite.

With the understanding of antibody diversity at the molecular level, and the advent of genetic engineering, recombinant antibodies became a reality and constitute a major class of therapeutic biologics with their current global market at more than USD 100 billion. Although, the antibodies have found major applications in the management of Cancers and inflammatory disease conditions, there have been many approved antibodies for the treatment of viral infections such as Ebola virus, Respiratory Syncytial Virus, Human cytomegalovirus (HCMV), Influenza and Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV2) [Pantaleo et al., 2022, Nature Reviews Drug Discovery, 21(9):676-96.]. Recently, Human Antibody cocktails have been successfully employed for the treatment of COVID-19.

Techniques such as PCR-based cloning of antibody-encoding genes, coupled with technologies to produce antibodies in cell culture using hyper expression vectors and cell lines, have enabled researchers to produce human antibodies for therapeutic purposes. A variety of strategies have been used to develop therapeutic antibodies. The lecture will elaborate on the use of antibodies for viral infections and describe our efforts to utilize Phage displayed naïve human antibody libraries (PDHAL) for the discovery of therapeutic neutralizing antibodies against some of the targets including SARS-CoV2.

Keywords: Recombinant therapeutic antibodies, Phage display, SARS-CoV2, Neutralizing antibodies, Human antibodies

NS-MTAMR-7

Expression Patterns and Functions of Toxin-Antitoxin Loci in *Mycobacterium tuberculosis*

Amita Gupta
amitagupta@south.du.ac.in

Department of Biochemistry and Center for Innovation in Infectious Disease Research Education and Training (CIIDRET), University of Delhi South Campus, New Delhi (110021), India

Abstract: Toxin-antitoxin (TA) systems have ubiquitous presence in bacterial genomes with observed roles in stress survival, persistence and drug tolerance. They are usually two component systems comprising of a stable protein toxin that inhibits an essential cellular process, such as translation, replication, membrane integrity or peptidoglycan synthesis, leading to cell growth arrest/ cell death. An unstable antitoxin, that maybe an RNA or a protein, neutralizes its cognate toxin. TA systems are grouped into several types and families based on their and mode of antitoxin regulation as well as sequence and structure similarity. The most well characterized TA systems are type II systems where the antitoxin is a protein that binds with the toxin to form a complex and inactive the toxin. The TA genes are transcribed as an operon and the antitoxin generally auto-regulates the transcription, often in complex with the toxin.

Mycobacterium tuberculosis (*M.tb*) harbors more than 90 TA systems in its genome and majority of them are Type II TA systems. These TA systems are often located within regions of the genome that also have genes involved in virulence, dormancy, cell entry, cell signaling, suggesting that they could also contribute to the stabilization and maintenance of essential genes and the success of *M.tb* as a human pathogen. TA systems play essential roles in stress adaptation, survival and pathogenesis. We have demonstrated that the genome-encoded TA loci in *M.tb* are bonafide pairs where the toxin shows cell killing activity that can be neutralized by the cognate antitoxin. Through whole-genome microarray studies, the genes of TA systems were identified to be differentially expressed during active infection, oxidative stress, low pH stress, nutrient starvation, as well as antibiotic stress. Certain TA modules exhibited co-activation across multiple growth conditions suggesting a common regulatory mechanism. Further, deletion mutants of TA genes showed impaired host infection and survival.

Keywords: Toxin-antitoxin (TA) loci, *Mycobacterium tuberculosis*, Type-II TA system, Stress response, Microarray

NS-MTAMR-8

Investigation of G-Quadruplex DNA Motifs in the H*elicobacter pylori* Genome and their Potential as a Target for Pharmacological Intervention

Monika Kumari[1], Priyanka Payal[2], Neha R Sahu[3], Uma Shankar[2], Amit Kumar[2], Debasis Nayak[3], Sharad Gupta[2], Vikas Yadav[4] and Puja Yadav[1]*
*pujayadav@cuh.ac.in

[1]*Department of Microbiology, Central University of Haryana, Mahendergarh, Haryana, India,*
[2]*Department of Biosciences and Biomedical Engineering Indore, Simrol, Indore, Madhya Pradesh, India,*
[3]*Department of Biological Sciences, Indian Institute of Science Education and Research Bhopal, Bhopal, Madhya Pradesh, India*
[4]*School of Life Sciences, Jawaharlal Nehru University, New Delhi, India*

Abstract: *Helicobacter pylori*, a significant human pathogen associated with duodenal ulcers and gastric cancer, poses an escalating health threat marked by rising resistance and resulting clinical complications. The diminishing efficacy of *H. pylori* treatment is attributed to the growing antibiotic resistance. Recent studies emphasize the role of DNA secondary structures, specifically G-quadruplexes, in various organisms, influencing biological processes and pathogenesis.

This study aimed to investigate the presence of putative G quadruplex (PGQs) motifs in the *H. pylori* genome and explore their significance in *H. pylori* pathogenesis and biological functions.

Utilizing the QGRS mapper algorithm, we identified a non-random distribution of G-quadruplexes, predominantly within ORF regions, enriching gene categories associated with cell wall/membrane/envelope biogenesis, and amino acid transport and metabolism. Evaluation of cytotoxicity revealed that G-quadruplex ligands (Braco-19, TMPyP4, and 360A) inhibited *H. pylori* growth, demonstrating IC_{50} values of approximately 26, 45, and 15.48 µM, respectively, indicating a potential therapeutic strategy against *H. pylori* infections. qPCR-stop assay, exhibited retardation in replication of G4- motifs containing genes with increasing concentrations of K^+ ions and G4 ligand- TMPyP4, suggesting the stabilization of PGQ motifs. Additionally, the mTFP-based reporter assay showed a decrease in mTFP gene expression on Braco-19 treated cells as compared to the untreated and further affirmed the formation of stable G-quadruplex structures in the HPGQ motifs *in vitro*. Subsequently, we found the downregulation of G4- harboring gene- *imaA* and *hopG* when treated with G4- ligands and observed morphological changes in shape of G4 ligands treated *H. pylori* cells compared to untreated control bacteria.

In conclusion, this study underscores the significant impact of G-quadruplexes on *H. pylori* pathogenesis and biological processes, proposing a promising therapeutic approach for combating *H. pylori* infections by targeting G4 structures.

Keywords: *Helicobacter pylori*; G-Quadruplex DNA motifs; Pharmacological intervention

NS-MTAMR-9

The Role of Mitochondrial Genetics and Epigenetics in COVID-19 Pathogenesis

Yamini Singh*, Diksha Kumari, Sayar Singh, Deepika Chauhan
*yamini29@gmail.com

DDT division, Defence Institute of Physiology and Allied Sciences (DIPAS), DRDO, Delhi, India

Abstract: Missense mitochondrial mutations and DNA methylation patterns have previously been linked to a number of disorders. Pathogenic mitochondrial DNA (mtDNA) alterations might unveil the potential involvement of the mitochondrial genome in SARS-CoV-2 infection. Existing evidences suggest that apart from many other factors, genetic and epigenetic factors may play a significant role in COVID-19 pathophysiology. The precise mechanism underlying the connection of mtDNA variants and methylation with COVID-19 remains unclear. The aim of the present investigation is to elucidate the role of mtDNA mutations and methylation patterns in disease severity. The study was performed on 25 subjects comprising COVID-19 positive {severe deceased (n=8), severe recovered (n=8)} and negative (n=9, healthy control) individuals. We performed next-

generation sequencing of mtDNA for variant analysis and bisulphite sequencing for identification of differentially methylated regions (DMRs) in COVID-19 patients and healthy control individuals. The computational approach was applied for functional annotation. DMRs were subjected to gene annotation to identify differentially methylated genes. Gene ontological analyses and pathway analysis was carried out. The study showed the association of unique mutations with alterations of mitochondrial pathways in COVID-19 severity. KEGG pathways revealed the association of DMGs with mitochondrial biogenesis, mitophagy and OXPHOS. In conclusion, DNA methylation may influence the expression of genes involved in COVID-19 progression and should be studied further to understand the prognosis of disease.

Keywords: COVID-19; Mitochondrial pathways; Pathogenic mitochondrial DNA (mtDNA); Epigenetics

NS-MTAMR-10

DNA Damage Response and Cell Cycle Regulation of Bacteria: A Twist around the Paradigm

Hari Sharan Misra
harimisra38@gmail.com

Distinguished Professor of Biological Sciences
Narsee Monjee Institute of Management Sciences (NMIMS),
A Deemed to be University Mumbai, Maharashtra (400056), India

Abstract: The co-protease activity in RecA-ssDNA complex cleaves auto-repressor LexA resulting to the de-repression of a large number LexA controlled genes in majority bacteria. This process is called SOS response and genes that are expressed in response to DNA damage are called SOS genes. The proteins encoded by SOS genes are involved in both DNA repair and to keep the functions of crucial cell division protein (e.g. FtsZ) under check, till the damaged DNA is repaired and cells are ready to division. For a long time, this mechanism of SOS response is the only known mechanism of DNA damage response and cell cycle regulation in bacteria. However, there are bacteria including the radioresistant bacterium, *Deinococcus radiodurans* that do not obey this rule of DNA damage response and cell cycle regulation, yet they respond to DNA damage, repaired it and survive. That means, such bacteria would have had some alternate mechanism(s) of DNA damage response and cell cycle regulation beyond the canonical pathway of SOS response. Our finding supporting a new mechanism of bacterial response to DNA damage and cell cycle regulation in the radioresistant bacterium *Deinococcus radiodurans* and proposed it to be an alternate to the canonical SOS response would be discussed.

Keywords: RecA-ssDNA complex; *Deinococcus radiodurans;* DNA damage; Cell cycle regulation

NS-MTAMR-11

Triggering of TLRs Mediated Signalling Pathways by Mushroom Polysaccharide for Immune Enhancing in Cancer Management

Swapan Kumar Ghosh
gswapan582@gmail.com

Molecular Mycopathology Lab., Cancer Research Unit, PG Department of Botany,
Ramakrishna Mission Vivekananda Centenary College (Autonomous),
Rahara, Kolkata, West Bengal (700118), India

Abstract: "Immunomodulation" term is now generally used in medical science and it means modification of our immune response (enhancement or suppression) by using a natural compound or a drug. Already some chemical immune modulators are in the market for examples prednisone, dexamethasone, etc are being used to manage some inflammatory diseases. Immunosuppressant compounds or drugs (e.g. Cyclosporin A, a fungal peptide) are also in market and administered during organ transplantation to arrest the rejection of organs. Unfortunately, these commercial immune modulators are causing health complications like reduced bone marrow, gastric and intestinal damage, etc. Under such circumstances, more safe and active agents are needed as alternatives for this

purpose. So, natural products from different sources are searching and screening as immunomodulating agents. Mushroom polysaccharides are the most commonly reported natural immunomodulators. The diversity of the sugar compositions, main chain polymer structures, degrees of branching, conformations, molecular weights, and other physical properties are responsible for significant effects on the bioactivity and mode of action of each immunomodulating polysaccharide (Ghosh and Chakraborty 2018; Chakraborty et al 2019; Ying and Hao 2023). Based on the monosaccharide unit, polysaccharides are basically two types like homopolysaccharides and heteropolysaccharides. Heteropolysaccharides are better than homopolysaccharides in this purpose. The relationship between the polysaccharide's composition and bioactivity has gained attention during the past decade. Polysaccharides with monosaccharide residues such as Mannose, Rhamnose, and Fucose are known to have better bioactivity (Deveci et al 2019). Currently in some laboratories including my lab., isolation, purification of mushroom polysaccharides from both edible and medicinal mushrooms, their structure determination by HPTLC, HPLC, GC-MS, 2/3 D-NMR, etc and application in immune enhancement for cancer management are going on. Among the reported polysaccharides which have immunomodulatory and antitumor activities, the two best-known polysaccharides are lentinan, isolated from *Lentinus edodes*), and *schizophyllan*, isolated from *Schizophyllum commune* and also both lentinan and schizophyllan contain β-1,3-d-glucans with β-1,6 branches. Lentinan exhibited immunomodulatory properties against gastric cancer whereas schizophyllan was effective against head and neck cancer. This immune enhancement by external natural products occurs in different signalling pathways in immune cells like macrophage, monocytes, etc. There are some antigen receptors like dectin-1, Complement receptor 3 (CR3), Lactosylceramide (LacCer), and Toll-like receptor (TLR) in human immune cells. Mushroom polysaccharides are unable to rich inside of the immune cells due to their high molecular weight, so, they bind with those receptors and trigger different signalling pathways like Dectin mediated signalling pathway, TLRs mediated signalling pathway, etc. Similarly, other scientists noted the NF-kB and MAPK signal pathways via TLR-2 and TLR-4 for immunomodulation (Yin et al 2021). Yan et al (2019) demonstrated activation of murine macrophage cells via TLR-2 pathway and stimulation of the secretion of cytokines and other immune mediators by 3-O-methylated heterogalactan of *Pleurotus eryngii*. Here our concern with TLRs mediated signalling pathway. In our lab. we (Bera and Ghosh 2024; Sanyal and Ghosh 2024) isolated homopolysaccharides and heteropolysaccharides from mushrooms (*Candolleomyces candolleanus, Trechispora pallescens, Pleurotus* sp,etc.)and applied in mice model (isolated lymphocyte and macrophage) and found that they after binding with TLR4 receptor of macrophage, activated immune cells. qPCR results of both *in vivo* (mice) and *in vitro* (mice cell line) experiments, indicated that polysaccharide activated TLR4 mediated MyD88 dependent signalling pathway, inducing serially like TLR4, MyD88, TRAF6 and NF-κB. By immune phenotyping study (Flow cytometry), it was observed that polysaccharides activated the $CD8^+$ T cells, $CD19^+$ B cells and CD 3 protein complex which activated both T cells and B cells. The experiment data exhibited that mushroom polysaccharides enhanced the immune function by promoting cytokine expression levels for both T lymphocytes and macrophages *in vivo*. In this study, we will discuss, in details of TLR4 mediated signaling pathway for immunomodulation in cancer management.

Keywords: Immunomodulation; Cancer management; TLR4 mediated signaling pathway; Mushroom polysaccharide

NS-MTAMR-12

Gut Metabolite Indoxyl Sulfate has Selective Deleterious and Anticancer Effect on Colon Cancer Cells

Anil Kumar
anilk@nii.ac.in

Gene Regulation Laboratory, National Institute of Immunology, New Delhi (110067), India

Abstract: There are number of reports about anti-cancer activity of indole derivatives and some of them such as Vinblastine have been used in clinic evaluations. In this study, we investigated the role of indoxyl sulfate (IS), an indole derivative, for its selective anti-cancer activity on colon cancer cells. Whether indoxyl sulfate has any harmful effect on normal colonic cells has also been studied. IS treatment on HCT-116 and HT-29 human epithelial adenocarcinoma cell lines led decrease in cell proliferation efficiency, cell viability and ATP content and showed 10% increase in cell apoptosis in comparison to control. Indoxyl sulfate also caused cell cycle to cease at G2/M phase. During animal study, balb/c mice were treated with 100mM of indoxyl sulfate to check colonic inflammation, if any, by IS administration and level of inflammatory cytokines IL-17A, IL-1β and TNF-α were studied. The change in the level of inflammatory cytokines after IS treatment was found statistically

insignificant, hence IS was found not causing inflammation. No significant change in the length of intestine and spleen was noted after IS treatment. In conclusion, we found IS has selective deleterious and anticancer effect on colon cancer cells and does not cause harm to normal colonic cells.

Keywords: Indoxyl Sulfate, Anticancer effect; Colon cancer cells; Inflammatory cytokines

NS-MTAMR-13

Probing the role of Interfacial Residues in the Activity and Stability of Adenylosuccinate Lyase from *Leishmania donovani*

Jignesh kumar A Mochi, Jaykumar Jani and Anju Pappachan*
*anju.p@cug.ac.in

School of Life Sciences, Central University of Gujarat, Gandhinagar, Gujarat (382 030), India

Abstract: Purine salvage enzymes have been of significant interest in anti-Leishmanial drug development due to the parasite's critical dependence on this pathway for the supply of nucleotides in the absence of a *de novo* purine synthesis pathway. Adenylosuccinate lyase (ADSL) one of the key enzymes in this pathway is a homo-tetramer, where the active site is formed by residues from three distinct subunits. Analysis of the subunit interfaces of LdADSL, revealed certain conserved residues- R40, E334, N335 and R370 forming critical inter-subunit interactions and also involved in substrate binding. Mutating these residues resulted in reduced activity, stability and affinity towards the substrate, SAMP as shown by enzyme kinetics, fluorescence spectroscopy and thermal stability studies. MD simulation studies also supported this. Structural analysis points to disrupted interactions with the catalytic base, H196, reduced hydrogen bonds and electrostatic interactions between the substrate and the enzyme, C3-loop conformational changes and altered conformation of active site residues as reasons for reduced activity and stability. Incubation of pairs of the mutant enzymes restored partly the functional active site by subunit complementation. Studies so far have majorly focused on the ADSL active site for designing drugs against it. Our work indicates that an alternative inhibitory mechanism for the enzyme can be designed by targeting the inter-subunit interface.

Keywords: Interfacial residues; Adenylosuccinate lyase; *Leishmania donovani;* Inhibitory mechanism

NS-MTAMR-14

An Interplay between Viruses and Host for microRNAs during Infection

Sunit K. Singh
Ph.D, FNASc, FRSB, FAMS[1,2]
sunitsingh2000@gmail.com

[1] Director, Dr. B R Ambedkar Centre for Biomedical Research (ACBR)
University of Delhi, New Delhi (110007), India
[2] Laboratory of Human Molecular Virology and Immunology
Molecular Biology Unit, Faculty of Medicine, Institute of Medical Sciences (IMS)
Banaras Hindu University (BHU), Varanasi, Uttar Pradesh (221005), India

Abstract: MicroRNAs are small non-coding RNAs fine tune the posttranscriptional gene regulation. Cellular microRNAs have been involved in the regulation of many cellular pathways. The viruses have evolved different strategies to exploit the cellular pathways by perturbing the expression of cellular microRNAs. The perturbations in the cellular microRNAs during viral infection play an important role in pathogenesis of viruses. This complex interaction between host and viruses to control the microRNA pathway usually favours viral infection and virus persistence by immune evasion strategies. Viruses use these miRNAs to manipulate both cellular and viral gene expression. Viruses have evolved the ability to modulate the expression of specific cellular miRNAs in order to enhance their replication. We reported the mechanism of exploitation of cellular microRNA by human immunodeficiency virus (HIV) to breach the Blood

brain barrier for entering into brain and the mechanisms utilised by Japanese Encephalitis virus (JEV) to target the important adaptor proteins of the immune cell signalling pathways as a strategy for the immune evasion.

Keywords: MicroRNAs; Cellular pathways; Human immunodeficiency virus (HIV); Japanese Encephalitis virus (JEV); Immune evasion

NS-MTAMR-15

Microbiome and Drug Resistance

Nirmal Kumar Ganguly
ganguly1nk@gmail.com

Ex-DG, ICMR, New Delhi, India

Abstract: The title Microbiome and Drug Resistance describes the rise and dissemination of antibiotic resistance among the typically commensal bacteria in the human digestive system. These commensal microbes, which form a normal part of the gut microbiota, can acquire and spread resistance genes through various processes such as mutations or horizontal gene transfer. Antibiotics can significantly disrupt robust microbiomes, which are diverse and balanced microbial communities in the gut. While antibiotics aim to eliminate harmful bacteria, they also destroy beneficial commensal bacteria, reducing microbial diversity. This disruption can cause an imbalance, known as dysbiosis, making the gut more vulnerable to infections, inflammation, and the proliferation of resistant bacteria. Such disturbances can have long-term effects, compromising the overall health and resilience of the microbiome and potentially affecting the host's immune system and metabolism. The growing prevalence of these resistance traits is alarming because it can result in the transfer of resistance genes to harmful bacteria, diminishing the efficacy of antibiotic treatments and posing a serious public health risk. This situation highlights the critical need to monitor and understand the factors driving antimicrobial resistance in the human gut microbiome. Precision bio-therapeutics effective in the gut, it is crucial to develop targeted treatments that adjust the microbiome without disturbing its overall balance will be hovering the markets soon. This includes creating probiotics, prebiotics, and synbiotics customized to individual microbiome profiles, encouraging the growth of beneficial bacteria and inhibiting harmful ones. Utilizing advanced methods like metagenomic sequencing and bioinformatics can help identify specific microbial strains and their roles, facilitating the development of personalized therapies. Moreover, these precision bio-therapeutics are both effective and safe.

Keywords: Microbiome and drug resistance; Dysbiosis; Bio-therapeutics; Human digestive system

NS-MTAMR-16

Translating and Integrating Molecular Codes of Microbes and Mosquitoes with Indian Vedic Science to Solve Lifestyle-associated Diseases

Rajnikant Dixit
dixit2k@yahoo.com; rkdixit@icmr.gov.in

Department of Vector Genomics, ICMR-National Institute of Malaria Research, Sector-8, Dwarka, Delhi (110077), India

Abstract: In the age of genomics, decoding the basic principles of biology for treating lifestyle-associated diseases is currently being explored with advanced technologies. However, modern technologies also pose a challenge in maintaining one's talent for a peaceful and balanced life, resulting in increased mental stress, negative thinking, depression, anger, lust, drug addiction, vindictiveness, and suicidal thoughts among the youth. The only possible way to solve this problem is to trace the epistemological essence contained in the Indian Vedic texts, such as Srimad Bhagavad Gita which defines all the elements of nature, animate and inanimate, and their interrelation and correlation with human intellectual power and behavior. We need to understand and interpret these mysteries of the Gita text through modern science, especially biological science which deals with all the complexities associated with lifestyle. The author has personally been inclined towards spiritual thoughts,

particularly the long-term impact of internal feelings and influences on ideological power, mental development, and intellectual balance due to repeated study of Shrimad Bhagavad Gita. This experience provided a unique opportunity to understand and carry forward new experiments on the genetic basis of living beings deeply. The research being conducted in the author's laboratory on mosquito lifestyle has multidimensional and long-term benefits not only to provide effective solutions for mosquito control but also a core knowledge that can be translated and integrated into the science of spirituality. What is needed is an inclusive plan that promotes research and an education system on spiritual knowledge along with science. A brief overview would be presented in the talk if provided the opportunity.

Keywords: Molecular codes; Microbes; Mosquito; Indian Vedic Science; Lifestyle-associated diseases

NS-MTAMR-17

Caerulomycin A: A Novel Immunosuppressive Molecule Targeting Autoimmune Disorders

Javed N Agrewala
jagrewala@iitrpr.ac.in

Immunology Laboratory, Department of Biomedical Engineering, Indian Institute of Technology Ropar, Rupnagar, Punjab, India

Abstract: Cytokines are crucial in maintaining immune homeostasis, particularly in regulating peripheral tolerance through regulatory T cells (Tregs) activity. This study reveals a novel function of Caerulomycin A (CaeA), a bipyridyl compound, in promoting Treg generation. Our findings show that CaeA markedly increases the population of CD4(+) Foxp3(+) Tregs and reduces Th1 and Th17 cells, indicated by the diminished frequencies of CD4(+)/IFN-γ(+) and CD4(+)/IL-17(+) cells, respectively. Mechanistically, CaeA inhibited IFN-γ-induced STAT1 signaling by upregulating SOCS1 expression while concurrently enhancing TGF-β-mediated Smad3 activity. Additionally, CaeA rescued Tregs from inhibition induced by IFN-γ. Blocking Smad3 signaling reversed the CaeA-driven expansion of Tregs. These results highlight the potential of CaeA as a promising therapeutic agent for treating autoimmune diseases by promoting Treg generation.

Keywords: Cytokines, Caerulomycin A, Immunosuppressive molecule, Autoimmune disorders

NS-MTAMR-18

In Silico Bioprospecting and Chemoinformatics Screening of Potential Inhibitors against Drug Resistant *Acinetobacter baumanii* and *Pseudomonas aeruginosa*

Sinosh Skariyachan
sinoshmicro@stpius.ac.in, sinoshskariya@gmail.com

Department of Microbiology, St. Pius X College Rajapuram, Kasaragod-Kannur University, Kerala, India

Abstract: Multidrug-resistant Acinetobacter baumannii (MDRAb) and Pseudomonas aeruginosa (MDRPa) were declared as priority-I & II pathogens, respectively by WHO (2019) and screening of potential therapeutic agents have profound scope and applications. This study aimed to identify natural lead molecules as potential inhibitors against MDRAb and MDRPa by in silico bioprospecting. Based on the metabolic pathway analysis, protein RecA (RecA) and orotate phosphoribosyltransferase (PyrE) were identified as potential drug targets for MDRAb. The three-dimensional structure of RecA and PyrE were computationally predicted. Library natural molecules were constructed and subjected to virtual screening, molecular docking, and molecular dynamic simulation. The therapeutic potential of computationally predicted molecules was validated by in vitro studies. Computational screening suggested that out of 236 molecules selected from the library, 06 leads were qualified for drug likeliness, and pharmacokinetic features, and one molecule-natural epiesteriol exhibited significant binding towards RecA and PyrE in comparison with the binding of faropenem and polymyxin E towards their usual targets. MD simulations suggested that epiesteriol-receptor complexes demonstrated stability throughout the simulation. The in vitro assay substantiated the finding. Similarly, Celastrol in Celastrus paniculatus and

Rotiorinol in Chaetomium cupreum showed better binding with GacA (binding energy -7.2 kcal/mol) and RhlR (binding energy -8.0 kcal/mol) of MDRPa, respectively, when compared to the binding of Meropenem and its target. MD simulation studies and the in vitro studies confirmed the inhibitory potential of these molecules ($p \leq 0.05$). The present study suggested that natural molecules screened by in silico bioprospecting can be used as potential binders towards the identified targets of MDRAb and MDRPa.

Keywords: Drug-resistant *Acinetobacter baumannii*; *Pseudomonas aeruginosa*; In silico bioprospecting; chemoinformatics; molecular docking; molecular dynamic simulation

NS-MTAMR-19

Managing Antimicrobial Resistance (AMR) with One Health Approach

Urmi Bajpai
urmibajpai@andc.du.ac.in

Department of Biomedical Science, Acharya Narendra Dev College, University of Delhi, New Delhi, India

Abstract: Antimicrobials are essential for preventing and treating infections caused by bacteria, fungi, parasites, and viruses in humans, animals, and plants. However, antimicrobial resistance (AMR) has become a global crisis driven by overuse and misuse—especially in non-human sectors, where the sub-therapeutic doses far exceed the consumption in human medicine. This misuse accelerates the emergence of multi-drug-resistant strains and renders conventional treatments ineffective. Immediate action is crucial to ensure our planet's safe, healthy future. Key steps include promoting preventive measures, discovering new treatments, improving access to antimicrobials, and fostering stronger antibiotic stewardship.

The One Health paradigm, an age-old wisdom which recognises the interconnectedness of humans, animals, and ecosystem health, has gained global recognition as an integrated solution to complex global challenges such as AMR, climate change, and food safety. Forming a Quadripartite alliance in 2022--comprising the FAO, WHO, WOAH and the UNEP)—marks a significant step in mainstreaming the One Health paradigm to combat AMR. Phage Therapy, with its advantages in both plants and animals and being ecologically friendly, presents promising alternatives to traditional antibiotics. Given the urgency, integrating AMR-mitigating strategies into the One Health framework is pivotal to expediting our efforts and safeguarding against this global crisis. In my talk, I will explore how adopting a One Health strategy can facilitate cross-sectoral initiatives to control AMR.

Keywords: Antimicrobial; Antibacterial; Antimicrobial Resistance (AMR); One Health Approach

NS-MTAMR-20

Channelizing Biosynthetic Capabilities of Actinobacteria for Industrial Application

Sheetal Bhasin
sheetalrbhasin@gmail.com

Department of Biosciences, Maharaja Ranjit Singh College of Professional Sciences, Indore Madhya Pradesh, India

Abstract: Biocatalysis using microbial enzymes is a large platform for solving industrial bottlenecks. Actinobacteria, a complex group of organisms, possess huge reservoir of metabolic capacities owing to their large genome size as compared to other bacteria. This heterogenous group encompasses industrially and environmentally useful representatives. Being common inhabitants of soil, these organisms are adapted to biodegradation of varied complex organic biomolecules which makes them prolific producers of numerous enzymes. Two third of the bioactive compounds of health care and agricultural use are produced using Actinobacteria. Actinobacterial diversity was worked upon to investigate glucose isomerase and amylase producing organisms. Actinobacterial enzymes were employed for the production of High Fructose Corn Syrup (HFCS) using a non-sweet source. Production process of glucose isomerase and amylase was optimized. Saccharification of corn starch was performed. Glucose resulting from this process was isomerized to fructose with the help of glucose isomerase. To increase the functional efficiency of the process we immobilized glucose isomerase and amylase. This increased the percentage of saccharification and isomerization. The immobilization

process also increased the thermostability as well as the pH stability of the enzymes. Production of HFCS is carried out in two steps, saccharification and isomerization, however we attempted to execute the two processes simultaneously. The glucose isomerase and amylase were co-immobilized to increase the efficiency. The implications and working for co-immobilization and simultaneous saccharification and isomerization shall be discussed.

Keywords: Biocatalysis; Actinobacteria; Industrial application; Saccharification

NS-MTAMR-21

Evolutionary Conserved Microbial Proteins: Targets Controlling Key Molecular Events and Pathogenesis

Bishwajit Kundu
bkundu@bioschool.iitd.ac.in

Kusuma School of Biological Sciences, IIT Delhi, Hauz Khas, New Delhi, India

Abstract: Conserved molecular signatures in multidrug-resistant intracellular pathogens can serve as novel therapeutic targets for mitigation of infection. Here we present the identification, characterization analysis, and molecular mechanisms of three such targets and their possible intervention strategies. The first is the *S. typhi* cell division activator protein (StCAP), which we found as a DNA-binding protein. Apoptotic protease activating factor1 (Apaf1), emerged as an StCAP-interacting partner. StCAP-transfected T1Mac showed a significant increase in LC3 II (autophagy marker) expression and downregulation of caspase 3 protein.
The second is the HtpX protein, found conserved in the drug-resistant and susceptible isolates of N. gonorrhoeae (NgHtpX). HtpX is a transmembrane metalloprotease that has a role in stress response. We identified pemirolast and thalidomide as high-energy binding ligands of NgHtpX which imposed a dose-dependent reduction in viability of cultured *N. gonorrhoea*.
The third is a cytoplasmic enzyme L -L-asparaginase, conserved in many bacteria and intracellular pathogens, which displays a critical metabolic role in acid regulation and drug efflux resistance. When targeted with in-silico identified inhibitors showed a drastic reduction in viability.

Keywords: *S. typhi* cell division activator protein (StCAP); HtpX protein; L -L-asparaginase; Conserved microbial proteins

IS-MM-1

Importance and Role of Biotechnology on Sustainable Food Sources and Environmental Health in Southern Africa

Thierry Regnier*, M. Thaoge –Zwane and B. Meiring
*regniert@tut.ac.za

Department of Biotechnology and Food Technology, Faculty of Science,
Tshwane University of Technology, Pretoria, South Africa

Abstract: According to the latest statistics, Africa hosts almost 282 million undernourished people. The absence of significant progress toward the WHO global nutrition targets is a concern. Despite the increase of biotechnology studies in Africa, the gap between processes and implementation remains high in all subregions with some exceptions of countries in Southern Africa. One of the challenges despite conflicts and climate change are the lack of regulation and energy/funding allocated to such projects. Therefore, the presentation focuses on assessing the current use of current biotechnology processes in South Africa to improve food security and cellular agriculture *via* selected key studies. The data presented were gathered using the different databases considering theses, reports and articles published in the time interval between 2010 and 2023. A search filter was applied for entering keywords, articles, titles, and years of publication. The bibliometric analysis, based on the metadata of the documents obtained from the different platforms between 2010 and 2023, showed that biotechnology and microbiological research and development have already produced significant products on the market, and will further have a pivotal role to play in encouraging and enhancing food production. This includes

the intervention in increasing crop yield through introducing high-yielding varieties resistant to biotic and abiotic stresses, the main important approach in developing Southern African countries is to intensify the nutritional values of foods. Another consideration that has not been fully explored is that fermentation using indigenous traditional microbial agents also plays a vital role in the production of novel foods since fermented foods can enhance food quality, safety and security. It is evident from the literature that the ability of biotechnology to act as a tool to assist in solving the issue is far from being fully exploited. Current trends highlight the need for more skill transfer and sustainable processes, to provide safe and secure food, which eventually can act as a valuable tool to reduce poverty.

Keywords: Biotechnology; Sustainable food sources; Environmental health; Southern Africa

IS-MM-2

Biodiesel Production from Optimized *Aloe vera* rind Hydrolysate, Lipid Profiling, and Biodiesel Properties Prediction

Ameera Al Shehhi and Nallusamy Sivakumar*
*apnsiva@squ.edu.om

Department of Biology, College of Science, Sultan Qaboos University,
PO Box 36, PC 123, Muscat, Oman

Abstract: Exploring low-cost feedstock for bioenergy production to replace a non-renewable energy source is gaining attention nowadays. *Aloe vera* rind (AVR) is considered a discarded waste in the *A. vera* products industries, which mainly focus on the gel. However, the presence of cellulosic components in AVR makes it an alternative, renewable bioresource to produce bioproducts. In this study, AVR was used as a novel substrate for biodiesel production by oleaginous yeasts, *Rhodosporidium toruloides* and *Cryptococcus curvatus*, using mono and co-culture methods. Different pretreatments were used in the preparation of the AVR substrate, and different analytical techniques (X-ray diffraction, Fourier transform infrared, and dynamic light scattering) were used to characterize the pretreated AVR. The pretreatment results showed that the H2SO4 pretreatment has the highest effect by increasing the saccharification percentage by 14%, followed by HCl. Double pretreatment with Triton X-100 decreases saccharification percentages. The Box-Behnken design was used to optimize the enzymatic saccharification conditions. The predicted optimum conditions for enzymatic saccharification of AVR were 47.91°C, 70 U/g cellulose, and 4.75% substrate loading for a 50 mL working volume. The maximum reducing sugar obtained in the validation experiment was 34.78 g/L with 65.89% saccharification. The increase in saacharification could be explained by the crystallinity reduction, lignin destruction, and particle size decline of AVR after acidic treatment. The result shows that *R. toruloides* produces about 5g/L (32%) of lipid, which is significantly more than *C. curvatus*and co-culture. The lipid profiles of mono and co-culture were similar and showed the presence of 13 fatty acid methyl esters. The predicted properties of the produced biodiesel, such as cloud point, cetane number, iodine value, and density, met the international standards (EN14214 and ASTM D6751). Consequently, the AVP could be a potential renewable feedstock for producing microbial lipids, which are crucial for biodiesel production.

Key words: *Aloe vera*rinds; Enzymatic saccharification; Reducing sugars; pretreatments; biodiesel; lipid profile

IS-MM-3

Combating Infectious Diseases: A Continuing Journey

Harshini Mukundan
hmukundan@lbl.gov

Scientist, program development, AAAS Ambassador, AAAS Fellow, Senior Policy Advisor,
The Council on Strategic Risks

Abstract: Emerging infectious diseases are a major concern to our health security. As was evidenced during the COVID-19 pandemic, the impact of a pandemic associated with a newly evolving pathogen can cause grave impact to our health. In addition, emerging crises such as antimicrobial resistance are a huge concern for our health and vitality. Our team has been working on addressing these challenges - and building in resilient science in order to help us address future outbreaks better. In this presentation, we will discuss the journey thus far, and

the lessons learned from it - and where we can go in the future to prevent impact on human life and economy associated with infectious diseases.

Keywords: Covid-19, Economy, Infectious-diseases, Human health

IS-MM-4

Human gut microbiome with rare diseases: A new paradigm of metagenomics approach

Santasree Banerjee[1*], Chen Li[2], Parimal Das[3], Anjana Munshi[4], Kausik Mandal[5], Rakesh Kumar Panjaliya[6], Mainak Sengupta[7] and Muhammad Ayub[8]
*santasree.banerjee@yahoo.com

[1]Department of Genetics College of Basic Medical Sciences Jilin University Changchun China
[2]Department of Human Genetics and Department of Ultrasound, Women's Hospital School of Basic Medical Science Zhejiang Provincial Key Laboratory of Genetic and Developmental Disorders Zhejiang University School of Medicine Hangzhou China
[3]Centre for Genetic Disorders Banaras Hindu University Varanasi, India
[4]Department of Human Genetics and Molecular Medicine Central University of Punjab Bathinda India.
[5]Department of Medical Genetics Sanjay Gandhi Postgraduate Institute of Medical Sciences Lucknow Uttar Pradesh India
[6]Department of Zoology, University of Jammu, Jammu and Kashmir, India
[7]Department of Genetics, University of Calcutta, Kolkata, West Bengal (700019), India
[8]Department of Psychiatry, University College London, London, UK

Abstract: The human microbiome is comprising of bacteria, archaea, protozoa, fungi, viruses and eukaryotic microbes that reside in our bodies. However, the human body carries approximately 10^{14} cells of diverse group of microorganisms. In addition, microbial population inhabiting our gastrointestinal tract, commonly referred to as the "human gut microbiome". These microbes have significantly impact in our physiology, specifically in both health and disease. In general, human gut microbiome majorly contribute to metabolic functions, provide protection against pathogens, activate the immune system, which cumulatively affect directly or indirectly most of our physiologic functions. So, alteration of usual microbial population in human gut microbiome leads to the dysbiosis which finally causes diseases. Human gut microbiome plays an important role in human health, specifically it influences the progression of colorectal cancer as well as other disorders associated with the nervous system, immunity, and metabolism. The human gut microbiome is thought to play a key role in the etiology of inflammatory bowel disease, type 2 diabetes, hypertension, colorectal cancer and rare diseases. Here, we intend to investigate and understand the significance of human gut microbiome for underlying rare diseases. Moreover, human gut microbiome is recently reported to be associated with ten rare diseases, including Pediatric Crohn's disease, Lichen planus, Hypophosphatasia, Discitis, Cogan's syndrome, Chancroid disease, Sennetsu fever, Acute cholecystitis, Grave's disease and Tropical sprue. Hence, next-generation sequencing based human metagenomics study is allowing us to address the individual's genetic and genomic pathography, and tackles the illness with specific and effective personalized medicine based therapeutic interventions.

Keywords: Human gut microbiome, Metagenomics, Rare diseases, Personalized medicine, Therapeutic intervention

NS-MM-1

Ending Tuberculosis from India by 2025: How Challenging is the Task?

Sarman Singh
MD, FRCP, FRSC, FAMS
sarman.singh@gmail.com

Director Medical Research,
AVMC&H, Vinayaka Mission's Research Foundation, Pondicherry, India

Abstract: Tuberculosis (TB) is one of the deadliest infectious diseases killing millions of people every year. Resistance to standard anti-tuberculosis drugs has become a major challenge in the treatment and control of TB around the globe. The resistance to mycobactericidal drug rifampicin with or without isoniazid resistance is

known as multidrug resistant tuberculosis (MDR-TB). MDR-TB threatens the progress made so far by the TB elimination programs. Patients infected with MDR-TB, are practically refractory to standard first-line treatment. The number of primary DR-TB decreased from 3.90% in 2015 to 3.10% in 2020 but again started increasing in 2021 and reached to 3.60%. India notified 24.20 lakh MDR cases in the year 2022; an increase of 13.0% in comparison to 2021 and reported a total number of 63,801 MDR cases. In 2017, India launched its revised national Strategic Plan (NSP) (2017-2025) with the ambitious and challenging goal of eliminating TB by 2025, 5 years before the 2030 target set by the United Nations Sustainable Developmental Goal (UN-SDG) and WHO End Tuberculosis Strategy. The World Health Organization (WHO) is aiming to eliminate TB by the year 2030. However, the target looks very difficult if not impossible.

Though world health organization (WHO) has committed to end tuberculosis by 2030, while some countries like India have proactively advanced this target to end tuberculosis by 2025. Though ending tuberculosis in India in next 1 year is seemingly a herculean task. Nonetheless, this optimistic short duration was questioned even at the time of declaration. However, various stakeholders are working on various fronts, yet the progress in achieving the targeted goal is far, especially after the COVID-19 epidemic. There are several reasons why this elimination of TB is far more difficult than a few viral diseases world could eliminate. To achieve this goal, a multipronged approach is required, but most importantly clarity from WHO needs to be issued to the inventors and pharma-enterprises to invest in rapid and point of care serological tests. Without prompt diagnosis of infected individuals and active case finding through such RDTs, the target may look even far more distant.

Keywords: Tuberculosis, MDR-TB, National Strategic Plan, UN-SDG

NS-MM-2

Importance of Molecular Epidemiology: Learning from SARS-CoV-2

Mahesh Dhar
maheshdhar@gmail.com

DSIDC Complex, Okhla-1, New Delhi, India

Abstract: Molecular epidemiology has proven crucial in understanding and combating the COVID-19 pandemic, highlighting its significance in modern public health. By analyzing the genetic makeup of SARS-CoV-2, researchers have tracked its origin, spread, and evolution, providing valuable insights for disease control and prevention. This approach enabled the rapid development of diagnostic tests and vaccines, demonstrating the power of genomic surveillance in pandemic response. It allowed for the identification of new variants, such as Delta and Omicron, helping health authorities adapt strategies to combat emerging threats. Molecular epidemiology also revealed patterns of transmission, aiding in contact tracing and informing public health measures. It exposed the virus's ability to cross species barriers, emphasizing the importance of the One Health approach in preventing future pandemics.

Furthermore, this field facilitated global collaboration, with researchers worldwide sharing genomic data to track the virus's spread and evolution in real-time. INSACoG, setup in Dec. 2020 bought together national institutes of diverse research mandates for a sole purpose of whole genome sequencing of prevalent SARS-CoV2 strains. This unprecedented cooperation has set a new standard for international scientific collaboration in the face of global health crises. The SARS-CoV-2 pandemic has underscored the critical role of molecular epidemiology in modern disease surveillance, prevention, and control, paving the way for more effective responses to future outbreaks.

Keywords: Molecular epidemiology, SARS-CoV-2, Diagnostic tests and vaccines, INSACoG

NS-MM-3

Shared and Disease-Specific Microbiome Signatures across Human Diseases

Bhabatosh Das
bhabatosh@thsti.res.in

Centre for Microbial Research, BRIC-Translational Health Science and Technology Institute, NCR Biotech Science Cluster, Faridabad, Haryana (121001), India

Abstract: Our recent studies identified gut microbiome dysbiosis as a potential risk for several metabolic and infectious diseases, including severe acute malnutrition, ulcerative colitis, type 2 diabetes, non-alcoholic fatty liver disease, and gall bladder cancer. A meta-analysis of the gut microbiome diversity and dynamics in the disease state revealed that several bacterial species, including *Escherichia coli, Streptococcus, Collinsella*, *Salmonella,* and *Fusicateni bacter,* shared a signature of increased abundance compared to the healthy controls, while *Faecali bacterium, Roseburia*, and *Butyricoccus* showed lower abundance in the disease state. More interestingly, we observed that some of these microbial signatures are disease-specific, while others are common across diseases. Our further mechanistic studies established that microbial-derived metabolites like ethanol, lipopolysaccharides and others play a crucial role in modulating host cellular metabolic activity and transforming into a disease-specific state. We address a critical knowledge gap in microbiome-based biomarker discovery and understanding complex diseases by exploring the functional potency of the signature microbiota.

Keywords: Disease-specific microbiome signatures; Human diseases; Meta-analysis; Gut microbiome diversity

NS-MM-4

Mitochondrial Dynamics: Regulation and Functional Role

Sanjay Kumar
sanjay28@gmail.com

Indian Institute of Science Education & Research (IISER), Tirupati, Andhra Pradesh, India

Abstract: Mitochondria is a dynamic organelle that continuously undergoes fission and fusion to meet cellular demand. The balanced state of mitochondrial fission and fusion keeps mitochondria healthy and ensures optimal mitochondrial functions. I will talk about the crosstalk of canonical and noncanonical TGF-β signaling and regulation of mitochondrial fission and fusion, followed by the role of altered mitochondrial dynamics in ovarian cancer cell proliferation, migration, invasion, F-actin remodeling, EMT, and restoration of mitochondrial fusion by genetic or pharmacological activation of Mfn2 reduces ovarian cancer progression.

Keywords: Mitochondria; Pharmacological activation; Mfn2; Ovarian cancer progression

NS-MM-5

Microbes as Ecosystem Guardians Integrating Traditional Wisdom and Modern Innovations for Human Welfare

Baljeet Singh Saharan
baljeetsaharan@hau.ac.in

Department of Microbiology
Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana (125 004), India

Abstract: Ubiquitous nature of microbes is very important. Microorganisms are fundamental to Earth's ecosystems, performing essential roles that sustain the balance of natural processes. These microscopic entities contribute to biogeochemical and nutrient cycling, soil health, and the regulation under environmental conditions, making them indispensable to ecological stability. This lecture will explore how we can harness the

power of microbes to address some of the most pressing global challenges of this era, including climate change, food security, and pollution. We will delve into the multifaceted roles of microbes as stewards of nature, focusing on their innovative applications in enhancing human welfare. By examining cutting-edge research and technological advancements, the lecture will illustrate how microbes are pivotal in fostering sustainable development. Key areas of discussion will encompass microbial diversity and their essential ecosystem services, which include supporting agricultural productivity, advancing medical therapies, and driving industrial applications. Additionally, we will investigate the critical role of the human microbiome in maintaining health and combating diseases. Through this comprehensive exploration, the lecture aims to underscore the indispensable contributions of microbes to human well-being and environmental sustainability. It will highlight their potential to address global challenges and secure a healthier, more resilient future for all of us.

Keywords: Microbes; Human welfare; Traditional wisdom; Modern innovations

NS-MM-6

Interplay between Microbiota and Endocrine-disrupting Chemicals: Implications on Ecosystem and Human health

G. Velmurugan
vel@kmchrf.org

Chemomicrobiomics Laboratory, Department of Biochemisty & Microbiology, KMCH Research Foundation, Coimbatore, Tamil Nadu (641 014), India

Abstract: Microbes and chemicals are omnipresent in all different strata including extraterrestrial space. The interplay between them happens continuously and they are double-edged swords i.e., the chemicals will undergo changes due to microbial action and in parallel the chemicals will also influence the microbial diversity and physiology. During the last few decades, there has been enormous production and release of both natural and synthetic chemicals into the environment including human body. Most of these chemicals, interfere the endocrine function of the mammals and hence termed as "Endocrine-disrupting chemicals". The fate of these EDCs in the environment are largely determined by the microbiome. Here, we will be discussing on the gut microbial metabolization of different EDCs (including toxic elements, pesticides, persistent organic pollutants, food additives, etc.,) and its influence on aetiology of metabolic diseases in humans. In addition, there is increasing evidence on the emergence of antimicrobial resistance due to the crosstalk between EDCs and microbiome. This interplay between the EDCs and microbiome in different environments drives the whole planet and determines the One Health.

Keywords: Endocrine-disrupting chemicals; Gut microbial metabolization; Whole plant; One health

NS-MM-7

Effects of Air Pollution Particulate Matters on Bacterial Biofilms

Mukesh Kumar Yadav
mukesh.yadav@cup.edu.in

Department of Microbiology, Central University of Punjab, Bathinda, Punjab (151401), India

Abstract: Background: Increasing air-pollution is major concern for human health. The particulate matters (PM) present in air-pollution exerts toxicity and deposits in the respiratory tract and increases microbial infections. The exact mechanism by which PM such as Urban particles (UP), Asian Sand Dust (ASD) particles, Diesel Exhaust particles (DEP) exposure interact and contribute in microbial infection is not well studied. We evaluated the effect of urban particles UP, ASD and DEP particles on Streptococcus pneumoniae (pneumococcus) in vitro biofilm formation, colonization of human middle ear epithelium cells (HMEECs) as well as mouse nasal cavity and also evaluated bacteria transition to the middle ear and lungs from nasopharynx.
Methods: The in vitro biofilms and planktonic growth of S. pneumoniae were evaluated in metal ion free medium in the presence of PM (UP, ASD and DEP). Biofilms were quantified by crystal violet (CV) microplate

assay, colony forming unit (cfu) counts and resazurin staining. Biofilm structures were analyzed using a scanning electron microscope (SEM) and confocal microscopy (CM). Gene expressions of biofilms were evaluated using real time RT-PCR. Effects of PM exposure on S. pneumoniae colonization to HMEECs were evaluated using fluorescent in-situ hybridization (FISH), cell viability was detected using the Ezcyto kit, apoptosis in HMEECs were evaluated using Annexin-V/ PI based cytometry analysis and reactive oxygen species (ROS) production were evaluated using the Oxiselect kit. Alteration of HMEECs gene expressions on UP exposure or pneumococci colonization was evaluated using microarray. In vivo colonization of pneumococci in the presence of UP and transition to middle ear and lungs were evaluated using an intranasal mice colonization model.

Results: The PM exposure significantly increased (*$p < 0.05$) pneumococcal in vitro biofilms and planktonic growth. In the presence of PM, pneumococci formed organized biofilms with a matrix, while in absence of UP bacteria were unable to form biofilms. The luxS, ply, lytA, comA, comB and ciaR genes involved in bacterial pathogenesis, biofilm formation and quorum sensing were up-regulated in pneumococci biofilms grown in the presence of UP. The HMEECs viability was significantly decreased ($p < 0.05$) and bacteria colonization was significantly elevated ($p < 0.05$) in co-treatment (UP + S. pneumoniae) when compared to single treatment. Similarly, increased apoptosis and ROS production were detected in HMEECs treated with UP + pneumococci. The microarray analysis of HMEECs revealed that the genes involve in apoptosis and cell death, inflammation, and immune response, were up-regulated in co-treatment and were unchanged or expressed in less fold in single treatments of UP or S. pneumoniae. The in vivo study showed an increased pneumococcal colonization of the nasopharynx in the presence of UP and a higher transition of bacteria to the middle ear and lungs in the presence of UP. The UP exposure elevated S. pneumoniae in vitro biofilm and colonization of HMEECs, and in vivo mouse nasopharyngeal colonization, and increased dissemination to mouse middle ear and lungs.

Conclusion: The PM exposure elevated *S. pneumoniae in vitro* biofilm and colonization of HMEECs, and *in vivo* mouse nasopharyngeal colonization, and increased dissemination to mouse middle ear and lungs.

Keywords: Air-pollution; Particulate matter; Biofilms; Respiratory infection; Colonization

NS-MM-8

Decoding the Enigma of COVID-19 Associated Pulmonary Mucormycoses (CPAM) through the Transcriptomic Lens

Khem Raj
khemrajthakur@gmail.com

Department of Microbiology, Basic Medical Sciences, Block – 1, South Campus
Panjab University, Chandigarh, India

Abstract: The coronavirus pandemic (COVID-19) is associated with secondary bacterial and fungal infections globally. The COVID-19 pandemic has brought to light an alarming surge in mucormycosis cases in India, particularly among recovering and recovered COVID-19 patients. This phenomenon, termed as COVID-19 associated Pulmonary Mucormycoses (CPAM). The main risk factors identified for COVID-19 associated Pulmonary Mucormycoses (CPAM) in our country are inappropriate use of glucocorticoids, zinc supplementation, diabetes mellitus, diabetic ketoacidosis and renal transplantation. However, there is limited data pertaining to the alterations in innate immunity and cellular metabolism in COVID-19 patients and their possible role in increasing susceptibility to mucormycosis that lead to the development of CPAM. Thus, the present talk will revolve around the identification of differentially expressed genes (DEGs), and metabolic pathways analysis associated with dysregulation of host immune responses in patients developing CPAM using a RNA-Sequencing based transcriptome approach. This will shed a light on how complex immunological and cellular metabolic perturbations during COVID-19 may results into a CPAM condition.

Keywords: COVID-19 pandemic; COVID-19 associated Pulmonary Mucormycoses (CPAM); Differentially expressed genes (DEGs); Transcriptomic Lens

IS-MSD-1

Algal Biotechnology a Tool for Future Sustainable Food and Feed Production

Avigad Vonshak
avigad@bgu.ac.il

Ben-Gurion University of the Negev, Jacob Blaustein Institutes for Desert Research Microalgal Biotechnology Sede-Boker Campus, 84990 Israel

Abstract: The increased awareness to the problem of climate change, increase in world population and the need to better manage available resources are pointing out to the need to explore better modes of food and feed production that will make better and more efficient use of land and water resources.
Algae have attracted the attention of the scientific and biotech community for their unique characteristics, such as remarkable efficiency in harnessing solar energy, growth using seawater, and nutrient side streams. The outcome is sustainable production of biomass with a variety of metabolites and commodities for the benefit of humanity.
From a modest beginning of Chlorella tablets in Japan in the late fifties, new endeavours have emerged as specialized industries the world over aiming at producing health food, food additives, animal feed, biofertilizers, and an assortment of natural products.
During the lectures an attempt will be made to point out what are the real major obstacles for improved algal productivity in large scale production systems in order to make it available sustainable mode of production for future benefit of mankind.
While significant knowledge on Algae has been generated in the academic forum, there are still major gaps which hinder the development of algae-based industries on land and in the sea since efficient mechanisms of knowledge transfer to potential users and stakeholders are notoriously lacking.

Keywords: Algal biotechnology; Sustainable production; Humanity

IS-MSD-2

Microbial Valorization of Agri-food Waste to Produce Natural Pigments for Innovative Food Applications: A Sustainable Approach

Minaxi Sharma
Minaxi.Sharma@nottingham.edu.cn; minaxi86sharma@gmail.com

Research Centre for Life Science and Healthcare, Nottingham Ningbo China Beacons of Excellence Research and Innovation Institute (CBI), University of Nottingham Ningbo China, Ningbo, China

Abstract: As the global population expands rapidly, the demand for healthy food has surged, driving a significant rise in agricultural productivity. Massive volumes of food waste are being produced because of the increased agricultural and overall food production, endangering both the environment and humankind. In this regard, the UN's set aims to achieve Sustainable Development Goals (SDGs goal 12) for efficient resource management to realize the success of green/circular bio-economy principles can be aided by the valorization of food wastes and by-products. Encouraging people to embrace potential green technologies to manage and valorizeagri-food waste into useful food additives is now critical to address these concerns. One of the ways that the circular economy model is influencing approaches globally is the recovery of value-added natural pigments from agri-food waste. The production of natural pigments from agri-food waste is advantageous since it is nontoxic, high quality, biodegradable, environmentally friendly, and not affected by seasonal variations. Therefore, the least expensive method of producing natural pigments is biotechnologically using inexpensive substrates such leftovers from agri-food waste. These natural pigments have a plethora of bio-therapeutic potential and are anticipated to have a significant influence on the creation of functional food formulations. While removing the use of artificial, petroleum-based food colors from the food chain, the production of naturally safe food pigments from agri-food waste is a more environmentally friendly approach within the framework of the circular economy. In this presentation, we will explore the recent developments & trends in microbe-based valorization technologies to exploit the pigment potential of agri-food waste, and, their

application in sustainable production of smart & functional foods, challenges & way forward in application towards the circular bioeconomy.

Keywords: Microbial Valorization; Agri-food waste; Natural pigments; Sustainable approach

IS-MSD-3

Bioprospecting of Lignocellulolytic Microorganisms and their Enzymes for Valorization of Waste Biomass

Namrata Joshi*, Kumar Pranaw and Łukasz Drewniak
*N.joshi@uw.edu.pl

Department of Environmental Microbiology and Biotechnology, Institute of Microbiology, Faculty of Biology, University of Warsaw, Poland

Abstract: The present study addresses the challenges of lignocellulosic biomass (LCB) conversion by optimizing fungal strains for enhanced enzymatic hydrolysis. Two potent fungal strains, *Aspergillusfumigatus* ZS_AF and *Penicilliumfuscoglaucum* JAM-1, were meticulously isolated and optimized for producing hydrolytic enzymes crucial for LCB valorization. Through optimization, ZS_AF achieved a two-fold increase in enzyme production using pine sawdust (PSD), with significant yields of CMCase, xylanase, β-glucosidase, and FPase. Similarly, JAM-1 demonstrated superior enzyme activity with rapeseed cake (RSC) over PSD. Secretome profiling of both fungi highlighted the critical role of carbohydrate-active enzymes (CAZymes) and auxiliary enzymes in biomass degradation, with 77% of ZS_AF's secretome comprising CAZymes, predominantly glycoside hydrolases (66%). JAM-1's secretome, enriched with 153 CAZymes when grown on RSC, underscored their significance in effective biomass saccharification.
To further address LCB recalcitrance, three lytic polysaccharide monooxygenase (LPMO) genes from *Cellulosimicrobiumcellulans* were heterologously expressed, resulting in thermostable enzymes that significantly boosted reducing sugar yields when combined with commercial cellulase. The study also explored enzyme immobilization on Faujasite Na-X zeolite, achieving a 73% immobilization efficiency, enhanced enzyme stability, and reusability. Structural analyses confirmed the catalytic efficiency of immobilized enzymes in valorizinglignocellulosic waste.
Additionally, applying a fungal consortium comprising ZS_AF, JAM-1, and *Trichodermadeliquescens* in composting waste biomass and sewage sludge demonstrated improved compost quality, reduced moisture content, and enhanced organic matter mineralization. In conclusion, this research illustrates the potential of optimized fungal strains and enzyme engineering in overcoming LCB recalcitrance, offering sustainable and efficient solutions for biorefinery processes and the composting of lignocellulosic waste, thereby contributing to environmental sustainability.

Keywords: Lignocellulolytic microorganisms; Carbohydrate-active enzymes; Enzymatic hydrolysis; Immobilization; Cellulase; Composting

IS-MSD-4

Green Manufacturing of Biopolymers in Extremophilic Consolidated Mini Cell Factories

Rajesh Sani
rajesh.sani@sdsmt.edu

Department of Chemical and Biological Engineering
South Dakota School of Mines and Technology, Rapid City, SD 57701, USA

Abstract: This talk provides screening for and isolating unique thermophiles with the dual capability of i) utilizing unprocessed lignocellulosic biomass as a sole carbon source and (2) producing biopolymers. On the upstream side, the thermophiles *have been adapted to depolymerize >65* wt.% of the unprocessed (not subjected to physical, chemical, and enzymatic pretreatment) agri-residues. A comparative analysis of the transcriptomes

of a thermophile on different carbon sources corroborates phenotypic observations at the genotypic level. Genomic insights identify essential candidate genes expressing the necessary ligninolytic enzymes and participating pathways for degrading and metabolizing lignin, xylan, cellulose, starch/pullulan by cnambio1.
On the downstream side, with Single-Step Biomass-to-Biopolymer property, the thermophile can synthesize a semi-crystalline medium chain length PHA (mcl-PHA) in unprocessed corn stover-containing medium. The produced mcl-PHA shows exceptional thermal stability of 420°C and a relatively high final melting point of 210°C and is capable of thermally induced crystallization. A deletion mutant of the thermophile for the PHA depolymerase gene (*phaZ*) is being tested to improve the PHA titers and demonstrate it as a strategic industrial platform for carbon-optimized conversion of agri-residues to biobased chemicals.
Further, work is in progress to i) rewire the depolymerization of unprocessed corn stover to PHA by the thermophile, to simultaneous manufacture of exopolysaccharide, nanocellulose, and other green biopolymer precursors and ii) their applications in biomedical and agriculture sectors. Together, the vision and future of this work are to systematically move the biomanufacturing pipeline of this novel form of consolidated bioprocessing from lab scale in SD Mines to ultimately end up at the 2000L commercial scale production system.

Keywords: Bioplastic; Omics; Non-model host; Synthetic biology; Thermophilic bioprocessing

IS-MSD-5

Biobased Bioproducts in a Sustainable Biorefineries

Vijai Kumar Gupta
vijaifzd@gmail.com

Deputy Chair, Bioprocess Engineering, School of Biotechnology Dublin City University, Glasnevin, Dublin D09 K20V, Ireland

IS-MSD-6

Algal Biotechnology and Emerging Blue Economy in Nigeria

M.B. Yerima
belyerima@gmail.com

Department of Microbiology, Faculty of Science, Sokoto State University, Sokoto, Nigeria, Africa

Abstract: United Nations estimation has it that, the world population will exceed 10 billion people by 2050 and Africa is likely to be among the densely populated continents. Agriculture is already nearly maximally exploited and climate challenges are eminent. Emerging technologies such as Synthetic Biology, high throughput phenomics and the application of internet of things (IoT) automation to algal manufacturing technology can advance the understanding of algal Biology and, ultimately drive the much beneficial algal based Bioeconomy. Photosynthetic microalgae are microbes that have colonized every habitat on earth and exhibit extraordinary biological diversity of more than 200,000 species. Unlike other microbes often exploited for bio-based manufacturing such as yeast and bacteria, phototrophic algae have the advantage of using sunlight which is free to fix carbon dioxide another naturally free substance in abundance. Hence, algal bioproducts can be cheaper and more affordable to developing economies like that of Africa. In addition, massive cultivation of algae can significantly reduce carbon dioxide concentration and global warming. More so, bioprocessing of algal biomass can lead to production of Biofuels such as Biogas, Bioethanol and Biodiesel. The utilization of these Biofuels also curtails emission of greenhouse gases.

Keywords: Algae, Bioeconomy, Biotechnology, Biofuels, Africa

NS-MSD-1

The Current Status and Future of Marine Fungal Research in India

Belle Damodara Shenoy
belleshenoy@nio.org; shenoynio@gmail.com

CSIR-National Institute of Oceanography, Regional Centre, Visakhapatnam, India

Abstract: Marine fungi, encompassing mycelial microfungi, yeasts, and zoosporic fungi, play crucial roles in marine ecosystems. This talk will explore the current understanding and future prospects of marine fungal research in India. Historically, marine fungal studies have progressed from early deep-sea isolations to sophisticated investigations using next-generation sequencing (NGS) tools. Recent research highlights the diversity and ecological significance of marine fungi, including their presence in unique environments like tarballs, where *Aspergillus* species are prevalent. Key research areas include deep-sea fungi, marine fungal cultures, and their biotechnological applications. Despite advancements, challenges such as limited sampling resources and preservation techniques remain. Future directions emphasise the need for enhanced infrastructure, a national repository, increased funding, interdisciplinary collaborations, and specialised training programs. By intensifying efforts in bioprospecting and integrating marine fungal research into broader conservation initiatives, we can unlock their potential for novel secondary metabolites, benefiting medicine, agriculture, and various industries.

Keywords: Marine fungi, Deep-sea fungi, Tarballs, Ecological significance, Diversity

NS-MSD-2

Microwave-assisted- THF-Water system for Bioconversion of Rice Straw for Biofuels and Value-added Platform Chemicals

Pradeep Verma* and Lakshna G Nair
*pradeepverma@curaj.ac.in

Bioprocessing and Bioenergy Laboratory, Department of Microbiology, School of Life Sciences, Central University of Rajasthan, Bandarsindri, Ajmer, Rajasthan (305817), India

Abstract: Lignocellulosic biomass (LCB) conversion into value-added products and platform chemicals contributes to reducing carbon footprints and helps in maintaining a circular economy. The current study employs microwave-assisted organosolv pretreatment, using Tetrahydrofuran (THF), a high lignin dissolution solvent, for the pretreatment of Rice straw. The system was monitored using 50% THF with a solvent-biomass ratio of 20:1 at different temperatures (80 °C, 100 °C, and 115 °C) and time intervals. The saccharification using cellulase on the pretreated biomass revealed that the pretreatment system at 100°C and 40 min under microwave heating was most efficient, with a sugar yield of 62.42% (72 h). Moreover, the FTIR analyses confirmed structural changes, and the calculation of the crystallinity index (CrI) using XRD techniques reported the reduction of crystallinity of the pretreated biomass (~33%) compared to the untreated sample (~46%). Further, LC-MS analysis of the liquid hydrolysate from the pretreatment reveals the presence of 13 important platform chemicals. The system was also compared using a thermal heating apparatus designed in the laboratory with a conventional heating system. Pretreatment performed in the heating apparatus with similar conditions to the microwave reported sugar yields of 24.02% for saccharification using cellulase (72 h). The FTIR analysis and CrI calculation using XRD showed less considerable changes to the untreated biomass. The LC-MS analysis of the hydrolysate from this experiment revealed only the presence of 9 platform chemicals. Thus, the microwave-assisted-organosolv THF-water pretreatment system can be validated as an efficient strategy in the bioconversion of LCB into value-added platform chemicals.

Keywords: LCB, THF, Pretreatment, Organosolv, Microwave, Platform chemicals

NS-MSD-3

Microbial Technology and Sustainable Agriculture

D. J. Bagyaraj
djbagyaraj@gmail.com

INSA Hon. Scientist & Chairman
Center for Natural Biological Resources and Community Development
41 RBI Colony, Anand Nagar, Bangalore, Karnataka (5650 024), India

Abstract: The current day emphasis is on sustainable agriculture which uses less of chemical inputs like fertilizers and pesticides having adverse effect on soil health, and environment. Thus use of organic inputs including microbial inoculants play an important role in sustainable agriculture. Microbial inoculants serve as bio-fertilizers supplying major plant nutrients N, P and K, and also as biocontrol agents suppressing root pathogens. Nitrogen abundantly present in the atmosphere is fixed by bacteria, living freely in soil or in symbiosis with plants. Rhizobia living in symbiosis with legumes forming root nodules are known to fix atmospheric nitrogen. Experiments conducted in India have shown that nearly 25-50% of nitrogenous fertilizer can be saved through inoculation with efficient rhizobia, associative and free-living soil bacteria like *Azotobacter* and *Azospirillum*.
Most of the tropical soils are not only P deficient but also P fixing; hence, 75% of super phosphate applied to the crop is fixed and not available for plant growth. There are some microorganisms which can solubilize unavailable form of P to available form. The cheaper sources of rock phosphate available in our country can be used along with these phosphate-solubilizing microorganisms. This will save a considerable amount of foreign exchange, as the raw material for the manufacture of super phosphate is imported. Microorganisms like potassium mobilizing bacteria and plant growth promoting rhizomicroorganisms also help in enhancing plant growth and productivity. Some microorganisms play an important role in protecting plants against plant pathogens and insect pests. The most common type of mycorrhizal association in crops important in agriculture is the arbuscular mycorrhizal (AM) fungi. They help plant growth through improved phosphorus nutrition and protect the roots against pathogens. Recent studies have brought out that yeasts, actinobacteria and cyanobacteria also can enhance plant growth which needs more investigation.
These studies have brought out that use of microbial inoculants not only enhance the growth and yield of crop plants but also reduce the application of fertilizers and pesticides.

Keywords: Microbial technology; Biofertililzers; Sustainable agriculture; Mycorrhizalassociation

NS-MSD-4

Bioprospective Potentials of Novel Actinobacteria from Liem Stone Quarries

Dayanand Agsar
vcgug@rediffmail.com

Gulbarga University, Jnana Ganga, Kalaburagi, Karnataka (585 106), India

IS-PMI-1

Plant Growth-promoting Bacteria Inoculation to Enhance Vegetative Growth and Physiological Traits of Turmeric (*Curcuma longa* L.)

Dilfuza Jabborova
dilfuzajabborova@yahoo.com

Institute of Genetics and Plant Experimental Biology, Uzbekistan Academy of Sciences
Kibray 111208, Uzbekistan

Abstract: Turmeric is a rhizomatous plant. Rhizomes of turmeric contain essential oil and curcuminoids and have high medicinal value. Plants growth promoting bacteria (PGPB) plays an important role in increasing the

growth, yield and physiological traits of turmeric plant. Plants growth promoting bacteria colonize roots, improve seed germination, plant growth and promote soil enzyme activities. PGPB improve plant growth through the synthesis of growth hormones, nitrogen fixation and phosphate solubilization. In this study, the role of plant-growth promoting bacteria on plant growth, physiological properties and yield of turmeric was investigated. The experiments were conducted under field conditions at Termez district, Uzbekistan. Eight treatments such as control, *P. koreensis*IGPEB 76, *P. rhodesiae* IGPEB 60, *P. fluorescens*IGPEB 51, *P. proteolytica*IGPEB 62, *P. chlororaphis* IGPEB 57, *B. pumilus* IGPEB 73 and *B. endophyticus* IGPEB 68 were used in the experiment. Physiological traits such as total chlorophyll, chlorophyll a, chlorophyll b and carotenoid contents in turmeric were measured by the method of Hiscox and Israelstam. Fresh leaf (50 mg) of turmeric sample was cut and added dimethylsulfoxide (5 mL) to test tubes. The test tubes were incubated at 37 °C for 4 h. Then absorbance of extract was determined using a spectrophotometer. The relative water content of leaves in turmeric was analyzed by the method of Barrs and Weatherly. Fresh leaf (100 mg) of turmeric sample was placed in petri plates and added water in plates for 4 h. After 4 h, water content of leaf in turmeric was measured. The results showed that plant-growth-promoting *P. rhodesiae*IGPEB 60, *B. endophyticus*IGPEB 68 and *P. koreensis*IGPEB 76 significantly increased the plant height, leaf number, leaf length and leaf width as compared to the control treatment. *B. endophyticus*IGPEB 68treatment significantly increased the relative water content, chlorophyll a, chlorophyll b, total chlorophyll and carotenoid contents compared to the control. Additionally, inoculation *B. endophyticus* IGPEB 66 treatment significantly enhanced soil enzyme activities and fresh yield of turmeric. As a result, it can be said that inoculation of turmeric with plant-growth-promoting *P. rhodesiae*IGPEB 60, *B. endophyticus*IGPEB 68 and *P. koreensis*IGPEB 76 may lead the increases in yields of turmeric.

Keywords: Turmeric; Plant growth promoting bacteria; Plant growth; Total chlorophyll content; Yield

NS-PMI-1

Production of High-value Plant Derived Terpenes in Yeast through Application of Synthetic Biology

Dinesh A. Nagegowda[1,2]
da.nagegowda@cimap.res.in; dinu33@yahoo.com

[1]*Molecular Plant Biology and Biotechnology Lab, CSIR- Central Institute of Medicinal Aromatic Plants, Research Centre, Bengaluru, Karnataka (560065), India*
[2]*Academy of Scientific and Innovative Research, Ghaziabad (201002), India*

Abstract: Terpenes are one of the largest classes of phytomolecules and are classified based on the number of carbon units in their structure such as hemi (C_5), mono (C_{10}), di (C_{20}), tri (C_{30}), tetra (C_{40}) and ploy ($C_{>40}$). Several compounds belonging to these classes have found immense utility due to their aromatic or medicinal value. The overall market for terpenes is around USD 1.25 billion in 2024 and is expected to grow at a CAGR of 8.3%, pushing the market size to USD 2.36 billion in 2031. Despite the huge demand and great interest for these compounds, their supply is limited due to low production in their natural source and unsustainable process used for their extraction. In most cases, chemical synthesis of these molecules is not a viable alternative as it involves multiple steps, and with low yield and can never match the natural properties. These aspects make the price of the naturally derived terpenes highly expensive in the market. Thanks to scientific efforts, the biosynthetic pathways for many of these molecules have been elucidated, paving the way for heterologous production. Microbial systems such as yeast provide an enticing alternative for the production of high-value terpenes as they circumvent many of the limitations of their natural source. Yeast in particular offers several advantages over other microbial systems for the production of terpenes, including their ability to produce the precursors for terpenes naturally as a part of their ergosterol biosynthetic pathway and their ability to express functionally active plant cytochrome P450 enzymes, allowing for the decoration of the basic terpenes skeleton to more complex terpenoids. This talk covers the use of yeast as a powerful synthetic biology / metabolic engineering platform for the production of commercially important terpenes in general, along with recent engineering studies for production of specific sesquiterpenes and monoterpenes being pursued in our lab.

Keywords: Phytochemicals, Terpenes, Yeast, Synthetic biology, Cytochrome P450 enzymes

NS-PMI-2

Microbial Volatile Organic Compounds for Plant Health and Productivity

Sivakumar Uthandi
usivakumartnau@gmail.com

Biocatalysts Laboratory, Department of Agricultural Microbiology, Tamil Nadu Agricultural University, Coimbatore-3, Tamil Nadu, India

Abstract: Volatile metabolites are low molecular weight (< 300 Da) organic compounds, with low polarity and high vapor pressure. Over the past few decades, scientists have identified diverse chemical compounds emitted by rhizobacteria that acts as antagonistic agents and signaling molecules. Microbial volatile organic compounds (mVOCs) are chemically diverse and include alkenes, alcohols, ketones, terpenes, benzenoids, aldehydes, pyrazines, acids, esters, and sulfur-containing compounds. The mVOCs are produced through diverse metabolic pathways such as fatty acid metabolism, shikimate pathway, mevalonic acid biosynthesis, and amino acid oxidation.

Signature Volatiles

Each microbial strain releases a specific blend of mVOCs, which plays a significant role in its lifecycle and interaction with other organisms including plants. Some mVOCs are unique to specific microbes, termed as signature volatiles, while some are common to most microbes. For instance, Benzathiazole compounds are unique to *Bacillus* sp. and certain fungi, whereas quinolonine for *Pseudomonas* sp. (mVOC 2.0). Apart from its plant growth promotion ability, certain VOCs elicits plant systemic defense by modulating physiological pathways. Therefore, these mVOCs are significant and have great potential for use in agriculture.

mVOCs in intra and inter-coMSDunity signaling

Certain mVOCs act as signaling molecules in intra- and interspecific interactions and mediate cell-to-cell communication. They are also potent antimicrobial as well as nematicidal agents. However, the biochemical mechanisms of the mVOCs remain mostly unknown. Sesquiterpenes (SQTs) can quickly move through pores in the soil matrix and mediate below-ground, long-distance chemical signaling. One of the major volatile compounds, 2-3 butanediol (2,3-BD) mediates growth promotion in *Arabidopsis* (Ryu et al., 2003). Further studies indicated that 2-3 BD controls the production of signaling molecules such as acyl-homoserine lactones (AHLs), which requires the sensor kinase GacS (Han et al., 2006). However, the mVOCs are ideal for use under airtight conditions, owing to their small molecules that can quickly diffuse through porous structures and over vast distances.

mVOCs and mineral uptake

Microbial volatile organic compounds from some PGPR strains facilitate the uptake of iron, copper, selenium, and sulfur. For example, *Arthrobacter agilis* UMCV2 volatiles improve iron acquisition in both monocot and dicot plants. *B. subtilis* GB03 primed in *Arabidopsis* increased iron uptake up to 2-fold in even under alkaline conditions. *B. amyloliquefaciens* BF06 volatiles increased selenium uptake by inducing the expression of sulfate transporter genes than in untreated plants (Wang *et al.*, 2017). Furthermore, some BVCs act as a nutrient source also. DImethyl- disulfide (DMDS), as a source of sulfur, increased*Arabidopsis* growth under sulfur-deficient condition.

mVOCs in stress alleviation

mVOCs indirectly improve plant growth by alleviating biotic and abiotic stress. Some mVOCs can also induce systemic tolerance to soil salinization and drought stress, which pose significant threats to crop production. Treatment with rhizobacteria can help alleviate these problems by improving root system architecture for more efficient water uptake. Rhizobacteria confer systemic tolerance to abiotic stress by modulating proline, antioxidant, and hormone production and reducing Na^+ accumulation in plants. The volatile 2,3-butanediol helps protect plants from abiotic stress. Treatment with the *Pseudomonaschlororaphis* O6 mutant, which cannot synthesize 2,3-butanediol, failed to increase drought stress tolerance in *Arabidopsis* compared with the wild type. The plant hormones salicylic acid and NO are required for the plant response to 2,3-butanediol under abiotic stress.

Likewise, DMDS and 2-methylpentanoate, are highly toxic to plant pathogens, and some, such as acetoin, 2,3-butanediol, and tridecane, induce plant systemic resistance (ISR) against these pathogens (Lee *et al.*, 2012). However, ISR appears to be the primary mechanism of disease suppression *via* mVOCs under natural conditions. The enhanced ISR mediated by MVs was confirmed by the modulation of phytohormones (SA, JA,

ET, and auxin, etc) signaling cascades and activation of both pathogenesis-related (PR) proteins and stress enzymes.

mVOCs in hormonal modulation

Several mVOC can regulate plant growth by modulating the biosynthesis, perception, and homeostasis of ethylene, auxin, cytokinin, abscisic acid (ABA) and gibberellin. The *Arabidopsis ethylene insensitive 2* (*ein2*) mutant is less responsive to *B. subtilis* GB03 volatiles compared with the wild type. Rhizosphere bacteria also promote plant growth by stimulating auxin production or by modulating auxin homeostasis. Plants treated with *B. subtilis* GB03 volatiles display enhanced root proliferation via increasing lateral root formation through the auxin-dependent pathway. Indole compounds modulate auxin signaling in *Arabidopsis.* Where plants uptake indole and use it as a precursor for auxin synthesis.

VOCs also play a crucial role in cytokinin signaling. For instance, volatiles from *A. alternata* increase cytokinin accumulation (3-fold) in *Arabidopsis* (Sánchez and López *et al.*, 2016), and they increase photosynthesis and reduce the time of floral bud appearance through cytokinin signaling *in vitro*. Although fungi and bacteria produce different volatile profiles, transcriptome analysis showed that the plant response to *A. alternata* is quite similar to the response to *B. subtilis* GB03. ABA biosynthesis occurs when sugar accumulates as an end product of photosynthesis (Sánchez-López *et al.*, 2016). ABA inhibits the accumulation of additional sugar by negatively affecting photosynthesis (Cho et al., 2010). However, B. *subtilis* GB03 volatile increases ABA biosynthesis (Zhang *et al.*, 2008).

Metabolites in plant-microbe interaction

Metabolomics profile comprises the characterization of all the secondary metabolites produced by organisms under certain environmental circumstances. Metabolome pattern generally varies according to the environmental flux that causes direct physiological changes in an organism since it has been directly correlated with the diverse metabolic process, which represents the corresponding genetic information (Bundy *et al*., 2005). Metabolomics is progressively used to achieve profound insight into the responses of abiotic stress. Recent advances in high throughput techniques in molecular detection methods have boosted metabolomic research. Plant metabolomic studies (Burns *et al*., 2003) showed the existence of distinct bioactive molecules. Plant roots secrete a variety of compounds into the soil, including carbohydrates, amino acids, and organic acids (Jones 1998; Bais et al. 2006) by diffusion, ion channels, and vesicular transport (Bertin et al. 2003). These compounds alter soil chemistry and provide nutrient sources for microbes in the rhizosphere

Root secretome aids microbial recruitment

The root exudates and microbe- derived signal molecules are a bilateral process that depicts communication between soil microbial communities and plants (Peiffer *et al*., 2013). These facts relate to the results concerning the detection of various plant exuded signal molecules to attract and trigger the typical biochemical pathways in the microbial communities that colonized plants. *Trichoderma* sp. produces two secondary metabolites, namely harzianolide and 6-pentyl-a-pyrone which exhibited auxin like effects in pea stems, helps for stress alleviation, and thereby it improves the plant growth. Changes in environmental conditions influence the variations in plant metabolism and exudation pattern of plants and composition of exuded molecules, and it consequently impacts the level of root colonization. Bioactive metabolites *viz.,* IAA, trehalose, glycine betaine, etc., accumulated in plants as a result of abiotic stress.

Moreover, ***chemoattraction and biofilm promotion*** activity of a secreted component is an enantiomeric-dependent response. Root secreted malic acid selectively signals and recruits the beneficial rhizobacterium *Bacillus subtilis* FB17 in a dose-dependent manner (Rudrappa et al., 2008).

Microbial metabolites in plant growth

Metabolic products released by microorganisms both directly and indirectly influence the plant growth. Rhizospheric plant growth-promoting bacteria synthesize bioactive molecules such as cytokinins, gibberellins and IAA evidenced the plant growth promotion under a non-stressed and stressed condition. Certain metabolites produced by rhizospheric PGPR, such as auxins and cytokinins, modulates root system architecture (RSA). Other indirect mechanisms include the effects of antibiotics and hydrogen cyanide, which promote plant growth by inhibiting the growth of deleterious microorganisms in the rhizosphere. PGPR can induce defense programs such as systemic acquired resistance (SAR) and induced systemic resistance (IST) thus reducing phytotoxic microbial communities. They also can elicit induced systemic tolerance (IST) to abiotic stress.

Microbial metabolites as MAMPs

Furthermore, metabolites also confer plant immunity by acting as elicitors. To counteract pathogen attacks, plants have evolved set of defense responses in a cascade of serine and threonine kinases. These inherent defenses (which includes physical and chemical barriers, as well as inducible) are activated after pathogen perception.This recognition step can be achieved by microbe-associated molecular patterns (MAMPs), which are vital molecules common to many classes of microbes. Hence MAMPs, are regarded as general elicitors in

plants involved in non-specific immunity and effective against broad spectrum of pathogens. MAMPs include proteins, glycans, and lipids. For instance, rhamnolipids from PGPR conferred resistance to pathogenic fungi in grapevine (Varnier et al., 2009). The schematic representation of metabolite mediated plant-microbe interaction is depicted in Figure.

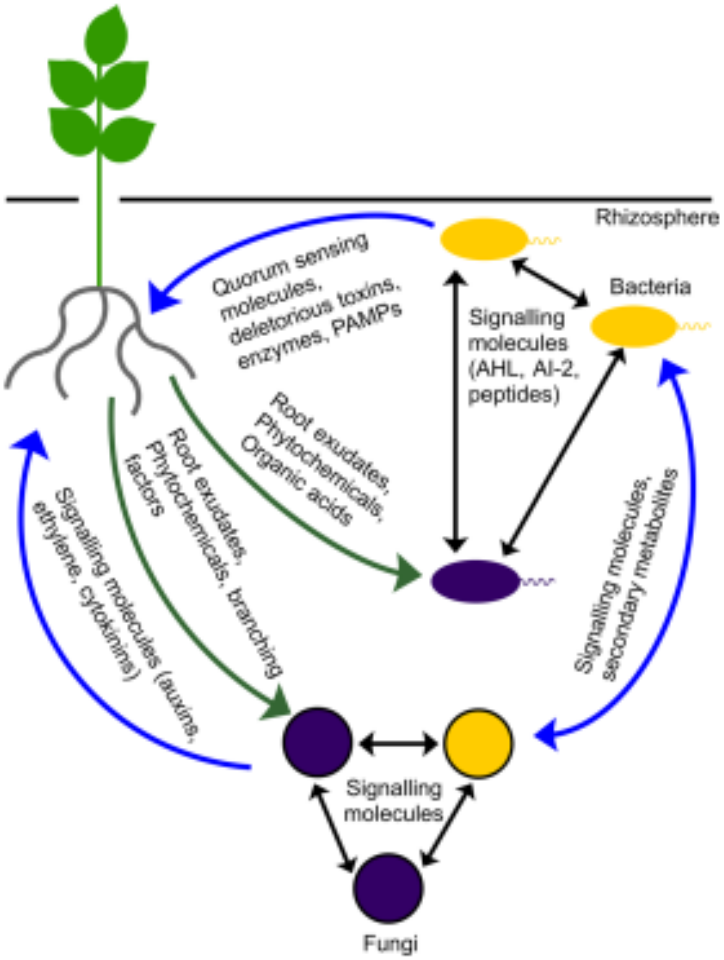


Fig: Schematic representation of root secretome and microbial metabolites, with their role in plant-microbe interaction

(Adapted from Lareen et al., 2016)

Future prospectus

The above facts imply that *in situ* mechanisms influencing microbial metabolism need to be evaluated thoroughly. Besides, most of these metabolites are still need to be identified. The state of the art metabolomics technology could serve as a potent tool for the assessment of metabolites and environmental interferences in microbial metabolism. Besides, understanding host metabolomics is vital to obtain information regarding the impact of microbial metabolisms in the host after colonization, which paves the way for the simulation of the convoluted endophytic environment. Trapping mVOCs is a highly crucial and most mVOCs occur in blends rather than a pure single compound. Hence, identifying mVOCs and metabolites responsible for biotic and abiotic stresses may provide new solutions for sustainable organic farming.

Keywords: Microbial metabolites, Hormonal modulation, MAMPs, Plant-microbe interaction

NS-PMI-3

The Invasive Microbiome: Mapping rhizosphere Modulation by *Lantana camara* in Invaded Habitats

Gitanjali Yadav
gy@nipgr.ac.in

National Institute of Plant Genome Research (NIPGR), New Delhi, India

Abstract: In this work, I will talk about how below ground microbial communities contribute to the establishment and success of invasive alien plant species though an integrated approach combining modern data science with traditional field based strategies. We focus on *Lantana camara,* an extremely noxious weed, considered to be one of the world's worst invasive species, having devastating impact on forested regions, local livelihoods as well as human health. To uncover the genomic basis of invasion, we performed whole genome assembly, followed by de-novo as well as reference-based transcriptomics, developing combinatorial and comparative analytical strategies for Lantana across diverse spatio-temporal scales. We use a three pronged strategy of mapping the Genotype and Phenotype to Chemotype, and this enabled us to step beyond invasion genomics to explore soil metagenomes as well as rhizophere communities in both native and invaded habitats. This work shows how Big Data, Machine intelligence and geo-spatial techniques can be successfully applied to field ecology. Our work also paves the way for connecting below ground microbial communities to above ground macro (vegetative) communities, and how this crosstalk mediated by chemical fingerprints, is able to modulate both the productivity and adaptive potential of plants.

Keywords: Invasive microbiome, *Lantana cámara,* Invaded habitats, Machine intelligence

NS-PMI-4

Crop Nitrogen use Efficiency for Sustainable Agriculture - Balancing Bacterial N-Fixation with Plant N-Assimilation

Nandula Raghuram
raghuram@ipu.ac.in

Centre for Sustainable Nitrogen & Nutrient Management (USBT),
Guru Gobind Singh Indraprastha University, New Delhi (110078), India
Sustainable India Trust, NASC complex, DPS Marg, Pusa New Delhi (110012), India
Centre for Sustainable Agriculture and Environment, Prof. HS Srivastava Foundation for Science and Society,
Eldeco Xpress Plaza, Uttrathia Raebareli Road, Lucknow, Uttar Pradesh (226025), India

Abstract: Poor agricultural Nitrogen Use Efficiency (NUE) is increasingly becoming a major economic and environmental problem, ever since Green Revolution ignored biological nitrogen fixation and legume-based crop rotations in favour of cereal-centric monocropping. In India, this tremendously enhanced the dependence on N-fertilizers, which in turn inhibit bacterial nitrogen fixation and promote microbial decarbonisation of farm soils. Further, the divergent trajectories of green and white revolutions delinked their interdependence for manure and animal feed and converted the nutrient biogeochemical cycles into environmental cascades. Consequently, at least two-thirds of the added N-fertilizer does not contribute to the crop harvest in intensive cropping zones and instead causes pollution, ill-health and climate change. The Indian, south Asian and global nitrogen assessments indicated that the declining role of biological N-fixation in general and legumes in particular could explain our poor systemic NUE. Restoration of legume-based cropping systems, improving manure management by integrating crops and livestock farming and recycling of nutrients from sewage can hugely save fertilizers while reducing nutrient pollution and protein malnutrition. Our early studies on nitrate assimilation in *Arthrospira* (Spirulina) *platensis* revealed that its genes are induced and regulated by externally supplied nitrate and that its enzymes have higher activities and stabilities than in rice. Our later efforts to understand the genetic basis of NUE in rice independent of soil microbial influences led to the development of methods such as nutrient-free soil, modal weight seeds and lifelong phenotyping in the greenhouse. We showed that flowering time and crop duration can be a convenient proxy for screening our huge rice germplasm for nitrogen use efficiency. We used the shortest duration varieties and the longest duration varieties among a

thousand released varieties of Indian rice to establish their contrasting NUE. We also identified and segregated the traits and genes for N-response from NUE for crop improvement.

Keywords: Sustainable agriculture; Bacterial N-Fixation; Plant N-assimilation; N-use efficiency

IS-VDL-1

Meeting the Challenge of Controlling Viral Immunopathology

Barry T Rouse
btr@utk.edu

College of Veterinary Medicine, University of Tennessee, Knoxville TN 37919, USA

Abstract: The mission of the talk is to recall the ways by which a virus infection can cause disease focusing on those infections where tissue damage is mainly the consequence of a host immune reaction to the infection. In such situations, not all immune activities participate in causing damage with some acting to regulate or even negate the inflammatory components. This opens up the prospect of rebalancing the participation of different immune events so as to achieve less tissue damaging consequences or even resolve lesions. Some strategies involve rebalancing the participation of immune components through various approaches, such as redirecting the nature of innate reactions, removing or blocking proinflammatory T cell products, expanding regulatory cells, restoring lost protective cell function, using monoclonal antibodies to counteract inhibitory molecules, and exploiting metabolic differences between inflammatory and immuno-protective responses. Ideally, we need to identify therapeutic approaches that can reverse ongoing lesions that lack unwanted side effects and are affordable to use, but in practice rebalancing is more readily achievable if performed early after infection before lesions are at their peak. We describe various strategies that are used successfully in model studies and the prospect of using them in clinical situations to control chronic viral induced lesions.

Keywords: Viral immunopathology; Strategies; Viral induced lesions; Therapeutic approach

NS-VDL-1

The Journey of Indigenous Vaccine in COVID-19 Pandemic

Pragya D. Yadav
hellopragya22@gmail.com, yadav.pragya@gov.in

Director-In-Charge, National Institute for One Health, Nagpur, Maharashtra, India
Scientist 'F', Group Leader, Maximum Containment Facility, Indian Council of Medical Research-National Institute of Virology, Sus Road, Pashan, Pune, Maharashtra (411021), India

Abstract: Accelerated research toward vaccine development was the primary focus of the global scientific community during the early stages of the COVID-19 pandemic. Early in March 2020, the SARS-CoV-2 was isolated at the Indian Council of Medical Research-National Institute of Virology (ICMR-NIV), Pune, marking the beginning of India's path towards indigenous vaccine development. Later, Bharat Biotech, an Indian biotechnology company, worked with the ICMR-NIV to produce the first indigenous COVID-19 vaccine in India, called Covaxin, based on an inactivated virus. It also included an adjuvant called Algel-IMDG, which helps to boost the vaccination's efficacy by promoting a strong immune response. Animal challenge experiments in hamsters and non-human primates showed significant immunogenicity and protective efficacy, according to preclinical research. In July 2020, the Drugs Controller General of India (DCGI) approved the vaccine for Phase I and II Human Clinical Trials. With 25,800 individuals, India undertook the first and largest Phase III efficacy study. The results showed that the vaccine was effective against symptomatic COVID-19 disease in 77.8% of cases, severe symptomatic COVID-19 disease in 93.4% of cases, and asymptomatic COVID-19 in 63.6% of cases. Safety study shows that the adverse events that were reported were comparable to placebo, with less than 0.5% of participants having significant adverse events and 12% of subjects reporting side effects that were frequently known to occur. Moreover, it has been demonstrated to neutralize the Omicron, Zeta, Kappa, Gamma, Beta, and Delta variants. The Central Drugs Standard Control Organization (CDSCO) recommended the

emergency user authorization for Covaxin on January 3, 2021. About 36,39,30,701 doses of the COVID-19 vaccine had been administered in India, making it the second vaccination of its kind in the country. The other COVID-19 vaccine indigenously then developed in India, in addition to Covaxin, are ZyCoV-D (DNA vaccine), Corbevax (Protein subunit vaccine), Covovax (Protein subunit vaccine), Gemcovac (mRNA vaccine), iNCOVAC (Viral vector). The knowledge acquired from the indigenous COVID-19 vaccine development process can be utilized to create vaccines against other diseases of public health importance. This methodical strategy lays the groundwork for India's future efforts to develop new vaccines.

Keywords: Indigenousvaccine development; COVID-19; Covaxin; ZyCoV-D (DNA vaccine); Corbevax; Covovax; Gemcovac; iNCOVAC

NS-VDL-2

Combating Anti-microbial Resistant Microbes with Vaccine Innovations

Ravi P. N. Mishra
ravi.mishra@imtech.res.in

Principal Scientist, CSIR-Institute of Microbial Technology, Chandigarh (160036), India

Abstract: Vaccines are considered as one of the most sustainable medical interventions to combat infectious diseases. The world has witnessed the potential of vaccines in controlling recent COVID-19 pandemic. Emerging vaccine technologies are utilizing the pivotal knowledge of comparative genomics, proteomics, immunoinformatic, modern bioprocess techniques and AI-ML in order to develop vaccines against infectious and non-infectious diseases, with warp speed. The present talk is focused on use of the above tools for discovery and rational design of effective vaccines against anti-microbial resistant microbial pathogens.

Keywords: Vaccines; Anti-microbial resistant microbes; Vaccine innovations

NS-VDL-3

Development of Novel Antivirals against Dengue and Chikungunya Viruses

Deepti Parashar
deeptiparasharster@gmail.com

Scientist F, Dengue & Chikungunya Group,
Group leader Diagnostic Reagent Facility, ICMR-National Institute of Virology,
Pune, Maharashtra, India

Abstract: Dengue (DENV) and chikungunya (CHIKV) viruses and their co-infections have emerged as major public health threats in tropical and sub-tropical regions. In case of both viral infections, initial viral load has been reported to be contributor to disease severity. With the lack of effective vaccines and antivirals, there is a need of effective drug with anti-dengue and anti-chikungunya activity.
Using *in vitro* cell culture methods, our studies have identified anti-dengue activity of bioactive compounds such as mangostin, chebulinic acid and carpaine from medicinal plants, plant extracts of *P. alba, A heyneanus, B monnieri, C papaya, V negundo, Sauropus androgynus L. Merr.* (Patil et al 2021, Thomas et al 2022, Alagarasu et al 2023; Alagarasu et al 2022, Joshi et al 2022), silver nanoparticles and supercritical fluid extract of *Carica papaya* leaves formulations (Patil et al 2022). Anti-CHIKV activity of bioactive compounds from medicinal plants (mangostin and arctigenin) (Panda et al 2021; Shukla et al., 2024) and plant extracts of *P. alba, A. heyneanus, B. monnieri, C. papaya, C. maxima* (Alagarasu et al 2022), papaya leaves in powder form (Patil et al 2022) and stearylamine (Jeengar et al 2021) have been reported. Using systems biology approach, we identified nine repurposed drugs viz., temsirolimus, 2-fluoroadenine, doxorubicin, felbinac, emetine, lomibuvir, enalaprilat, metyrapone and resveratrol to exert anti CHIKV activity and resveratrol, doxorubicin, lomibuvir, elvitegravir, and enalaprilat, to exert significant anti-DENV activity (Punekar et al 2022, Kasbe et al 2023).
Pioneering work done in the area of RNA interference agent (siRNA) for the inhibition of chikungunya virus which was published (Parashar et al, 2013, Parashar & Cherian 2014, Parashar & Cherian 2016) and patents

granted in US (2017), China (2019) Europe (2019), Australia (2021) & India (2021). The utility of solid lipid nanoparticles in delivery of antiviral siRNA in *in-vitro* and *in-vivo* model systems was demonstrated. Nanoparticles containing the siRNA approach can be considered for developing a delivery system for the treatment of other viral disease (Jeengar et al 2022). Another delivery system ZIF-C, for siRNA enhances the antiviral activity of chikungunya virus E2 and nsP1 genes directed siRNAs (Tagore et al 2022).
The findings from the studies may provide a basis for the future development of a novel therapeutic strategy to treat patients infected with dengue and chikungunya virus.

Keywords: Dengue (DENV); Chikungunya (CHIKV); Novel antivirals; Therapeutic strategy

NS-PCW & SCL-1

Nanotechnology in One Health: Enhancing Synergies across Health Systems

Anju Manuja*, Balvinder Kumar and Minakshi Prasad
*amanuja@rediffmail.com

ICAR-National Research Centre on Equines, Hisar, Haryana (125001), India

Abstract: The "One Health" model integrates the health of humans, animals, plants, and the environment to advance healthcare through multidisciplinary approaches, including nanotechnology. In drug delivery, nanotechnology enables the precise manipulation of molecules to create nanomaterials with targeted functions, leading to innovative nanobiotics and delivery systems. These nanoformulations, shown to be more effective and safer than conventional drugs, have successfully treated fungal, protozoan, and bacterial infections, particularly benefiting animal and plant health through biodegradable polymers.
Antimicrobial resistance (AMR) poses a significant health risk, driven by antibiotic-resistant bacteria and the resurgence of infectious diseases. As alternatives, inorganic nanoparticles like zinc oxide nanoparticles (ZnO NPs) have shown promise for their antibacterial properties. However, while nanoparticles offer wide applications, their safety in biological systems remains a concern. To mitigate toxicity, ZnO NP delivery systems have been developed, demonstrating both antibacterial efficacy and tissue repair.
Zinc oxide, commonly used as a dietary supplement, improves the bioavailability of zinc and iron—essential elements often inhibited by phytates. However, nanoscale formulations carry potential health risks. To enhance safety, ZnO NPs were encapsulated in alginate/gum-acacia (SAGA ZnO NPs) hydrocolloids and conjugated with iron oxide, resulting in higher Zn/Fe uptake in intestinal cells, showing alginate and gum acacia's protective effect in harsh digestive environments and an efficient delivery system when combined with iron oxide.
We formulated ZnO nanoparticles with flower-like morphology and further decorated with chitosan along with hydroxychloroquine (as a zinc ionophore) and evaluated successfully the formulations for cytotoxicity, and biocompatibility in embryonated chicks and their efficacy against bovine coronavirus (BCoV). We also demonstrated the cellular internalization of zinc ions and better synergy of chitosan, zinc oxide nanoparticles, and hydroxychloroquine to inhibit the bovine coronavirus.
An innovative trypanocidal drug delivery system for quinapyramine sulfate has proven highly effective against *Trypanosomaevansi* at reduced doses, while a new formulation with isometamedium chloride offers biocompatibility and efficacy at low doses.
Nanomaterials are considered for creating amazing efficiencies due to their properties being lighter, smaller, and stronger than the material they replace. Despite nanomaterials' lightweight and enhanced strength, their impact on human health, agriculture, and the environment requires careful consideration. Therefore, understanding the role and potential ecosystem impacts of nanoparticles, delivery systems, and carriers remains essential.

Keywords: Nanobiotics, Nanomaterials, One Health, Zinc oxide

NS-PCW & SCL-2

Deciphering the Microbiome Applications for Criminal Investigations

Jaskaran Singh[1*] and Minakshi Parsad[2]
*jaskaransingh630@gmail.com

[1]Department of Forensic Science, Geeta University, Naultha, Panipat, Haryana, India
[2]ICAR-National Research Centre on Equines (NRCE), Hisar, Haryana, India

Abstract: Forensic Microbiology is embarking its importnce and potential to aid in criminal justice system. The micro faunais prompting in personal identification by linking criminals with crime, crime with victim and victim with extent of severity The forensic perspective of microbiology aids in analysis & identification of physical evidences such as soil & hair. Furthermore, the microbial aspect also prompts in identification of post mortem intervals of decomposing corpses, and helps in metagenomics data generation analysis and interpretation. The scarce work on the subject and lack of expertise, trainings & protocols makes the branch more unique. An attempt is made to showcase one such microbe used for investigation in drowning cases is diatoms depending upon variable environmental conditions, the species of these Diatoms varies in geographical ranges. Thus, the identification of such species makes forensic investigation to narrow down the line of investigation in finding the approximate location of the deceased at time of death. This workshop will help to get better understanding of collection, preservation, packaging of water samples for isolation and identification of diatoms for forensic investigations.

Keywords: Crime, Criminals, Forensic Microbiology, Metagenomics

NS-PCW & SCL-3

Smart Nanomaterials for Medical and Agricultural Applications

Neeraj Dilbaghi
ndnano@gmail.com

Department of Biotechnology, Guru Jambheshwar University of Science and Technology, Hisar, Haryana (125001), India

Abstract: Innovations based on nanotechnology are crucial to international healthcare and environmental initiatives. As a result, nanomaterials are being thoroughly investigated by the scientific community for a wide range of biomedical, agronomic, catalytic, and diagnostic uses. We have developed a porous MNP-loaded hydrogel-based wound healing bandage using biologically synthesizing metallic nanoparticles (MNPs) and integrating them into a polymeric gel matrix based on natural plant gum. The ability of nanogel bandages to suppress multidrug-resistant (MDR) infections and promote wound site cell proliferation has been demonstrated through biomedical evaluations. Significant *in vitro* antioxidant and anti-inflammatory properties have also been established by the nanogel based bandages. Additionally, the nanogel-based bandages have demonstrated exceptional *in vitro* cell viability, demonstrating its suitability for wound healing. In addition, *a low-cost*, point-of-care diagnostic kit based on gold nanoparticles has been developed for the early, effective, and robust detection of trypanosomosis in equines. Compared to the traditional ELISA-based diagnosis, the developed trypanosomosis diagnostic kit is less expensive and prompt. We have also explored the use of smart nanomaterials in agriculture. Nanoemulsions based on carvacrol, thymol, and naringinin were tested for stability and potential to manage *Xanthomonas axonopodis*-caused bacterial blight disease in cluster bean. In another study, a novel fluorescence sensor based on molecular organic framework/quantum dots (MOF/QD) nanocomposite has been developed and evaluated to detect phosphate in soil samples.

Keywords: Metallic nano particles, Multidrug-resistant, Trypanosomosis, Xanthomonas axonopodis

NS-PCW & SCL-4

Role of Microbiology in Animal Forensics

Minakshi Prasad[1*], Jaskaran Singh[2], Basanti Brar[3], Gaya Prasad[4]
*minakshi.abt@gmail.com

[1]*ICAR-National Research Centre on Equines, Hisar, Haryana (125001), India*
[2]*Geeta University, Naultha, Panipat, Haryana, India*
[3]*Om Sterling Global University Hisar, India;* [4]*IIVER, Rohtak, Haryana, India*

Abstract: Microbiology has become an integral tool in the field of animal forensics, aiding in the investigation and resolution of animal-related crimes. By analyzing microbial evidence, forensic microbiologists can identify pathogens, establish links to specific environments or species, and determine cause of death in animal fatalities. Microbial communities, particularly in soil, carcass decomposition, and bodily fluids, offer unique and stable signatures that can help distinguish between natural death and foul play. Molecular tools including DNA profiling and metagenomics are particularly valuable in understanding the microbial flora associated with individual animal species, enabling the identification of geographical locations, diets, and even specific environmental exposures. Moreover, microbiological analyses can reveal time-since-death estimates, helping investigators establish timelines critical in forensic investigations. Through these methods, microbiology enhances forensic accuracy and provides essential information in cases of wildlife trafficking, illegal poaching, animal abuse, and environmental crimes, contributing significantly to justice in animal-related investigations.

Key words: Microbes; Animal forensics; Metagenomics; Pathogens; Poaching

NS-PCW & SCL-5

Innovation and Intellectual Property Rights

Rahul Taneja
rahulipr@hotmail.com

Registered Patent & Trademark Agent, Haryana State Council for Science and Technology
Department of Science and Technology, Bays 35, Sector -2, Panchkula, Haryana, India

Abstract: The Indian pharmaceutical and Biotechnology industry has changed remarkably over the last few decades, from being traders in imported drugs in the fifties, to major bulk drug producers by the eighties. During this transitional period Indian pharmaceutical and Biotechnology units have learnt the importance of Intellectual Property Rights and challenges faced by them during their marketing, production and exporting their products. There was a time when property of any individual or organization was measured in terms of physical tangible assets like land, buildings, valuables like cars, gold, machinery etc. But with passage of time, intangible assets also got recognition, and now we know these intangible assets as Intellectual Property or IP. Now, in modern concept of ownership, we count both intangible and tangible property as property associated with an individual or an organization. Intellectual Property is the Property, which has been created by exercise of Intellectual Faculty. It is the result of persons Intellectual Activities. Thus Intellectual Property refers to creation of mind such as inventions, designs for industrial articles, literary, artistic work, symbols which are ultimately used in commerce. Intellectual Property rights allow the creators or owners to have the benefits from their works when these are exploited commercially. These rights are statutory rights governed in accordance with the provisions of corresponding legislations. Intellectual Property rights reward creativity & human endeavour which fuel the progress of humankind. The intellectual property is classified into seven categories i.e. (1) Patent (2) Industrial Design (3) Trade Marks (4) Copyright (5) Geographical Indications (6) Lay out designs of integrated circuits (7) Protection of undisclosed information/Trade Secret according to TRIPs agreements. First of all, an Idea is generated in mind and these are converted in some form of property. For instance an idea is either converted into an Innovation or invention; some literary or artistic work; some aesthetic or decorative feature of article; brand name, trade dress or packaging style etc. Role of Trademark and Patent are widely involved in the field of Pharmaceutical Industries. All these forms of property are protected by various legal instruments.

Key words: Copyright; Geographical; IPR; Industrial design; Patent; Trade Marks

NS-PCW & SCL-6

Genetically diverse and symbiotically efficient Nitrogen-fixing rhizobia are root nodule symbionts of various wild/native and invasive legumes found in different agro-climatic conditions of India

Hukam Singh Gehlot
hsgehlot@gmail.com

BNF and Microbial Genomics Lab, Department of Botany, Centre of Advanced Study, Jai Narain Vyas University, Jodhpur-342001 (Rajasthan) India

Abstract: Legume-Rhizobia symbiosis and biological nitrogen fixation is a dynamic process having ample ecological and environmental impact. More than one hundred species of root nodule nitrogen fixing rhizobia have been known since the discovery of single species in 1889 by German Botanist Frank. For improving the soil fertility and enhancing the crop production in India the rhizobia-based biofertilizers were incorporated long back in our agricultural practices. We are still looking for efficient rhizobia which has broad host range and can adapt in wide agro-climatic conditions of India. In search of some efficient nitrogen-fixing rhizobia, we began our exploration in the arid and semi-arid regions of India with special focus on native and wild legumes of Indian Thar Desert. More than thirty species of native and invasive legumes were surveyed for their nodulation status, with few first reports of nodulation. After creating the nodulation database, the root nodule symbionts (>150) were characterized at molecular level. A significant genetic diversity was observed among these strains isolated from papilionoid, mimosoid, and caesalpinoid legume hosts. Using the polyphasic approach several potential new species were identified. The dominating symbionts were novel strains of *Sinorhizobium* (*Ensifer)* and strains of *Bradyrhizobium* sharing close affinity to *B. yuanmingense*. The symbioticgene-basedphylogenies gave information about the novel *nod* and *nif*genes harbored by these strains. Interestinglya significant incongruences were observed in core and *'sym'* gene phylogenies suggesting the occurrence of horizontal gene transfer under the stressed environmental conditions of Thar Desert.Based on genomic characterization the dominant symbiont of various legumes was described as new species *Ensifer* (*Sinorhizobium*) aridi. Genetically similar strains were reported from African and American alkaline-hot deserts, however these strains has geographiclocation specific nodulation genes. Among several Ensiferaridi strains, the PC2 strain was found interesting with multiple genes related to symbiosis and stress tolerance that found fixing nitrogen efficiently in species of Vigna and Macroptilliu mother than wild legumes.These well charaderized symbionts were checked for their N-fixing efficacy under glass-house conditions. Symbiotically efficient strains with broad host range were screened and have been cross-inoculated on several papilionoid crop legumes. So we have now several candidates which can be used as bio-inoculants for the various cultivars of *Vignaradiata, V. unguiculata, V. aconitifolia*, and *Cyamopsistetragonoloba*.

Keywords: *B. yuanmingense*, Legume-Rhizobia, root nodule, Nitrogen-fixing rhizobia

AWARDEE ABSTRACTS

AWA-1

Lifetime achievement Award, 2024

Dr. (Mrs.) Praveen Rishi, FABMS, FAMSc

Professor (Retd.), Department of Microbiology
Former Dean (Faculty of Science), Panjab University, Chandigarh

Cross-Roads Journey in Science: A Multi-Dimensional Approach

Abstract: Typhoid fever caused by *Salmonella enterica* serovar *Typhi* remains a common serious disease, particularly in tropical developing countries. Moreover, relentless emergence of antibiotic-resistant Salmonella strains coupled with the drawbacks associated with available therapeutic armamentarium and prophylactic measures warrants an urgent need to explore newer antimicrobial agents, vaccine candidates along with the development of more sensitive and specific diagnostic tools. Owing to multifactorial pathogenicity of *Salmonella*, initial research was conducted on host-parasite interactions, in view of various stresses which the organism encounters within the host at various stages of infection process. Further, to combat emerging AMR, various agents, for example, antimicrobial peptides, probiotics alone or with prebiotics as well as certain natural compounds were explored and found to be efficacious as biotherapeutics either alone or as combination therapy. It has also been documented by us earlier that *Salmonella* once exposed to cadmium in the environment can maintain the reservoir of resistant genes. This is one of the factors for inducing AMR in the pathogens. Thus, various metal inhibitors were developed to reverse the situation. Thereafter the bi-directional elucidation of probiotics administration as psychobiotics has also been documented to manage *Salmonella* brain infection at gut-brain axis. Along with such studies, double layered microencapsulated probiotic and micro-structured synbox system comprising of L. periplantarum and EGCG was also developed. In addition, a novel composition for encapsulating TRPV1-targeting siRNA within solid lipid nanoparticles was developed to reduce the pain sensation (Patent granted). Further, a hydrogel based antimicrobial wound dressing was developed, which promotes healing of Staphylococcus infected wounds by releasing Lactobacillus plantarum and curcumin or curcumin-loaded solid lipid nanoparticles (Patent published). Furthermore, microbial enzyme consortium obtained from Aspergillus niger, a soil isolate was also found to eradicate biofilms from biomedical surfaces and clearance of biofouling and black gunk developed on kitchen drainage pipes (Patent filed). In context to prophylactic measures, dual immunization using the combination of newly identified immunogenic CdtB (Cytolethal distending toxin subunit B) protein and bioinformatically identified flagellin epitope has also been reported as successful vaccination strategy against typhoidal serovars of Salmonella. Apart from this, a diagnostic kit to detect *Salmonella* has also been developed (Patent granted) and the technology has been transferred to the industry. Recently, possible mapping of audiometric analysis with the aerobic bacteriological findings in patients with Chronic Suppurative Otitis Media has also been put forward. During this research journey, crossing the boundaries from microbiological techniques to biochemical, biophysical, immunological, bioinformatics as well as nanobiotechnological tools helped in drawing meaningful conclusion with a multi-dimensional approach.

AWA-2

AMI- Life Time Achievement Award, 2024

Prof. Kamla Chaudhary

Prof. (Retd.) Department of Biotechnology and Molecular Biology
CCS Haryana Agricultural University Hisar, India
Prof. Emeritus Department of Microbiology,
Maharshi Dayanand University, Rohtak, India

Strategy for fractionation of rice straw components for a biorefinery setup and ethanol production from cellulosic fraction by yeasts

Abstract: Agro-industry plays a major role in the overall growth of world economy. India is the second largest agro-based economy with year-round crop cultivation in various parts of the country. Among the various crops grown in India, rice, wheat, and pulses are still the part of the staple diet of most of the population and these crops are preferred by the farmers because they provide a higher economic return. The multipurpose uses of crop residues are not limited to animal feeding only, but also used for other purposes which include soil mulching, bio-manure, thatching of rural homes and fuel for domestic and industrial applications. Despite of their known benefits, the burning of a significant part of crop residues on-farm to clear the field for cultivation of the succeeding crop is still in practice which is intensifying in recent years particularly in mechanized rice-wheat system of the north-west India. The adverse effects of crop residue burning includes the emission of greenhouse gases (GHGs), resulting in global warming, increased levels of particulate matter (PM) and smog, causes health hazards, loss of biodiversity of agricultural lands, and the deterioration of soil fertility. As per the latest data available, India produced 138 million tons of rice and 126 million tons of rice straw in 2024. Presently efforts are on to use rice straw for biomass power generation (burning), bio CNG and bioethanol production only. But the best option is to utilize rice straw through the production of bio-based products in a bio refinery set up wherein whole crop is being processed both for grains as well as straw. In a bio refinery, grains are used for production of food products and the lignocellulosic biomass can be utilized with multiple end goals i.e. to fractionate the rice straw biomass into its main components and these can be converted to valuable products for market use.

To make the process commercially viable, there is a need to develop low cost processes for separation of silica, lignin and other valuable fractions. It can generate extra revenue for the biorefinery instead of simply burning it to provide energy for the processing steps. We have used an integrated approach to separate various components of rice straw such as cellulose, hemicellulose, silica and lignin. Also improved procedural steps were used to save large quantity of water required for neutralization of treated rice straw. In the first step rice straw is treated with dilute alkali to obtain lignocellulosic residue and a dark brown supernatant. The residue is composed of major fraction of cellulose and some amount of hemicellulose. After saccharification of cellulosic fraction with cellulases, glucose, xylose, cellobiose, and xylooligosaccharides were produced. This sugar mixture was used for ethanol fermentation by yeasts. After ethanol distillation, yeast biomass and cellulose nanofibers can be utilized further. The dark brown supernatant so obtained contained silica, hemicellulose and lignin. Consecutively supernantant was subject to various treatment for precipitating and separating silica, hemicellulose and lignin using CO_2, ethanol and acid respectively.

AWA-3

AMSc Fellow - 2024

Prof. Sarman Singh

MBBS, MD, FRCP, FRSC, FAMS, FRSTMH, FSIIP, FATP, FIMSA, FABMS, FAAVR
Director (Medical Research and Institutional Collaborations)
AVMC, Pondicherry, Former Director, AIIMS, Bhopal

From a tiny village boy to highly recognized medical man: Tough but not impossible

Abstract: Born to illiterate parents in a small village in Aligarh, Uttar Pradesh, Dr. Singh faced significant challenges while growing up in extreme poverty. Despite these difficult circumstances, he pursued his education diligently, ultimately completing his undergraduate studies in Aligarh. His determination led him to secure a spot in the prestigious MBBS program at King George's Medical College in Lucknow, which he financed through borrowed funds. This foundational medical degree enabled him to sustain himself and further his education, specializing in Clinical Microbiology at the renowned Postgraduate Institute of Medical Education and Research (PGIMER) in Chandigarh.

In 1988, Dr. Singh joined the All India Institute of Medical Sciences (AIIMS) in New Delhi, where he transformed adversity into opportunity. At AIIMS, the Clinical Microbiology Division was a neglected sector of Laboratory Medicine. Within just 15 years, he elevated it to a world-class diagnostic facility. In 2018, he embraced a new challenge as the Director of AIIMS Bhopal, a prestigious position that is highly sought after by medical professionals in India.

Dr. Singh is a dedicated and industrious medical scientist, respected as a teacher and author of numerous research papers, and an editor for various medical journals and books. His administrative acumen is complemented by a deep understanding of institutional frameworks. Renowned both nationally and internationally for his remarkable research and academic contributions, Dr. Singh has faced various challenges and discrimination throughout his career but has remained resilient, serving as an inspiration for countless underprivileged students.

AWA-4

AMSc Fellow – 2024

Dr. Sunil Pabbi
Principal Scientist (Retd.) and Former Head & Professor, Division of Microbiology
ICAR - Indian Agricultural Research Institute, New Delhi
Former President, Association of Microbiologists of India

Bioprospecting microalgae biomass for high value bio-commodities for sustainable food, agriculture and environment

Abstract: Microalgae are light driven cell factories that thrive in freshwater or the marine environment and produce primary metabolites such as lipids, carbohydrates, proteins and amino acids including a diverse array of secondary metabolites *viz*. pigments, vitamins and sterols that have applications in food/feedas dietary supplements, as therapeutics for health management and wellbeing, biofuel for renewable energy, biofertilizers for agriculture and bio ameliorant for environment management etc. In many cases there is utilization of whole biomass or certain valuable metabolites and enzymes are extracted.The agricultural importance lies in the capacity of these organisms to fix atmospheric nitrogen, liberation of growth promoting substances, solubilizing phosphates, addition of organic matter and improving soil health. Similarly, microalgal pigments have gained much importance, with applications ranging from use as natural dyes and colours in textile, cosmetic and food industry as well as pharmaceutical and analytical use. Microalgal pigments and many other high value chemicals are now produced commercially. Microalgae accumulate significant amount of lipids mainly as triacylglycerides (TAGs) which are converted into biodiesel. These also serve as a sustainable and promising source of long chain omega-3 fatty acids due to the production of high-value EPA and DHA.

Besides the use of cyanobacteria as a biofertilizer for rice-based cropping system, microalgae offer one of the best options for sustainable next generation feedstock to use as platform feed for production of advanced biofuels and to address the rising demand for healthier, natural and sustainable products to satisfy the nutritional deficiencies of many foods and feeds in an economic way. There is a need to integrate the full production chain using multidisciplinary approach and also explore the development of technologies for sustainable and economic production of value-added biocommodities including bioplastics, nutraceuticals, novel and industrial platform chemicals through a biorefinery approach.

AWA-5

AMI Prof G S Rangasawamy Award, 2024

Dr. Livleen Shukla

Principal Scientist,
Division of Microbiology,
ICAR-Indian Agricultural Research Institute, New Delhi, India

Novel Microbial consortium an economical and viable solution for crop residue management for sustainable agriculture

Abstract: India is the global prime producer of rice (*Oryza sativa*) accounting for about 20% of world rice production. In India 43.2 m ha of area is under rice cultivation. The main byproducts of rice are straw, rice husk and rice bran. Approximately, 760 million tons of rice straw is produced per year globally, which is 1.5 times greater than per ton of rice-grain production. The disposal of this surplus straw creates a major concern in all the rice growing areas. Moreover, since last two decades' farmers prefer to burn this straw to clear the field for the timely sowing of wheat in northern and north-western parts of India. Open field-burning of straw release a large amount of pollutants including methane and fine/ inhalable particles, toxic gases such as carbon monoxide (CO), carcinogenic polycyclic aromatic hydrocarbons and volatile organic compounds (VOCs) which are responsible for various environmental pollution and human health hazards. Burning of rice straw emits 0.7- 4.1g of CH_4 and 0.019- 0.057g of N_2O per kg of dry rice straw and other gaseous pollutants such as SO_2, NOx, and to some extent, dioxins and furans. We have developed an effective microbial solution *Pusa Decomposer (liquid, capsule and wettable powder form)* for accelerated decomposition of paddy straw. Results show 90-95% degradation of the straw in a short period of 15 days, with concomitant improvement in soil OC, N and P availability and 15% increase in crop yield.There was marginal increase in soil health parameters like Microbial biomass Carbon (703-1222 mg/kg); Microbial biomass Nitrogen (82.86-207.96 mg/kg); Microbial biomass Phosphorus (5.44 – 9.22 mg/kg); and soil enzymes such as Dehyrogenase (249-296 TPF/g soil/day); Alkaline Phosphatase (127.1 – 159.9 µg/g/hr); Fluorescein diacetate (0.12-0.426µg/g/hr); Urease (488-509µg $N\text{-}NH_4^+$/g/hr). The research was carried out to decompose *ex-situ* flower and vegetable plants waste generated at CPCT, ICAR-IARI, New Delhi to value added product as compost. *Tagetes* sp., *Chrysanthemum* sp. and *Lycopersicon esculentum* showed pH 6.9- 7.2; EC 1.6-3.1; Potash (K) 0.74-0.9%; Phosphate (P) 0.38-0.44%; Organic carbon 22.61-36.09%; Nitrogen 0.38-0.49 % and C:N ratio 22.61: 0.38- 35.5:0.49, Humus 0.23-0.51% in 45-60 days. All the three composts were free from phytotoxicity and coliforms.

AWA-6

AMI- S R Vyas Memorial Award, 2024

Dr. Prakasham Reddy Shetty

Emeritus Scientist
CSIR-Indian Institute of Chemical Technology
Hyderabad, India

Mutan and Mutanase and their imperative role in biotech industry and oral health

Abstract: Glucans are biopolymers of glucose produced by plants, mushrooms and microbes. They are unique in nature with properties associated with human health. Among glucans, α and β glucans with 1-3 glycosidic linkages, differentiated by axial or equatorial position of glycosidic bond, play pivotal role in Pharmaceutical sector. α – glucan also termed as mutan. Two different approaches were adopted to produce them in the present study; a) isolation from cell walls of *Streptococcus mutans* (MTCC 497) and b) production using biocatalyst glucosyltransferase. Different hexose monosaccharide (glucose and rhamnose) and oligosaccharides like disaccharides (sucrose and maltose) and trisaccharide (raffinose) were used as substrates for in vitro synthesis. Molecular characterization of the enzyme glucosyltrasferase was performed by SDS-PAGE analysis which denoted that the biocatalyst produced by *S. mutans* has a molecular weight of ~125 kDa. Mutan as such is principle causative for dental decay. Hence efforts have been made to characterize the mutan followed by developing the microbial solution for its degradation. Acid hydrolysis of α-(1-3)-glucans revealed presence of glucose moieties which were characterized by Somogyi-Nelson method and also by phenyl hydrazine test (Osazone formation). Microscopic analysis of glucan hydrolyzed monomers revealed needle shaped crystals irrespective of substrates used for enzymatic synthesis of glucans. Water insoluble α-(1-3)-glucans (WIG) were converted to water soluble form by sulfation. The sulfation of WIG was confirmed by the presence of -O-SO_3- and C-O-SO_3- characteristic peaks at 1240 and 820 cm^{-1}. MALDI-TOF analysis of sulfated α-(1-3)-glucan revealed 1.2 to 9 kDa fragmentation. Antibacterial profile studies revealed higher growth inhibitory activity against gram negative than gram positive bacterial strains by sulfated α-(1-3)-glucans only. One-fold higher anti-inflammatory activity with IC_{50} value of 0.11 mg/ml was observed with sulfated α-(1-3)-glucans over WIG. Time dependent fibrinolytic potential without requirement of tissue plasminogen activators was observed for sulfated α-(1-3)-glucans. Using this substrate, mutanase producing microbial strain, *Paracoccus mutanolyticus*, was isolated and characterized its biochemical and molecular properties. The enzyme showed optimum activity at pH 5.5 and at 50 °C. It displayed Michaelis–Menten behaviour with a K_m of 1.263 ± 0.03 (mg/ml), V_{max} of 2.712 ± 0.15 U/mg protein. Thermal stability studies denoted that it required 55.46 and 135.43 kJ mol^{-1} of energy for activation and deactivation in the temperature range of 30–50 °C and 50–70 °C, respectively. Mutanase activity was enhanced ~ 50 and 75% by Fe^{2+} and EDTA, respectively, while presence of Hg^{2+} and Mn^{2+} inhibit > 90% of its activity. This enzyme has a molecular mass of 138 kDa and showed monomeric nature by Zymography. Scanning electron microscopy analysis of mutanase treated *Streptococcal* cells revealed cleavage of linkages among the cells and complete separation of cells, indicating its potential in dentistry as an anticaries agent in the prophylaxis and therapy of dental caries. In addition, antifungal activity of mutanase against *Colletotrichum capsici* MTCC 10147 and *Cladosporium cladosporioide* MTCC 7371 revealed that the enzyme has potential towards biological control of phytopathogens which could be used as an alternative bio-control agent against chemical pesticides in the future.

AWA-7

AMI- Soshil Kumar Panacea Award, 2024

Dr. Narottam Acharya

Scientist-F, Institute of Life Sciences,
Bhubaneswar, Odisha

Vaccines against fungal pathogens: A possible reality

Abstract: Disseminated fungal infections account for ~3.75 million deaths worldwide annually, and mortality may increase further due to a rise in the numbers of immune compromised individuals and drug-resistance fungal species. Recently, WHO reported a first-ever list of "priority fungal pathogens" mostly belonging to the genus *Candida*, *Cryptococcus*, and *Aspergillus*, and emphasized accurate and early diagnostics, monitoring drug resistance, and development of novel antifungal drugs and immune therapeutics. Although similar approaches have been taken as used for viruses and bacteria, a safe and effective antifungal vaccine is yet to be developed. Since every pathogen need to replicate in the host to survive and cause diseases, we targeted for the first time the replication machinery components by two distinct approaches to attenuate virulence of *Candida albicans*. CNA25 and CAET are two such strains those are a virulent and induce robust protective immune responses to prevent systemic candidiasis in pre-clinical models, and are the promising potential live whole-cell vaccine strains. These findings will be discussed.

AWA-8

AMI-Soshil Kumar Jain Panacea Biotech Award, 2024

Dr Goutam Ghosh

Ex-Vice Chancellor, Gandhi Institute of Engineering and Technology University
Ex-Vice President Asian Federation of Biotechnology
Director, Vaxfarm Life Sciences, New Delhi

Bridging the Gap in Translational Research: A must for Successful Development of Innovative Vaccines

Abstract: Scientific advancement and discoveries in Biological research outpaces the capacity to convert findings into commercially viable life-saving remedies. In reality, a lot of scientific findings never make it farther in the development process. However, many of these newer findings could have been saved from being "lost in translation" if there is greater partnership, sharing mindset, improved leadership and insights for translational research.

Although scientists are well-versed in the molecule or product in question, academia frequently fails to grasp the full scope of its development process and how to take a highly valuable scientific idea, translate it to the clinic and then bring it to market in the most efficient and economical way. It requires collaboration between academics and industry rather than small-scale initiatives with little support from a single lab in an academic environment. Translation of these discoveries into newer biological products such as vaccines and therapeutics has been far slower than anticipated, despite large investments in fundamental science, technological advancements, and improved understanding of human illness.

For translational research to operate more effectively, functional interactions should exist between Academia, Clinicians, Industry and Government since it offers an efficient platform for driving innovation and bringing cutting-edge solutions to the fore. Newer approaches to translational research in novel vaccine development need to focus on by integrating the role each specialty/stakeholder in a cooperation to accelerate the translational challenges in developing the product from the proof-of-concept stage to scale-up issues, reproducibility, preclinical and clinical evaluation, manufacturing and commercialization of processes and product. It's important that we acknowledge the enormous worth of these collaborations going forward and make sure they continue to be based on openness, trust, and reciprocity.

AWA-9

AMI- Louis Pasteur Award, 2024

Dr. Mahesh Dhar

Vice-President (Research)
Sunny Corporation Pvt. Ltd. DSIDC Complex, Phase- I Okhla, New Delhi

Role of Genome Sequencing in Molecular Epidemiology

Abstract: Molecular epidemiology has proven crucial in understanding and combating the COVID-19 pandemic, highlighting its significance in modern public health. By analyzing the genetic makeup of SARS-CoV-2, researchers have tracked its origin, spread, and evolution, providing valuable insights for disease control and prevention. This approach enabled the rapid development of diagnostic tests and vaccines, demonstrating the power of genomic surveillance in pandemic response. It allowed for the identification of new variants, such as Delta and Omicron, helping health authorities adapt strategies to combat emerging threats. Molecular epidemiology also revealed patterns of transmission, aiding in contact tracing and informing public health measures. It exposed the virus's ability to cross species barriers, emphasizing the importance of the One Health approach in preventing future pandemics.

Furthermore, this field facilitated global collaboration, with researchers worldwide sharing genomic data to track the virus's spread and evolution in real-time. INSA CoG, setup in Dec. 2020 bought together national institutes of diverse research mandates for a sole purpose of whole genome sequencing of prevalent SARS-CoV2 strains. This unprecedented cooperation has set a new standard for international scientific collaboration in the face of global health crises. The SARS-CoV-2 pandemic has underscored the critical role of molecular epidemiology in modern disease surveillance, prevention, and control, paving the way for more effective responses to future outbreaks.

AWA-10

AMI- Young Scientist Award, 2024 (Agriculture Microbiology)

Dr. Gaurav Raturia

Postdoctoral Research Associate, Institute of Genomics for Crop Abiotic Stress Tolerance, Texas Tech University, USA.

Decoding tripartite symbiosis relationships: Insights into AMF and *Rhizobium* Interactions for sustainable agriculture

Abstract: The increasing food demand and intensification of agriculture have resulted in the increased use of chemical fertilizers, which is a leading cause of soil degradation. It is essential to ensure sustainable agriculture to meet global food demand without compromising environmental safety. This agricultural sustainability can be achieved by leveraging the use of beneficial microorganisms. This study delves into the synergistic potential of Arbuscular mycorrhizal fungi (AMF), rhizobium, and plant interactions in sustainable agriculture. The mutualistic association of AMF and rhizobium with soybean roots facilitates nutrient uptake especially Phosphorus, Nitrogen, and different micronutrients. Our study focuses on the identification of genes, and signaling molecules involved in the tripartite symbiosis of soybean-AMF-Rhizobium, using genome-wide association studies (GWAS), metabolomics, and Single nucleus RNA sequencing (snRNA-seq). GWAS using more than 100 soybean germplasm was performed to identify single nucleotide polymorphisms (SNPs) associated with root nodule-related traits. To further investigate the potential signaling molecules responsible for successful association, root metabolomics analysis was performed on inoculated and non-inoculated plant roots. snRNA-seqwas then employed to unravel cell-specific gene expression patterns and pinpoint potential signal molecules facilitating this symbiosis. A hairy root transformation system is being used to validate the function of the identified genes. These findings could lead to the development of soybean varieties with improved responses to microbial inoculation, enabling more resilient, sustainable agricultural practices that minimize chemical inputs.

AWA-11

AMI- Young Scientist Award, 2024 (Dairy and Food Microbiology)

Dr. Somenath Das

Assistant Professor
Department of Botany,
Burdwan Raj College, Purba Bardhaman, West Bengal

Nanoencapsulation of essential oils as novel, green and consumer oriented approach to protect stored food commodities from fungi and aflatoxin contamination

Abstract: The sustainable development agenda of 2030 as described by United Nations in 2015 includes 17 sustainable development goals (SDGs) for improvement in quality life in a sustainable manner. Among these 17 goals, SDG 1, SDG 2, and SDG 3 are completely based on no poverty, zero hunger, and promote food security with sustainable agriculture. Contamination of postharvest food commodities in poor storage conditions, fungal attack, and aflatoxin biosynthesis would cause hurdle to achieve this SDGs. Synthetic chemicals have been indiscriminately used to avoid the fungi and aflatoxin mediated food contamination, however, they cause various health hazards and environmental non-sustainability problems creating a challenge to attain the SDGs. The present study demonstrates the nanoencapsulation of essential oils into biopolymer and assessment of preservative efficacy in various stored food system. The encapsulation of essential oil was confirmed through Scanning electron microscopy, Fourier transform infrared spectroscopy, dynamic-light-scattering, and X-ray-diffractometry analyses. The nanoencapsulation improved the antifungal efficacy against *Aspergillus flavus* and aflatoxin B_1 biosynthesis through their controlled delivery. Inhibition of ergosterol, enhanced leakage of cellular cations, and efflux of small proteins and nucleic acids suggested plasma membrane as a target site of antifungal action. Moreover, the impairment in methylglyoxal synthesis and antioxidant enzymes activity by nanoencapsulated essential oils validated the novel anti-aflatoxigenic mechanism of action. The molecular study of essential oil determined down-regulation of the genes (*afl-R*, *ver-1*, *omt-A*) involved in synthesis of aflatoxin B_1 and targeted action through bioinformatics based *in silico* investigation. The *in situ* application of nanoencapsulated essential oil was performed in rice, maize, dry fruits, and oil seeds in the form of fumigation. The encapsulated essential oils preserved the nutritional contents and organoleptic properties of foods along with inhibition of lipid peroxidation. The nanoencapsulated essential oils have been found as safe to mammalian system with very high LD_{50} values over synthetic preservatives. This nano-approach has been validated as cost effective, consumer oriented, and highly productive for food and agricultural industries. Thus the nanoencapsulated essential oils develop a controlled delivery and sustainable approach to ensure the nutritious food availability, address the food security challenges, and can fulfill the sustainable development goals.

AWA-12

AMI- Young Scientist Award 2024 (Environmental Microbiology)

Dr. Nirjara Singhvi

Dev Bhoomi Uttarakhand University, Dehradun, India

Harnessing Omics to Decipher Microbial Genomic Repertoires for Environmental Conservation

Abstract: Bioinformatics has emerged as an indispensable tool in unraveling the genetic blueprints of microbial communities, enabling a deeper understanding of their contributions to environmental health and sustainability. Microbial are essential in maintaining ecological balance, aiding in processes such as nutrient cycling, pollutant degradation, soil fertility, and ecosystem resilience. With advancements in bioinformatics, it is now possible to analyze massive genomic datasets from diverse microbial populations, uncovering genes, metabolic pathways, and interaction networks that reveal microbial functions crucial for environmental maintenance. By decoding the genomic repertoires of microbial communities, bioinformatics facilitates the identification of genes involved in key ecological functions like nitrogen fixation, carbon cycling, and organic pollutant breakdown. Furthermore, bioinformatic tools help predict how microbial communities may respond to environmental stressors, including pollution and climate change, thereby supporting targeted conservation efforts. This study emphasizes the potential of bioinformatics to drive innovative, microbially-based solutions for ecosystem restoration and sustainable natural resource management. By applying genomic insights to environmental science, bioinformatics opens new avenues for using microbial communities as ecological engineers in the quest to protect and rehabilitate our planet.

AWA-13

AMI- Young Scientist Award, 2024 (Industrial Microbiology)

Dr. Sandeep Kumar Singh

Senior Research Fellow
Division of Microbiology
ICAR-Indian Agricultural Research Institute, New Delhi, India

Refinement and characterization of microbial consortium for accelerated decomposition of paddy straw

Abstract: Lignocellulosic residues, such as rice straw, along with carboxymethyl cellulose (CMC), xylan, and lignin, were evaluated as substrates for cultivating lignocellulolytic fungi in submerged fermentation at 30°C over a 15-day period. Rice straw, constituting 40-60% of the rice plant's biomass and rich in cellulose (42.14%), hemicellulose (22.08%), and lignin (11.98%), was explored as a renewable resource for energy and biochemical production. In the qualitative screening of degradation, a total of thirty-nine fungal isolates were selected. These screened isolates were further subjected to quantitative estimation of different enzymes. The maximum enzyme production was observed infour fungal strains namely *Penicillium oxalicum* (F1), *Talaromyces pinophilus* (F12), *Penicillium griseofulvum* (F22), and *Trichoderma reesei* (F26). Enzyme assays at 3-day intervals revealed maximal production of CMCase (63.42-88.26 U/mL), FPase (46.01-80.66 U/mL), xylanase (1146.10-1640.52 U/mL), lignin peroxidase (0.192-0.287 U/mL), and laccase (0.193-0.434 U/mL). Molecular characterization using internal transcribed spacer (ITS) sequencing confirmed the identity of the fungal strains. These results demonstrate the significant potential of these fungi in producing hydrolytic enzymes and degrading lignocellulose, with rice straw serving as an economical carbon source for biotechnological applications in biorefineries. This study not only indicated a valuable paddy straw degrading strain but also offer meaningful evidence for further exploration of the microbial degradation mechanism.

AWA-14

AMI-Louis Pasteur Award, 2024

A promising approach for food safety and food pathogen control

Namita Singh, Madhavi Chahar, Vinay Gupta
namitasingh71@gmail.com

Lab No.202, Microbial Biotechnology Laboratory, Department of Biotechnology, Guru Jambheshwar University of Sciences and Technology, Hisar India-125001

Abstrct: This study reports the isolation and characterization of two novel bacteriophages, EC BD and ST BD, targeting *Escherichia coli* and *Salmonella typhimurium*, respectively, as potential biocontrol agents for foodborne pathogens in dairy products. Phage EC BD, isolated from cattle dung, belongs to the Myoviridae family and displays robust lytic activity with a large burst size and short latent period. It effectively reduced enterotoxigenic *E. coli* strains in milk, cheese, and paneer, achieving up to a 7.0 log CFU/mL reduction at 4°C. Similarly, phage ST BD isolated from buffalo dung, demonstrated high stability at 4°C and significantly inhibited *Salmonella Typhimurium* growth in dairy products, resulting in up to a 7.0 log CFU/mL reduction after 6 days. Both phages were found to be strictly lytic, with no toxins, virulence, or antibiotic resistance genes, making them safe for food applications. These findings suggest that EC BD and ST BD have strong potential as natural biocontrol agents to mitigate *E. coli* and *Salmonella* contamination in dairy food matrices.

Keywords: Myoviridae, *Escherichia coli*, *Salmonella typhimurium*, enterotoxigenic

CONFERENCE PRESENTATIONS

AMDT-1 (Oral)

invA gene of *Salmonella* Pathogenicity Island-1: A Dubious Target for *Salmonella* Detection?

Akanksha Joshi[1*], Kartikey Chaturvedi[2], Abhishek Kaushik[1], Komal Chauhan[3], Neetu Kumra Taneja[1] and Tarun Kumar Sharma[4]
*joshi.akanksha2495@gmail.com

[1]*Department of Interdisciplinary Sciences, National Institute of Food Technology Entrepreneurship and Management (NIFTEM), Kundli, Sonepat, Haryana (131028), India*
[2]*Translational Health Science and Technology Institute (THSTI), Faridabad, Haryana (121001), India*
[3]*Department of Food Science and Technology, National Institute of Food Technology Entrepreneurship and Management (NIFTEM), Kundli, Sonepat, Haryana (131028), India*
[4]*Department of Medical Biotechnology, Gujarat Biotechnology University (GBU), Gandhinagar, Gujarat (382355), India*

Abstract: *Salmonella*, a prevalent food-borne pathogen prevails as complex surface associated interacting communities of alike and/ or different cells (mixed-species) throughout the food supply chain and/ or inflamed gut. Under such scenarios increased donor-acceptor ratio increases the rate of inter-species and intra-species Horizontal gene transfer (HGT). Within such associations various events of HGT might have compromised the integrity and uniqueness of the *invA* gene, traditionally considered to be confined within *Salmonella spp.* This study explores different primer sets amplifying various regions of *invA* gene of dairy isolated AMR strain of *Salmonella*. The primers were thoroughly analyzed for their structural characteristics and specificity by NCBI-Primer BLAST and *in-silico* PCR. *In-situ* specificity analysis was done by conventional PCR. Homology of *invA* gene sequence with the whole genome of selected bacterial species was computed using open-source software packages like BioPython for Jupyter, MAFFT, MEGA11 and Jalview. While the *in-silico* PCR for all the primer sets, except for XinvA, computed high specificity for *Salmonella,* primer BLAST directed us towards a non-conventional trend depicting high cross-reactivity. *In-situ* analysis heightened concerns about the specificity of invA. An alarming False detection rate of 87.5% with *invA*-based detection was observed. Multiple sequence alignment of whole genome of selected non-*Salmonella* strains depicts the presence of various homologous sites to *invA*. This investigation questions the reliability of traditional and upcoming detection platforms using *invA* as the marker gene for *Salmonella* owing to a remarkably high false positive rate.

Keywords: *Salmonella*; HGT; invA gene; BioPython; in-silico PCR; BLAST

AMDT-2 (Oral)

Salivary Microbiome: A Non-Invasive Avenue for Detecting and Evaluating Oral Cancer

Rashmi Bhardwaj[*], Ravina Vats, Afsareen Bano and Pooja Yadav
*bhardwajrashmi3@gmail.com

Centre for Medical Biotechnology, Maharshi Dayanand University, Rohtak, Haryana, India

Abstract: Introduction: Oral cancer is the sixth most common malignancy to generate a significant mortality rate globally. Oral Squamous Cell Carcinoma is a widespread malignant neoplasm of oral cancer whose foremost risk factor includes tobacco consumption. The lack of a non-invasive diagnostic approach for early predictive biomarkers leads to late diagnosis, poor prognosis, and low five-year survival rate. Saliva can be a potential diagnostic fluid as it is non-invasive and in direct contact with the oral cancer lesion. Our study explores salivary microbiome alteration in oral cancer and tobacco consumers, a susceptible group for oral cancer.
Methodology: Salivary DNA samples from 90 study participants, including Oral cancers, Tobacco consumers, and control, were used next-generation sequencing of V3-V4 region of 16S rRNA. Raw reads were filtered and de-noised by DADA2 and analyzed by QIIME2 software for alpha and beta diversity variation analysis, including Simpson and Shannon index. Community structure difference and function prediction among study groups were analyzed by PICRUSt2 software.

Results: By investigating the Amplicon Sequence Variant and distribution of function number, 99 common ASVs were found between oral cancer and tobacco consumer. *Firmicutes*, *Fusobacteria*, *Bacteroidota*, *Actinobacteria,* and *Proteobacteria* found to be differentially expressed phylum in oral cancer, whereas *Bacteroidota* and *Actinobacteria* were deregulated in tobacco consumers. By LefSe- LDA Score analysis of beta diversity, genus *Rothia* and *Actinomyces* were differentially expressed in oral cancer as well as tobacco consumers.
Conclusion: These compositional changes in salivary microbiome may have the capacity to act as a biomarker to track the emergence of oral cancer. The shared microbial alteration found in tobacco consumers and oral cancer patients revealed that prolonged tobacco consumption is linked to oral cancer development.

Keyword: Microbiome; Oral Cancer; Cancer Biomarkers; Tobacco; Saliva; Non-invasive Diagnostics

AMDT-3 (Oral)

Development of a Novel Malaria Diagnostic Kit with High Sensitivity and Zero False Positives

Tarun Kumar Bhatt and Preshita Bhalerao
tarun@curaj.ac.in

Department of Biotechnology, School of Life Sciences, Central University of Rajasthan, Bandarsindri, Kishangarh, Ajmer, Rajasthan (305817), India

Abstract: A protozoan parasite from the family Plasmodium causes malaria, a vector-borne illness that is spread by the female mosquitoes. The World Health Organization (WHO) estimates that 250 million cases are recorded annually. To lessen the complications of the illness, it is crucial to diagnose the parasite and its causative species as soon as possible. Various techniques (RDT, PCR, microscopic analysis, etc.) are accessible and regularly used to identify the malaria parasite. However, each technique have advantages and disadvantages of its own. Rapid Diagnostic Tests (RDTs) based on HRPII protein approach is used most commonly. False-negative and False-positive reports, which are both connected to HRPII protein, are among the major RDT drawbacks. As a result, HRPII protein replacement is urgently required for the prediction of *P. falciparum* infection. We have chosen malaria proteins with a very high abundance but a very short half-life for the proposed research. With this approach, a diagnostic marker with extremely high specificity and no false positives would be developed for the first time. Through precise pre- and post-treatment detection, the chosen marker(s) will eliminate both the issues of false negatives and false positives and will contribute to the 2023 goal of 'Accelerating the fight against malaria'.

Keywords: Malaria; RDTs; Diagnosis; False positives; False negative

AMDT-4 (Oral)

Role of Microbiology in Animal Forensics

Minakshi Prasad[1*], Jaskaran Singh[2], Basanti Brar[3] and Gaya Prasad[4]
*minakshi.abt@gmail.com

[1]*ICAR-National Research Centre on Equines, Hisar, Haryana (125001), India*
[2]*Geeta University, Naultha, Panipat, Haryana, India*
[3]*Om Sterling Global University Hisar, India;* [4]*IIVER, Rohtak, Haryana, India*

Abstract: Microbiology has become an integral tool in the field of animal forensics, aiding in the investigation and resolution of animal-related crimes. By analyzing microbial evidence, forensic microbiologists can identify pathogens, establish links to specific environments or species, and determine cause of death in animal fatalities. Microbial communities, particularly in soil, carcass decomposition, and bodily fluids, offer unique and stable signatures that can help distinguish between natural death and foul play. Molecular tools including DNA profiling and metagenomics are particularly valuable in understanding the microbial flora associated with individual animal species, enabling the identification of geographical locations, diets, and even specific

environmental exposures. Moreover, microbiological analyses can reveal time-since-death estimates, helping investigators establish timelines critical in forensic investigations. Through these methods, microbiology enhances forensic accuracy and provides essential information in cases of wildlife trafficking, illegal poaching, animal abuse, and environmental crimes, contributing significantly to justice in animal-related investigations.

Key words: Microbes; Animal forensics; Metagenomics; Pathogens; Poaching

AMDT-5 (Poster)

Development of a Molecularly Imprinted Au-SPE Sensor for Rapid Microcystin Detection in Contaminated Water

Minakshi Lalit[1*], Vikas Hooda[2], Namita Singh[1]
pr.minal@gmail.com

[1]*Microbial Biotechnology Laboratory, Department of Biotechnology, Guru Jambheshwar University of Science and Technology, Hisar, Haryana (125001), India*
[2]*Centre for Biotechnology, Maharishi Dayanand University, Rohtak, Haryana (124001), India*

Abstract: Acute and chronic damage may arise in human and animal from exposure to cyanotoxins, especially microcystins, in water resources, which are linked to hepatotoxicity and carcinogenesis. Consequently, there is a need for an on-site diagnostic method that can rapidly measure microcystins in surface water. This study has developed an affordable, user-friendly sensor system for the detection of microcystins in cyanotoxin-contaminated water. A gold screen-printed electrode (Au-SPE) sensor, based on molecularly imprinted polymer (MIP), was designed, produced, and evaluated. The detection utilized differential pulse voltammetry (DPV) and electrochemical impedance spectroscopy (EIS) as measuring techniques.
The calibration curve for the DPV measurements of microcystins in cyanotoxin-contaminated water samples showed excellent selectivity, with a broad peak corresponding to their anodic current. Another measurement technique, EIS, demonstrated the high sensitivity and affinity of the sensor, with interference recorded in cyanotoxin-contaminated water samples showing decreased diffusion with the addition of biomolecules.
Our results suggest that the MIP-based Au-SPE sensor will play a significant role in environmental diagnostics and water monitoring in the near future.

Key words: Cyanotoxin; Microsystin; Differential pulse voltammetry; Electrochemical impedance spectroscopy

AMDT-6 (Poster)

Comparative Analysis of Antibiotic Resistance in Urban and Rural Soil Microbiomes through Computational Approach

Sandhya Devi[1], Neha Yadav[1,2] and Rakesh Yadav[1]*
ry.yadav01@gmail.com

[1]*Department of Biotechnology, Guru Jambheshwar University of Science and Technology, Hisar, Haryana, India-125001*
[2]*Central Instrumentation Laboratory, Central University of Punjab, Bhatinda, Punjab (151 401), India*

Abstract: The global rise in antibiotic resistance presents a significant health challenge, with soil microbiomes acting as key reservoirs for antibiotic resistance genes (ARGs). In this study, we utilized computational biology and bioinformatics methods to examine the prevalence and diversity of ARGs in soil microbiomes from both urban and rural environments, using publicly available metagenomic datasets. Our analysis encompassed metagenome sequences from 20 urban and 20 rural sites across various geographic regions, aiming to understand the influence of urbanization on the distribution of ARGs.
To achieve this, we developed a specialized bioinformatics pipeline to process the metagenomic data, identify ARGs, and assess their abundance and diversity in urban versus rural samples. This pipeline integrates advanced

tools for quality control, genome assembly, gene prediction, and ARG annotation, drawing on resources such as the Comprehensive Antibiotic Resistance Database (CARD) and ResFinder.
Our findings revealed notable differences in ARG profiles between urban and rural soil microbiomes. Urban samples demonstrated a higher abundance and diversity of ARGs, particularly genes associated with resistance to beta-lactams, fluoroquinolones, and tetracyclines. Meanwhile, rural samples exhibited a lower overall ARG presence but displayed distinctive resistance patterns, especially towards naturally occurring antibiotics.
The datasets are further subjected to the machine learning techniques to pinpoint the key characteristics that differentiate urban and rural resistomes, alongside network analyses to investigate ARG co-occurrence patterns. This allowed us to explore potential horizontal gene transfer events and the evolution of multidrug resistance in soil bacteria across diverse environments.
This study underscores the impact of urbanization on ARG distribution within soil microbiomes and illustrates the value of harnessing metagenomic data for novel insights. Our results contribute to the expanding knowledge of environmental reservoirs of ARGs and may help guide future strategies to curb the spread of antibiotic resistance within microbial communities.

Keywords: Antibiotic resistance genes; Soil microbiome; Metagenomics; Comparative genomics; Urban environments; Rural environments

AMDT-7 (Poster)

Development of a Multiple Genetic Marker-based Kit for the Detection of Bacterial Urinary Tract Infection

Archita Lenka and Sandip Kumar Dash*
*dashsandipkumar@gmail.com

Department of Zoology, Berhampur University, Berhampur, Odisha (760007), India

Abstract: Urinary tract infections (UTIs) are prevalent infections in the human urinary tract, mainly caused by bacteria (90-95% of cases), though they can also be caused by fungi or viruses. Six bacterial strains—*Escherichia coli.*, *Pseudomonas sp*., *Staphylococcus sp*., *Streptococcus sp*., *Enterococcus sp*., and *Proteus sp*.—are responsible for 95-97% of bacterial UTIs. UTIs affect approximately 8-10 million people each year, with a higher incidence in women. While several diagnostic methods have been developed for detecting these bacteria, many have limitations such as low sensitivity or specificity, long detection times, or high costs. Although culture-based detection remains the gold standard, it is time-consuming and can be misleading. There is a need for a simple, sensitive, specific, and cost-effective diagnostic method. To address this, we have developed a straightforward diagnostic kit based on multiple genetic markers for the rapid and economical detection of bacterial UTIs. We selected specific genes for each bacterial strain from NCBI GenBank and designed primer sets targeting partial sequences of these genes. We isolated genomic DNA from each bacterium and optimized the amplification of target sequences through adjustments in temperature and time. The amplicons were sequenced to confirm their identity against reported sequences in NCBI. We then created a reference ladder by mixing the amplicons in optimized proportions. The primers, mixed into a PCR master mix and lyophilized, were used to develop the diagnostic kit. This kit allows for efficient detection of bacterial UTIs and is suitable for mass screening.

Keywords: Bacterial infection; Diagnosis; Multiplex PCR; PCR; Human disorder

AMDT-8 (Poster)

SCC*mec* and AGR Typing of Methicillin-resistant *Staphylococcus aureus* and Methicillin-sensitive *S. aureus* Strains

Shweta Sinha* and Durg Vijai Singh
*shweta7865sinha@gmail.com

Department of Biotechnology, School of Earth Biological and Environmental Sciences, Central university of South Bihar, Gaya, Bihar, India

Abstract: Rapid and specific PCR-based methods offer the prospect of improved sensitivity and reduced turn-around time compared with standard phenotypic methods, potentially leading to appropriate and accurate therapy and infection control measures. A total of 65 *S. aureus* strains isolated from a variety of infections like ocular diseases, wound infection, sputum and environment were included in the study. We used hexaplex PCR assay for rapid detection of the antibiotic resistance genes and species-specific *nuc* gene, performed *SSC*mec and AGR typing in addition to ERIC and REP-PCR to look for genetic diversity. We identified all the 65 isolates by using biochemical tests including Gram staining, catalase production, fermentation of glucose and mannitol. The amplification of the *S. aureus nuc* gene in hexaplex PCR confirmed the identity of isolates. Hexaplex PCR differentiated isolates into two MSSA and MRSA. We found 40% isolates to be positive for *mec*, 9.2% isolates for *pvl* gene, 1.53% for *czr*C gene, but none for *qac*A/B gene. SCC*mec* typing of MRSA strains showed that 65.38% strains belong to type *SSC*mec type V and 26.92% were type IV. AGR typing showed that 30.76% *S. aureus* strains belong to *agr*-I, 13.84% strains to *agr*-II, 23.07% to *agr*-III and 12.30% belong to *agr*-IV respectively; however, 20% strains were not typeable by the method employed. This study provides evidence that *S. aureus* are mostly lacking the pvl gene, belong to different *SSC*mec types of which type V is dominant *SSC*mec types among MRSA strains, in addition to showing diverse *agr*-types indicating diversity among *S. aureus* irrespective of sources of isolation.

Keywords: SCC*mec*; AGR; MSSA; MRSA; Hexaplex PCR; ERIC; REP

AMDT-9 (Poster)

Recombinase Polymerase-Aided Amplification Combined with Lateral Flow (RPAA-LF) Assay for Rapid and Highly Sensitive Parallel Detection of *Bacillus anthracis* and *Yersinia pestis*

Moumita Paul, Suchetna Singh, Sanjay Kumar* and S. Ponmariappan
*drsanjay.drde@gov.in

Biodetector Development Test and Evaluation Division, Defence Research & Development Establishment, Defence Research and Development Organization, Jhansi Road, Gwalior, Madhya Pradesh (474002), India

Abstract: Bioterrorism is characterized by the intentional dissemination of biological agents to inflict significant harm or disruption. *Bacillus anthracis* and *Yersinia pestis* are particularly concerning due to their high potential to cause extensive damage and suffering within affected communities. Early detection and rapid investigation are the keys to containing outbreaks, quick implementation of suitable medical counter-measures, and also for general surveillance. Hence, a field-deployable, rapid, sensitive and specific detection method is required to contain the spread of these potential agents. A duplex recombinase polymerase-aided amplification combined with lateral flow strip based result read-out (RPAA-LF) has been developed to rapidly and accurately detect *B. anthracis* and *Y. pestis*. The assay has a total turn-around time of 20 min at 42°C. To the best of our understanding this is the first report describing the development of duplex RPAA-LF for simultaneous detection of *B. anthracis* and *Y. pestis*. The specific nature of the assay was established with a panel of 25 closely related and non-related organisms. The analytical sensitivity of the assay was found to be 10 copies per reaction for both *B. anthracis* and *Y. pestis*. Further studies were conducted to extend the assay's applicability to environmental and clinical matrices by artificially spiking the agents into natural water and human blood. The assay demonstrated the capability to detect up to 10 colony-forming units per milliliter (cfu/ml) of *Bacillus anthracis* in both water and blood, while the detection limit for *Yersinia pestis* was 15 cfu/ml in both the matrices. The straightforward operation of RPAA-LF, which does not depend on advanced equipment and utilizes low-cost lateral flow strip-based result read-out, combined with its high sensitivity and specificity,

positions it as a promising alternative to other nucleic acid amplification assays in both field and laboratory settings with extended turnaround times.

Keywords: *B. anthracis; Y. pestis;* Recombinase Polymerase-aided Amplification; Lateral flow assay; Rapid; Low-cost

AMDT-10 (Poster)

Development of an Internally Controlled Single-tube Hydrolysis Probe Based Multiplex Real-time PCR Assay for Simultaneous Detection of *Bacillus anthracis, Yersinia pestis* and *Francisella tularensis*

Suchetna Singh[1], Moumita Paul[1], Sanjay Kumar[1*], S. Ponmariappan[1] and Duraipandian Thavaselvam[2]
*drsanjay.drde@gov.in

[1]*Biodetector Development Test and Evaluation Division, Defence Research & Development Establishment, Jhansi Road, Gwalior, Madhya Pradesh (474 002), India*
[2] *O/o DGLS, Defence Research and Development Organization, SSPL Campus, Timarpur, New Delhi (110 054), India*

Abstract: New and emerging infectious diseases caused by pathogenic bacteria in the field of health- care, agriculture, bio-defence and the recent devastating COVID-19 pandemic has highlighted the importance for the development of rapid and reliable detection assays for environmental monitoring and better patient management. Nucleic acid based amplification techniques (NATs) such as real-time PCR are extensively used for sensitive and specific detection of micro-organisms present in varied samples. Most of the currently available NATs target single agent detection without inclusion of suitable internal controls. The use of internal control is imperative for development of a robust detection assay to avoid the possibility of false negative results due to inefficient sample preparation, presence of PCR inhibitors, and reagents as well as equipment malfunction. To address this challenge, this study deals with the development of a single-tube multiplex real-time PCR assay for simultaneous detection of three high priority Category A biothreat agents, namely, *Bacillus anthracis, Yersinia pestis* and *Francisella tularensis* along with an internal control to ensure efficient nucleic acid extraction and reliable amplification. The spores of *Bacillus thuringiensis* are used as an extraction and amplification control for environmental matrices. The developed assay was found to be highly specific when evaluated with closely related and non-related bacterial species and the analytical sensitivity of the assay was determined to be 50 GE/qPCR reaction of each target agent in multiplex format. In artificially spiked garden soil, the lower limit of detection was found to be 400 CFU/gram of soil for *Yersinia pestis* and *Francisella tularensis* and 4000 CFU/gram of soil for *Bacillus anthracis*. Hence, the developed multiplex assay provides a robust detection platform for simultaneous detection of *B. anthracis, Y. pestis* and *F. tularensis* from environmental matrices.

Keywords: Real-time PCR; Multiplex; Spiking; Internal Control; Environment Matrix; Detection

AMDT-11 (Poster)

Uricase from *Bacillus drentensis*: Production, Characterization and Heterologous Expression for Uric Acid Diagnosis

Ishita Awasthi[1*], Neena Capalash[2] and Prince Sharma[1]
*ishitaawasthi00@gmail.com

[1]*Department of Microbiology, Panjab University, Chandigarh, India*
[2]*Department of Biotechnology, Panjab University, Chandigarh, India*

Abstract: Uricase (urate oxidase, EC 1.7.3.3) is a pivotal theranostic enzyme widely utilized for the detection of uric acid and for the effective treatment of hyperuricemia and gout. In this study, four uricase-producing bacterial species were isolated from diverse environmental niches viz. fish markets, poultry farms and hilly regions, with Bacillus drentensis identified as the most promising candidate. Uricase production was optimized statistically by Response Surface Methodology (RSM), resulting in a three-fold increase under the standardised

conditions: pH 9, 0.2% uric acid and 2% sucrose concentration. De novo whole genome sequence analysis gave insights into the structural and functional properties of the uricase gene, while operon prediction was conducted to understand the genetic regulation of uricase production. Additionally, T-cell and B-cell epitope predictions, along with antigenicity and allergenicity analysis, were performed to assess the potential of using uricase as a therapeutic agent. The catalytic site of uricase was cloned and expressed in E. coli BL21(DE3) pLysS, yielding a 34 kDa protein with validated enzymatic activity, demonstrated by the degradation of uric acid within 24 h. This study underscores the immense potential of indigenous recombinant uricase in the development of diagnostic kits for uric acid detection, also addressing the challenge of high costs involved in importing uricase.

Keywords: Uricase; Uric acid; Optimization; *Bacillus drentensis*; Enzyme activity; Catalytic site

AMDT-12 (Poster)

Comparison of Serological Test and Real Time PCR for Diagnosis of Human Brucellosis Suffering from Pyrexia of Unknown Origin

Renu Kumari[1], Raj Kumar Kalyan[1], Kamlesh Kumar Gupta[2] and Sanjeev Kumar Verma[3]
*krenu9108@gmail.com

[1]*Department of Microbiology, King George's Medical University, Lucknow, Uttar Pradesh, India*
[2]*Department of Medicine, King George's Medical University, Lucknow, Uttar Pradesh, India*
[3]*Department of Pediatrics, King George's Medical University, Lucknow, Uttar Pradesh, India*

Abstract: Background: Brucellosis is a neglected zoonotic disease; it affects both human as well as animal's health, and therefore, directly affects animal productivity and human efficiency.
Objectives: The present study was aimed to compare results of serological test and Real Time polymerase chain reaction (RT PCR) for diagnosis of brucellosis in patients suffering from of Pyrexia of Unknown Origin (PUO).
Material and Methods: Blood samples from 270 suspected cases of Pyrexia of unknown origin (PUO) were subjected to Real time PCR and ELISA IgM and ELISA IgG.
Results: Out of 270 suspected cases, the test wise prevalence was 11.11% by Real Time PCR, 11.48% by ELISA IgM and 1.85% by ELISA IgG. Among the RT-PCR (30) positive serum samples 20 was serologically positive for Brucella, and among RT PCR positive serum samples Brucella abortus was detected in 23 (76.67%) and the remaining 7 samples (23.33%) had Brucella melitensis DNA.
Conclusion: Our results indicate that RT-PCR can be considered a useful diagnostic tool in patients who have negative serologic test results, and in detection of Brucella species. However, ELISA could be used as a supplement and complement test along with Real Time PCR for identification and differentiation of human brucellosis.

Keywords: PUO- Pyrexia of unknown origin; RT PCR-Real Time polymerase chain reaction; ELISA IgM-Enzyme linked immunosorbent assay Immunoglobulin M; ELISA IgG-Enzyme linked immunosorbent assay Immunoglobulin G

AMDT-13 (Participate only)

Antemortem Diagnosis of Bovine Tuberculosis in Reactor Animals: A Comparative Study using Tuberculin Skin Test and Molecular Methods

Mohit Kumar[1,2], Joginder Singh Duhan[2], Vaishali[1], Babu Lal Jangir[3], Ramesh Kumar[1] and Naresh Jindal[1]*
*nareshjindal1@gmail.com

[1]*Department of Veterinary Public Health and Epidemiology, Lala Lajpat Rai University of Veterinary and Animal Sciences, Hisar, Haryana (125004), India*
[2]*Department of Biotechnology, Chaudhary Devi Lal University, Sirsa (125055), Haryana, India*
[3]*Department of Veterinary Pathology, Hisar, Haryana (125004), India*

Abstract: Bovine tuberculosis (bTB), caused primarily by *Mycobacterium bovis* a member of *Mycobacterium tuberculosis* complex (MTBC), is a chronic infectious disease affecting cattle and other mammals, posing significant challenges to public health and the livestock trade. MTBC members including *M. bovis, M.*

tuberculosis, M. orygis, M. caprae, etc. caused opportunistic infection in different domestic and wild animals. This study aimed to diagnose *Mycobacterium* infections in bTB reactor animals using a comparative approach between the tuberculin skin test (TST) and molecular methods. A total of 150 samples (nasal swabs, fecal, and blood) were collected from 50 reactor animals from various farms in Haryana, India, after tuberculin skin testing. The skin test results showed 74% of the animals were positive for the Single intradermal test (SIT), while 26% tested positive for the single intradermal comparative cervical test (SICCT). Samples were tested using conventional polymerase chain reaction (PCR) with 16S rDNA and IS1081 primer sets for detecting the *Mycobacterium genus* and *Mycobacterium tuberculosis* complex (MTBC), respectively. PCR results revealed that 31 nasal swabs were positive for *Mycobacterium* (16S rDNA), and 19 were positive for MTBC (IS1081). However, only three fecal and blood samples were positive for the *Mycobacterium genus*, and none for MTBC. Statistical analysis using Chi-square and Pearson correlation tests showed insignificant correlations between reactor status and PCR results. Overall, molecular methods provided a more sensitive diagnostic approach, complementing the conventional tuberculin skin tests. The integration of testing of nasal swab samples by PCR alongside skin tests using purified protein derivatives may be a promising approach for the comprehensive evaluation of bTB status in bovines, enhancing diagnostic accuracy and epidemiological understanding.

Keywords: Bovine tuberculosis, *Mycobacterium bovis, Mycobacterium tuberculosis* complex, Tuberculin skin test, Polymerase Chain Reaction (PCR)

AIMA-1 (Oral)

Artificial Intelligence-Driven Profiling of Human Gut Microbiota: Classifying Healthy and Dysbiosis States for Population-Specific Health Insights

Jyoti Kaurav[1*], Ravi Kumar Chaudhary[2] and Sanjay Kumar Sharma[1]
*jyotikaurav.gbu@gmail.com

[1]*ICT, Gautam Buddha University, Greater Noida, Uttar Pradesh, India*
[2]*Department of Research & Development, Government Institute of Medical Sciences, Greater Noida, Uttar Pradesh, India*

Abstract: The human gut microbiome, a diverse ecosystem of bacteria, fungi, archaea, metazoa, and viruses within the gastrointestinal tract, plays a critical role in maintaining human health and has been linked to various psychological and physiological conditions. Dysbiosis, or imbalance in the gut microbiota, is increasingly recognized as a contributor to numerous diseases and disorders.
This study aims to analyze human gut microbiome data from both global and national (Indian) databases, with a focus on identifying population-specific microbial traits. By comparing the Indian microbiome to global datasets, we aim to uncover unique microbial patterns and their potential health implications. Such insights can pave the way for tailored health interventions and more effective disease diagnostics in the Indian context.
Our methodology involves pooling data from comprehensive microbiome repositories such as MG-RAST, HMP, EBI Metagenomics, and HMGA. AI and machine learning (ML) algorithms, including PERMANOVA and Random Forest classifiers, are employed to detect significant differences in microbial composition and functionality. Data preprocessing and mining techniques are utilized to ensure consistency and reliability across diverse datasets. The analysis is further enriched using bioinformatics tools like QIIME and MetaPhlAn, facilitating in-depth interpretation of microbial diversity and its relationship to health and disease.
The primary goal of this study is to define the microbial signatures associated with both healthy and dysbiosis states of the gut. By doing so, we hope to contribute to global microbiome research and drive improvements in population-specific healthcare strategies in India. Identifying shared microbiome patterns linked to diseases will also enhance our understanding of what constitutes a "healthy" or "unhealthy" gut microbiome, enabling timely diagnosis and treatment of gut-related diseases.

Keywords: Gut microbiome, Dysbiosis, AI, Machine learning, Indian population, Bioinformatics, Microbial diversity, Personalized health.

AIMA-2 (Poster)

Optimizing Health Monitoring Systems through Advanced Sensor Network Design and Analysis

Heena Mehta* and Mukesh Singla
*heena111mehta@gmail.com

[#] *Department of Computer Science and Engineering, Baba Mastnath University, Haryana, India*

Abstract: This article describes the creation and assessment of a new health monitoring system using sensor networks that gathers vast, real-time data on the condition of a patient. The system's goal is to deliberately position sensors on or around the user's body to monitor vital health data constantly. The study begins with establishing objectives and requirements, then proceeds to specifically address the selection and placing of sensors, architectural design for the sensor network, and lastly, data collection algorithm implementation. The obtained health data is gathered by a centralized monitoring system, which also processes and analyzes it in real-time. Our study mostly focuses on safeguarding the integrity and privacy of private information. User-friendly interfaces developed for both healthcare professionals and end consumers help to make data interpretation more efficient. Before implementation, the system is thoroughly tested and validated to guarantee its reliability in real-world healthcare environments; it also receives continuous monitoring and enhancements. This work advances customized health monitoring by offering a practical and extendable approach for continuous parameter tracking of health via the integration of sensor networks. Systems of health monitoring are gathering increasing popularity. Although a lot of research have concentrated on health monitoring, their subjects have only been limited. Accuracy and performance of data categorization should be improved. We investigate in this work a health monitoring system based on sensor networks. This paper reviews current studies on health monitoring systems including their approaches and constraints.

Keywords: Health Monitoring System; IoT Environment; Security; Sensor network

AIMA-3 (Poster)

AI-Mediated Designing of an Antimicrobial Peptide and its Expression as AMP-Nuclease Fusion Protein against MDR Pathogens

Anushree Patra[1], Neena Capalash[2] and Prince Sharma[1*]
*princess@pu.ac.in

[1]*Department of Microbiology, Panjab University, Chandigarh, India*
[2]*Department of Biotechnology, Panjab University, Chandigarh, India*

Abstract: Multidrug-resistant bacterial pathogens are posing fatal threats in both healthcare and community settings due to their ability to cause severe infections and form resilient biofilms, which complicate treatment and foster antibiotic resistance. Addressing this challenge requires novel antimicrobial strategies. Various approaches, including new antibiotics, antimicrobial peptides (AMPs), vaccines, enzymatic treatments are being explored. Enzymes, notably nucleases, have proven effective in disrupting biofilms by targeting extracellular DNA (eDNA). In this study, using machine learning, a novel 15-amino-acid peptide with promising antimicrobial, non-allergenic and non-hemolytic properties was designed. We engineered a fusion protein (AI-AMP: ΔNucAb34) by fusing this novel AMP with a truncated version of outer membrane nuclease (NucAb89) of *A. baumannii*, a conserved protein across multidrug-resistant strains that has emerged as a promising candidate for therapeutic applications. This chimeric protein was designed to perform dual functions: degrading biofilms through the nuclease activity while also killing the released bacteria by AMP. This fusion protein was cloned and expressed in *E. coli*-pET28a host-vector system and its DNA degrading and antimicrobial activities were examined against multidrug-resistant pathogens. This approach, which integrates advanced AI techniques with enzyme engineering, represents a promising strategy for combating biofilm-associated infections and improving treatment outcomes.

Keywords: Artificial intelligence; Multidrug-resistant bacteria; Machine learning; Antimicrobial peptides; Biofilms; Nuclease

AIMA-4 (Poster)

AI-Driven Discovery and Characterization of Polyethylene Terephthalate (PET)-Degrading Cutinase Homologs from Metagenomic Datasets

Shubham Kumar and Barkha Singhal*
*barkha@gbu.ac.in

School of Biotechnology, Gautam Buddha University, Greater Noida, Uttar Pradesh (201312), India

Abstract: Plastic pollution has become a global environmental crisis, with polyethylene terephthalate (PET) being one of the most prevalent pollutants due to its extensive use, durability, and non-biodegradable nature. Current estimates suggest that by 2025, global plastic waste generation will reach 220 million tons, with India contributing over 10,000 kilotons. PET, a widely utilized plastic due to its mechanical strength, low cost, and impermeability, poses a significant threat to ecosystems, accumulating in the environment and impacting biodiversity. We employed a bioinformatic approach to identify novel PET-degrading enzymes to address this challenge. Using a probability model built with artificial intelligence algorithms, including Hidden Markov Model (HMM), we screened metagenomic databases for homologous sequences of previously characterized cutinases, known for their PET-degrading capabilities. From an initial pool of the top 100 significant homologs, and further 23 enzymes were short listed on the basis of presence of PET degrading domains like dienelactone hydrolase (DLH) domain. Physicochemical properties of these enzymes were analyzed by Protparam. Numbers of amino acids were observed in range of 237 – 454 residues, instability index has been found between 21.58 to 50.25 and 13 enzymes have been found to have instability less than 40 which ensure their stability, aliphatic index has been observed between 60.77 to 83.66, 20 out of 23 enzymes were found to be hydrophilic in nature with negative GRAVY index. 4 most appropriate proteins with suitable physicochemical properties have been selected for 3D model prediction. These models have been verified on SAVEs server. We named these enzymes PETase1, PETase2, PETase3 and PETase4. Their interactions with PET substrates were evaluated through molecular docking simulations, providing insights into potential degradation mechanisms. This study highlights the utility of AI-driven bioinformatic tools in discovering novel biocatalysts for PET degradation. It contributes to the ongoing efforts to mitigate plastic pollution through biodegradation.

Keywords: Polyethylene terephthalate; PETase; Cutinase, Plastic, Biodegradation, Artificial intelligence

ENVM-1 (Oral)

Persistent Organic Pollutants in the Environment: Insights into Impact and Sustainable Remediation Strategies

Sonam Paliya
sonampaliya140@gmail.com

Institute for Organic Biogeochemistry in Geo-Systems, RWTH Aachen University, Germany

Abstract: Persistent Organic Pollutants (POPs) are a class of toxic chemicals that persist in the environment, bio accumulate in living organisms, and pose significant risks to human health and ecosystems. Their widespread distribution, long-range transport, and resistance to degradation have made them a global concern. This talk delves into the environmental behaviour of POPs, emphasizing their sources, pathways, and the multifaceted impacts they exert on natural systems. Drawing on recent advancements, we will discuss the intricate mechanisms through which these pollutants interact with abiotic and biotic components, causing long-term ecological disruption.

In light of the urgency to mitigate POP contamination, this talk also provides a comprehensive overview of current and emerging remediation strategies. These include chemical, physical, and biological approaches, with a particular focus on sustainable techniques such as bioremediation. We will discuss the efficacy, feasibility, and scalability of these solutions, highlighting innovative methods that minimize secondary pollution and energy consumption.

By integrating scientific insights with practical applications, this talk aims to inform about the path forward in addressing the persistent threat posed by POPs, ultimately fostering a more resilient and sustainable environmental management framework.

Keywords: Persistent Organic Pollutants, Emerging Contaminants, Toxicity, Sustainable, Remediation

ENVM-2 (Oral)

Utilization of sugarcane bagasse and poultry manure for compost preparation

Monika Kayasth*, Shikha Mehta and Jagdish Parshad
*monakayasth@gmail.com

[1] *Department of Microbiology, College of Basic Sciences and Humanities, Chaudhary Charan Singh Haryana Agricultural University, Hisar-125004, Haryana, India*

Abstract: Sugarcane Bagasse (B) is the fibrous waste produced in the sugarcane juice extraction process. It constitutes varying concentration of cellulose, hemicellulose and lignin. Disposal of sugarcane bagasse by dumping is unattractive process because of large requirement of land and pollution concerns. Composting is the good method of converting organic wastes into environmentally friendly products**.** Among the composting microorganisms, bacteria, actinomycetes and fungi constitute the major active groups. In the present work, sugarcane bagasse was subjected to composting for its conversion in to beneficial manure. Co-composting alongwith poultry manure and cattle dung helped to improve physico-chemical characteristics. As the decomposition progressed the carbon content of the compostable materials decreased with the time period and nitrogen content increased in all treatments. This resulted in a decline in C/N ratio during composting. However, after 45 days of composting, the maximum reduction (26.2%) in C/N ratio was observed in treatment T5 having sugarcane bagasse supplemented with poultry waste (15:1) and cattle dung (10%). The phosphorus content and potassium content increased in all treatments at different days of composting and maximum content was observed in treatment T5 i.e. 1.43% and 1.79%, respectively after 45 days of composting. Dehydrogenase activity was also found to be maximum (57.84 µgTPF/g soil/24h) in the same treatment. Thus, composting could be introduced as an efficient technology to convert bagasse into nutrient rich manure.

Keywords: Sugarcane bagasse, Poultry manure, Dehydrogenase activity, Composting

ENVM-3 (Oral)

Development of a Clean Bioprocess to Achieve High Microalgal Biomass Density Coupled with Facilitated Self-flocculation by Utilizing Bicarbonate as a Source of Dissolved Carbondioxide

Anirban Das Gupta
anirban.dasgupta@tnu.in

Department of Biotechnology, The Neotia University, West Bengal, India

Abstract: Microalgae feedstock-based bioprocesses are increasingly emerging as promising technologies towards achieving some of the major sustainable development goals (SDG17), mostly pertaining to clean energy and environment. The current technologies largely involve sparging flue-gas carbon dioxide (CO_2) directly into closed or open photobioreactors and thus suffer from very limited bioavailability of sparingly soluble CO_2 in dissolved form which leads to limited biomass production. Therefore, the present study has been designed to assess the ability of Chlorella vulgaris, a model microalga, to capture carbon from a dissolved inorganic carbon (DIC) source namely sodium bicarbonate ($NaHCO_3$) and grow within closed photobioreactors to high biomass density. With the aim to develop a proof of this concept, Chlorella vulgaris was grown in minimal medium supplemented with varying doses of initial bicarbonate (50–250 mM). The results demonstrated that with increasing initial bicarbonate (HCO3-) concentration, CO_2 fixation rate and algal biomass productivity were enhanced. At 150 mM initial HCO_3-, biomass concentration and CO_2 fixation rate were increased by about 145% and 38%, respectively, as compared to minimal medium. Biomass concentration was further improved by implementing a smart intermittent bicarbonate feeding strategy, which resulted in an overall enhancement by about 255%, as opposed to minimal medium. It was interesting to observe that Chlorella vulgaris facilitated its own harvesting by self-flocculation-cum-settling mechanism within a short period of time in presence of HCO_3-. The efficiency of self-flocculation was found to increase by about 55% in presence of 150 mM initial HCO_3-, when compared with minimal medium. High resolution microscopic analyses revealed that microalgal cells were embedded within a self-produced matrix of extracellular polymeric substances (EPS) and underwent

alterations in topological complexity that may have facilitated nutrient uptake and gaseous exchange across the cell surface, thereby resulting in enhanced biomass production and self-settling. Therefore, strategic utilization of bicarbonate as a source of DIC convincingly establishes the novelty of our rational approach towards enhancing microalgal biomass coupled with efficient CO_2 fixation and self-harvesting. This innovative and smart process may be scaled up and translated to efficiently sequester flue-gas CO_2 released by thermal power plants and other fossil fuel-based industries through algal cultivation.

Keywords: Bicarbonate utilization; CO_2 capture; Smart intermittent feeding; Self-harvesting

ENVM-4 (Oral)

Environmental Stressors and the Dynamics of Diatom Species Resilience

Gayatri Dave
gayatridave.bt@charusat.ac.in

P D Patel Institute of Applied Sciences, CHARUSAT, Anand, Gujarat, India

Abstract: Diatoms, unicellular photosynthetic microalgae account for 40% of global carbon sequestration. They are sensitive to environmental perturbations making them ideal bioindicators of aquatic ecosystems. Anthropogenic activates often surges nutrients in aquatic bodies. Further, the onshore accidents results in oil-spills. Usually, only the large oil-spills gains attentions of environment cleaning agencies, whereas micro oil-spills are remained unnoticed. This micro- oil spills may adversely impact the growth of phytoplankton. The present study aims to evaluate the resilience of marine diatom species under such crude oil stress. For laboratory simulation, the six membered diatom consortia were exposed to varied crude oil concentration (500, 750, 1000 ppm), nitrate and phosphate stress over 30 days. A decline in cell growth and chlorophyll levels was observed with rapid lipid formation. Out of six, three species; *Chaetoceros gracilis, Surirella librile* and *Halamphora coffeaeformis* survived at 750 ppm, while no species thrived at 1000 ppm crude oil stress. Lipid droplets (LD) developed in *S.librile, C.gracilis, H.coffeae formis* and *Navicula rostellata*. Recognizing these species as either tolerant or sensitive could make them valuable bioindicators or useful for ecological restoration in areas affected by crude oil contamination.

Keywords: Diatoms; Anthropogenic activities; Micro oil-spills; Nitrate-Phosphate stress; Lipid droplets; Ecological restoration

ENVM-5 (Oral)

An Innovative Device and Technique for Analyzing Bacterial Chemotaxis towards Chemoattractants

Sheetal Pardeshi[1,2] and **Prafulla Shede[2*]**
*pns.agc@mespune.in
ORCID ID: 0000-0001-9557-6632; ORCID ID: 0000-0002-0835-0246

[1]*Department of Microbiology, PES Modern College of Arts, Science and Commerce (Autonomous), Shivajinagar, Pune, Maharashtra (411005), India*
[2]*Department of Microbiology, MES Abasaheb Garware College (Autonomous), Karve Road, Pune, Maharashtra (411004), India*

Abstract: Capillary assemblies and microfluidic devices commonly used for bacterial chemotaxis assays have some limitations, presenting opportunities for further innovation. This study introduces a new, cost-effective device called the chemotaxis plate, along with a method for conducting chemotaxis assays with it. The device was validated using two bacterial strains, Pseudomonas putida MCC 2989 and Bacillus subtilis MCC 2049, which are chemotactic to L-aspartate. Results showed that 100 to 1000 times more cells were recovered in the presence of the chemoattractant compared to the control ($p<0.05$). The novel assay achieved 100% sensitivity and 99.21% specificity for detecting chemotaxis of *Pseudomonas putida* MCC 2989 towards 3mM L-aspartate

within 50 minutes. Additionally, the device was used to isolate bacteria that are chemotactic to caffeine directly from environmental samples. The optimized process yielded notably high chemotaxis response indices being reported for the first time.

Keywords: Chemotaxis; *Pseudomonas Putida; Bacillus Subtilis*, L-Aspartate, Caffeine, Chemoattractant

ENVM-6 (Oral)

Bioprospecting of Lignocellulolytic Microorganisms and their Enzymes for Valorization of Waste Biomass

Namrata Joshi, Kumar Pranaw, Łukasz Drewniak
n.joshi@uw.edu.pl

Department of Environmental Microbiology and Biotechnology, Institute of Microbiology, Faculty of Biology, University of Warsaw, Poland

Abstract: The present study addresses the challenges of lignocellulosic biomass (LCB) conversion by optimizing fungal strains for enhanced enzymatic hydrolysis. Two potent fungal strains, Aspergillus fumigatus ZS_AF and Penicillium fuscoglaucum JAM-1, were meticulously isolated and optimized for producing hydrolytic enzymes crucial for LCB valorization. Through optimization, ZS_AF achieved a two-fold increase in enzyme production using pine sawdust (PSD), with significant yields of CMCase, xylanase, β-glucosidase, and FPase. Similarly, JAM-1 demonstrated superior enzyme activity with rapeseed cake (RSC) over PSD. Secretome profiling of both fungi highlighted the critical role of carbohydrate-active enzymes (CAZymes) and auxiliary enzymes in biomass degradation, with 77% of ZS_AF's secretome comprising CAZymes, predominantly glycoside hydrolases (66%). JAM-1's secretome, enriched with 153 CAZymes when grown on RSC, underscored their significance in effective biomass saccharification.

To further address LCB recalcitrance, three lytic polysaccharide monooxygenase (LPMO) genes from Cellulosimicrobium cellulans were heterologously expressed, resulting in thermostable enzymes that significantly boosted reducing sugar yields when combined with commercial cellulase. The study also explored enzyme immobilization on Faujasite Na-X zeolite, achieving a 73% immobilization efficiency, enhanced enzyme stability, and reusability. Structural analyses confirmed the catalytic efficiency of immobilized enzymes in valorizing lignocellulosic waste.

Additionally, applying a fungal consortium comprising ZS_AF, JAM-1, and Trichoderma deliquescens in composting waste biomass and sewage sludge demonstrated improved compost quality, reduced moisture content, and enhanced organic matter mineralization. In conclusion, this research illustrates the potential of optimized fungal strains and enzyme engineering in overcoming LCB recalcitrance, offering sustainable and efficient solutions for biorefinery processes and the composting of lignocellulosic waste, thereby contributing to environmental sustainability.

Keywords: Lignocellulolytic microorganisms; Carbohydrate-active enzymes; Enzymatic hydrolysis; Immobilization; Cellulase; Composting

ENVM-7 (Oral)

Biotreatment of Extreme Ecological Niche by Diversified Native Microbial Consortia

Ragini Gothalwal
ragini_gothalwal@yahoo.com

Department of Biotechnology, Barkatullah University, Bhopal, India

Abstract: As the global population grows, so do the demands for water for drinking, sanitation, farming and energy production among many other uses. At the same time human activity and climate change are disrupting natural water cycles putting freshwater ecosystems under pressure. Pollution, infrastructure development and reserve extraction pose additional challenges (Davidsen, 2014). In India, lot of idols are worshiped with all rituals at different time in a year. Afterwards, these are immersed into the water bodies. The material used for making idols has led to the use of non-biodegradable materials like POP, plastic, thermacol synthetic colour,

synthetic fiber etc. which deteriorates the water quality (Kishor et. al., 2014). Moreover, the chemical dyes used to paint these idols contains potentially hazardous heavy metals.

The current agricultural practices are heavily dependent on the application of synthetic fertilizers and pesticides. Intensive tillage and over-irrigation have helped to meet the food requirement of the people. Despite that increased environmental and health problem, which includes deterioration of soil fertility, executive use of pesticides and also increased cost of agricultural production (Vanessa et. al. 2009). These soils are unproductive, impermeable and hard due to the presence of undesirable pollutants on the soil surface called extreme soil. Pesticide-contaminated soil has high pH and high electrical conductivity and is deficient in organic carbon, Na, K, and P. Nostoc 00246 strain is very useful in agricultural applications because of their N2 fixation activity, extracellular polysaccharides, photosynthesis system and particularly desiccation tolerance ability and their property to improve the quality of nutrient-poor soils. Cynoformulation can enhance the N2, phosphors and potassium content in soil and play a very important role in plant metabolism such as cell division, growth and development, breakdown of sugar and nutrient transport within the plants.

Quorum sensing bacteria produces and releases chemical signal modules termed auto inducer whose external concentration increases as a function of cell density. Quorum sensing thus enable bacteria to coordinate and respond quickly to environmental changes, such as the availability of nutrients, other microbes or toxins in the environment. The mix consortium of Micrococus sp. GS2-22, Corynebacterium sp. GS5-66, Flavobacterium sp. DS5-73, Bacillius sp. DS6-86 and Pseudonomonas sp. degraded maximum 78% of BH crude oil of 1% crude oil concentration at 33^0C and pH 7.5 (Rahman et. al. 2002). On the comparative study on the biodegradation of 2,6-dichlolorophenol indophenol of bacterium consortium and individual bacteria, the consortium showed the fastest utilization of 2,6-dichlolorophenol than the individual isolate (Varjani and Upasani, 2013). The study involves biodegradation of benzene, diesel, hexane, petrol, toluene and xylene. This approach could be a milestone between labs and field trial as a bioremediation technology in term of biofilm and biosplling in future.

Most contaminated sites are generally contaminated with multiple pollutants rather than a single type and harbour a variety of different environmental conditions for biological activity. Therefore, bioremediation using a single type of microorganism results in failure due to low biodegradability, adaptively and viability of the applied microorganism in a contaminated site with diverse environmental conditions. However, these limitations can be easily overcome by the application of a native microbial consortium containing multiple species with diverse biodegradation abilities for different types of pollutants. A native consortium was tried which can serve as a promising candidate for remediation of plastic and heavy metal degradation as well as dye decolorisation as no microorganism has been reported that can bioremediate all these together. The major advantage is low cost, low technology technique which generally has a high public acceptance and can often be operated on site.

Keywords: Non-Biodegradable materials; Chemical dyes; Corynebacterium; Bioremediation technology

ENVM-8 (Oral)

Revitalizing Contaminated Soils: Harnessing Fly Ashes to Enhance Soil Microbiota and Ecosystem Health

Łukasz Drewniak*, Szymon Rzuczkowski, Monika Dang, Dawid Gmitter and Mikołaj Iwan
* l.drewniak2@uw.edu.pl

Department of Environmental Microbiology and Biotechnology, Institute of Microbiology, Faculty of Biology, University of Warsaw, ul. Miecznikowa 1, 02-096 Warsaw, Poland

Abstract: Coal fly ash (CFA), a byproduct of coal combustion, constitutes 65–95% of the total waste generated during coal-fired power production. With an annual global output of approximately 800 million tons, CFA is predominantly produced in China (500 million tons), India (140 million tons), and the United States and European Union combined (115 million tons). While around a quarter of this global production finds economic applications in industries such as metallurgy, construction, and agriculture, the remainder is typically stored long-term in industrial heaps or landfills. One significant barrier to the broader industrial utilization of CFA is its residual unburned carbon content, often in the form of polycyclic aromatic hydrocarbons (PAHs) like naphthalene, fluoranthene, anthracene, and phenanthrene. These PAHs contribute to the toxicity of CFA, with established carcinogenic and toxic effects on living organisms. In addition to organic contaminants, stored CFA also contains heavy metals (Pb, As, Hg, Cd, Se, Cu, Cr, Ni) and valuable rare earth elements (REEs) such as Nd, Y, La, and Gd. The unique composition and alkaline nature of CFA suggest its potential as a soil amendment for the reclamation of agricultural and industrial lands.

This presentation will explore the potential benefits, limitations, and risks associated with the use of CFA in soil improvement. Key topics include the impact of CFA on soil structure, permeability, and aeration, particularly in heavy soils such as clay. Additionally, the enrichment of soil with essential trace elements and the regulation of soil pH through the alkaline properties of CFA will be discussed. The presentation will also address the implications of CFA application on soil microbiota structure and activity, and the broader consequences for soil ecosystem functioning.

This research was financed in full by the National Science Centre under the OPUS grant no. 2022/45/B/NZ9/02018 entitled Fly ash management - microbiological degradation of unburned coal.

Keywords: Coal fly ash**;** Polycyclic Aromatic Hydrocarbons; Heavy metals; Valuable rare earth elements

ENVM-9 (Oral)

Chitinolytic Potential of Gut Flora of Amphibians for Sustainable Development

Siddhesh Gaikwad and **R.S. Pandit***
*panditrao499@gmail.com

Savitribai Phule Pune University, Pune (411007), Maharashtra, India

Abstract: Amphibians and reptiles, known for their diverse and widespread presence, primarily feed on insects and small invertebrates, making chitin a significant component of their diet. While extracellular chitin digestion by gut microflora has been observed in mammals, this study focuses on identifying and characterizing chitinolytic bacteria from the gut of M. sahyadrensis and Hemidactylus varadgiri. The total viable count (TVC) of hindgut microflora of M. sahyadrensis and H. varadgiri were determined to be 137×10-5 CFU/g and 60.9 × 10-4 CFU/g respectively. Six chitinase-producing strains were isolated from M. sahyadrensis gut, while nine were isolated from H. varadgiri. Both primary and secondary screenings identified strains SS1 and NP5 as the most efficient isolates, showing high enzyme activities and a favorable CZ/CS ratio. These isolates exhibited cellulase and lipase production, with optimal growth conditions at 45°C, pH 6, and 0% NaCl concentration. Molecular characterization revealed SS1 and NP5 to be closely related to Enterobacter cloacae 'Hoffmann cluster IV and Paenanthrobacter ureafaciens, with 94.75% and 98.744% similarity, respectively. Notably, NP5 showed resistance to Erythromycin. Among the tested substrates, SS1 and NP5 exhibited the highest chitinase activities on crab chitin (CC). SS1 demonstrated 17% degradation of chitin flakes and 53% of fish scales, while NP5 degraded 75% of prawn shells and 14% of chitin flakes. These findings suggest the potential role of extracellular bacterial chitinases in the digestion of chitin-containing foods, possibly influencing the evolution of the digestive systems of amphibians and reptiles. Moreover, the study highlights the chitin degradation capabilities of bacteria sourced from unique environments such as the gut of insectivorous animals. These bacteria hold promise for various applications including N-acetyl D-glucosamine production, bioethanol production, single-cell protein production, and insect pest management.

Keywords: Chitinolytic bacteria; *M. sahyadrensis; Hemidactylus varadgiri;* Amphibians; Reptiles

ENVM-10 (Oral)

Microplastics in Wastewater and Sludge from Wastewater Treatment Plants: Identification and Biodegradation

Heena Bisht, K. Nantha Kumar, C Paul Jeyaseelan and Banwari Lal
heena.bisht_c@teri.res.in

Environmental and Industrial Biotechnology Division,
The Energy and Resources Institute (TERI), New Delhi (110003), India

Abstract: Microplastics (MPs) contamination has become a significant environmental concern in recent years, endangering both aquatic wildlife and humans. MPs are plastic particles smaller than 5 mm in size that have been categorized as emerging water pollutants because of their biological toxicity, bioaccumulation, and

biomagnification potential. MPs' toxicity is mostly determined by the cumulative effects of MPs, additives, and toxicants adsorbed on their surfaces. Major sources of MPs into nearby freshwater and soil habitats have been identified as partially treated or untreated industrial effluents and sewage discharges from wastewater treatment plants (WWTP). Our main objective is to study the occurrence and type of MPs in the wastewater and sludge from WWTP, as well as their biodegradation in different full scale anaerobic digesters (AD). In our study, we have collected wastewater and sludge samples from Keshopur STP, New Delhi, whose effluents often flow into Yamuna after treatment. The collected MPs were dried, digested with wet peroxide oxidation, separated, and evaluated based on their morphotype, size, color, and polymer type. It was observed that the dominant MPs were blue, red, and green in fibers, films, and pellets forms when observed under a microscope. Raman spectroscopy was utilized to determine the chemical composition of MPs, and it was found that the majority of them were Polyethylene Terephthalate (PET), High-density Polyethylene (HDPE), Polypropylene (PP), and Low-density polyethylene (LDPE). Our future research will focus on biodegradation of MPs using various full-scale anaerobic digesters, as there has been little research on this topic thus far.

Keywords: Microplastics; Pollutants; Wastewater treatment plant

ENVM-11 (Oral)

Profiling of Soil Microbial Communities Based on Substrate Utilization under Varied Salt Loads

Madhu Choudhary[*1], Hanuman S Jat[1,2], Rakesh Kumar[3], Hardev Jat[3], Avni, Sanjay Arora[4] and RK Yadav[1]
*madhucssri@gmail.com

[1]*ICAR- Central Soil Salinity Research Institute, Karnal (132 001), Haryana*
[2] *ICAR-Indian Institute of Maize Research, Ludhiana (141 004), Punjab*
[3]*ICAR-National Dairy Research Institute, Karnal (132001), India*
[4]*ICAR-CSSRI Regional Research Station, Lucknow (226002), India*

Abstract: Limited information is available on changes in microbial activities and their functional diversity under different types of salt affected soils. A micro plot study with - highly saline, moderately saline, highly sodic, moderately sodic and normal soils was conducted to evaluate the impact of salt type and load on soil physical, chemical and biological properties. Higher pHs, CEC, and ESP were observed in sodic soils (10.04, 10.19 cmol kg^{-1}, and 76.15) while higher EC_e was found saline soils (13.53 ds m^{-1}). Significantly higher concentration of Na^+, Ca^{2+} and Mg^{2+} was observed under highly saline soils (151.71 me L^{-1}, 11 me L^{-1} and 47.83 me L^{-1}) whereas the concentration of CO_3^{2-} and HCO_3^- found significantly higher under highly sodic soils (2.17 me L^{-1} and 11.28 me L^{-1}). Presence of high concentration of anions and cations influences microbial community composition as evident from the study of Community level physiological profiling by substrate utilization pattern. Average well color development (AWCD) was increased with incubation period. Highest AWCD was observed with normal soils followed by moderately saline and moderately sodic soils and lowest was found in highly sodic soils. The utilization of amino acids, amines, carboxylic acids, phenolic compounds and polymers was highest for normal soils followed by moderately saline and lowest was recorded for highly sodic soils. The carbohydrate utilization pattern was highest in highly saline soils, followed by highly sodic soils and lowest was for moderately sodic soils. The diversity index H was found highest (3.19) in normal soils followed by moderately saline (2.82), moderately sodic (2.67), highly saline (2.49) and lowest in highly sodic soils (1.57). Enzymatic activities and microbial populations were found to decrease with increasing salt load. The study suggested that poor soil physico-chemical and biological conditions are correlated with salt load therefore studies on the soil physicochemical and biological properties must be carried out before recommending any land use, reclamation strategies or nutrient management practices.

Keywords: Substrate utilization; Well colour development; Enzyme activities; Salt affected soils; Sodic soils; Saline soils

ENVM-12 (Oral)

Algal Biofilter Consortium in Recirculating Saltwater Aquaponic Systems with Marine Shrimps and Seaweeds

S. Rajakumar
kodairaj@gmail.com

Department of Marine Biotechnology, Bharathidasan University, Tiruchirappalli, Tamil Nadu, India

Abstract: A study was organized to improve the nutritional value of the *Penaeus vannamei* (White legged shrimp) with *Gracillaria* (Marine seaweed) in the saltwater aquaponics system. The *Penaeus vannamei* and *Gracillaria* were optimized to the experimental condition and the Aquaponics system was designed with a 200L capacity FRP tank for *Penaeus vannamei* as well as a culture tank for *Gracillaria* along with a filtration system containing bio-filter and mechanical filter. The system was initiated with 120 nos. of *Penaeus vannamei* and 200 g of *Gracillaria* in two different tanks. The *Penaeus vannamei* growth and its nutritional value total protein, total carbohydrate, and lipids were improved in the aquaponics system compared to the control system and also the survival rate of the *Penaeus vannamei* was 83% in the aquaponics system during the study period at its optimal temperature of 28 ^{0}C to 32 ^{0}C. along with the improved growth and nutritional and biochemical parameters in shrimps and seaweeds, the biofilter consortium seems to be dominated by salt-tolerant algal nitrogen fixers. On the oyster shell substratum, the rapid development of the algal community was observed, which in turn helped to maintain the dissolved oxygen (DO) and nitrate concentration better than the control. This helped the overall water quality parameters and the development of shrimps and seaweeds in combined systems.

Keywords: *Penaeus vannamei*, Dissolved Oxygen (DO); Gracillaria**;** Biofilter

ENVM-13 (Poster)

Plastic Eating Microbes: A Review of Achievable Catalysts for Alleviating Garbage

Natasha Charaya
natashacharaya@gmail.com

Department of Biotechnology, Guru Jambheshwar University of Science & Technology, Hisar, Haryana (125001), India

Abstract: The usability of synthetic plastics is an essential component of the international economy in the twenty-first century. The prolongation and consumption of non-recyclable petroleum-based plastics, such as polyvinyl chloride, polypropylene, and polyethylene terephthalate, has risen eighty percent globally in the last 50 years since its creation. Plastic has been recognized as a tenacious polymer, meaning that it is a cheap, flexible, and anticorrosion material. Long-term retention of these plastics has been shown to pose several risks to human well-being and the surroundings. Many people throughout the world are concerned about the distribution of these resistant plastics in crops, liquids, and soil. Their effect on the marine environment is even more detrimental because they can encompass or obstruct the intestines of aquatic beings. In addition, it has been discovered that plastics, particularly microplastics, disrupt chemical connections among marine organisms, induce innate toxicity through contamination, and soak up infectious agents and relentless biological pollutants. While non-recyclable petroleum-based plastics are immune to degradation by carrying hazardous additives, traditional petrochemical plastics break down via abiotic agents. Consequently, it is necessary to look for a viable remedy that might aid in the biological degradation of artificial polymers. Because advanced recycling operations only cover about 10% of petrochemical plastic waste, the degradation process of non-biodegradable plastics, therefore, depends on the development of new ways, which include microbes such as Ideonella sakaiensis 201-F6, Phormidium, Lewinella, Bacillus megaterium, Rhodococcusruber, Serratiamarcescens, Enterobacteraeburiae YT1, and Bacillus sp. YP1. This review's main goal is to highlight the origin, technique, and enzymes of the different microbes that can break down plastics made from petrochemicals concluded from the literature review. Utilizing advantageous microbes with the capacity to break down plastic may be a viable

and efficient solution to all of the issues raised while leaving a vast scope to research further about the possible application of the advantageous microbes.

Keywords: Plastic-eating microbes, Petrochemical plastics, *Ideonella sakaiensis*, Bioremediation, Degrading enzymes, Polyethylene terephthalate

ENVM-14 (Poster)

Isolation and Screening of Bacterial Isolates for Pesticide Degradation at Varying Concentrations

Poonam Ranga[1,2*], Baljeet Singh Saharan[2] and Sunaina Kumari[2]
rangamicro@yahoo.co.in

[a] *Department of Biotechnology, Deenbandhu Chhotu Ram University of Science & Technology Murthal, Sonepat, Haryana (131039), India*
[b] *Department of Microbiology, College of Basic Sciences & Humanities, Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana (125004), India*

Abstract: The extensive use of pesticides in agriculture has led to significant environmental contamination, posing risks to ecosystems and human health. Bacterial degradation of pesticides offers a promising solution to mitigate these adverse effects without posing any ill effect on environment in return by producing toxic byproducts. In this study, we isolated and screened bacterial colonies having potential to tolerate various classes of pesticides, including organophosphates, carbamates, and chlorinated hydrocarbons. Bacteria employ specific enzymes, such as hydrolases, oxidoreductases, and lyases, to break down complex pesticide molecules into less toxic or non-toxic compounds. The efficiency of bacterial degradation is influenced by factors such as the presence of co-metabolites, environmental conditions and the genetic adaptability of bacterial strains. Advances in biotechnological approaches, including genetic engineering and the use of microbial consortia, have further enhanced the tolerance and degradation capabilities of bacteria. This research underscores the potential of bacterial bioremediation as an eco-friendly and cost-effective strategy for managing pesticide pollution by taking Cartap Hydrochlorite as major one, thereby contributing to sustainable agricultural practices and environmental conservation.

Keywords: Bacteria, Pesticides, Cartap hydrochlorite, Insectisides, Bioremediation

ENVM-15 (Poster)

Microbial Diversity and their Functional Role in Himalayan High Altitude Hill Stream's Sediments

Laxmi, Rishikesh K*, Sharma Nitika**, Singh, Dileep K Sehgal and Neeta
*rishikesh@zoology.du.ac.in, **sharma1996nitika@gmail.com

Department of Zoology, University of Delhi, Delhi (110007), India

Abstract: Microbes play a significant role in the functioning and balancing of aquatic ecosystem. Sediment microbiota is highly sensitive and rapidly respond to environmental changes, serving as key drivers of material and energy flow in aquatic systems, yet they have received relatively little attention. These responses can be triggered by fluctuations in water temperature, organic matter concentration, land use patterns, and other hydrological dynamics. The microbial diversity of the sediment also indicate the overall health of aquatic ecosystem. This study focuses on the bacterial diversity and functional profiles of sediment samples collected from six sites (S1–S6) along the Pranmati stream, using the Illumina sequencing platform. The sampling sites were selected based on altitude and landscape characteristics. Proteobacteria was the dominant phylum across all sites, followed by Firmicutes and Actinobacteria. At the genus level, *Pseudomonas* (S1, S3), *Exiguobacterium* (S2), *Sphingomonas* (S4), *Microcoleus PCC-7113* (S5), and *Thermomonas* (S6) were the most prominent. Alpha-diversity indices revealed that sites S4 and S5 exhibited the highest species richness and diversity. Beta-diversity analysis indicated a close similarity between sites S4 and S5, as well as between S1, S2,

and S6, while S3 showed the most distinct microbial diversity according to the NMDS plot. Functional analysis based on 16S rRNA gene sequences indicated that DNA replication enzymes and histidine kinase activity were predominant along the stream. This study provides foundational insights into the bacterial community composition and functional roles within the stream.

Keywords: Aquatic ecosystem; Microbial diversity; Benthic microbiota; Himalayan; Sediment

ENVM-16 (Poster)

Nutritional Profiling of Chicken Feather Hydrolysate Produced from Feathers Waste via Keratinolytic Bacteria

Sunita Devi*, Kritika Kesta, Subhash Chand, Megha Sharma, Puneet and Parul Sharma
*sunitachamba@gmail.com

Microbiology Laboratory, Department of Basic Sciences, College of Forestry, Dr. YS Parmar University of Horticulture and Forestry - Nauni, Solan, Himachal Pradesh (173230), India

Abstract: The primary aim of this study was to evaluate the nutritional composition of chicken feather hydrolysate (CFH) derived from chicken feather waste using potent keratinolytic bacterial strains, including *Bacillus halotolerans* L2EN1, *B. cereus* N27, *B. cereus* N14, *B. megaterium* N35, and B. *halotolerans* DPE11, both individually and as a consortium. The results demonstrated that the bacterial consortium achieved a higher degree of feather degradation compared to individual strains, highlighting its superior efficacy. Nutritional analysis of the resulting CFHs revealed the presence of a range of amino acids, including essential amino acids (isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine) and non-essential amino acids (serine, cysteine, alanine, glycine, and arginine), along with macro (nitrogen, phosphorus, potassium, sulfur, and calcium) and micronutrients (zinc, iron, manganese, and copper), proteins, indole-3-acetic acid (IAA), and ammonia. The consortium-based CFH demonstrated significant advantages over those produced by individual strains, including a greater variety and higher concentration of amino acids (32.43 µg/mL), macro (nitrogen-20,672 ppm; phosphorus-164.11 ppm; potassium-510.20 ppm; sulfur-1,267.30 ppm; calcium-520 ppm) and micro (zinc-2.85 ppm; iron-210 ppm; copper-1.46 ppm; manganese-0.99 ppm) nutrients, protein content (2,795 µg/mL), antioxidant activity (0.31 mg/mL), indole-3-acetic acid (35.78 µg/mL), and ammonia production. These findings suggest that consortium-based CFH has considerable potential as a sustainable organic fertilizer for enhancing plant growth.

Keywords: Chicken feather waste, Chicken feather hydrolysate, Keratinolytic bacteria, Nutritional profiling, Organic fertilizer

ENVM-17 (Poster)

Evaluation of the Insecticidal Potential of Iron Nanoparticles against the Whitefly, Bemisia tabaci

Darshna Chaudhary*, Ankit kumari and Muskan Kaushik
*darshnarajan.cbt@mdurohtak.ac.in

Centre for Biotechnology, Maharashtra Dayanand University, Rohtak, Haryana (124001), India

Abstract: Whiteflies pose a significant threat to plants by directly damaging them through feeding and by serving as vectors for plant viruses. Their nymphs produce honeydew on the undersides of leaves, which reduces photosynthesis, lowers leaf quality, and fosters the growth of sooty mold. Traditional control methods have proven largely ineffective in managing whitefly populations and preventing virus transmission. In contrast, nanotechnology offers a novel and promising approach, providing new insights and strategies for the prevention and management of these disease-carrying insects. Consequently, we have focused on exploring nanotechnological interventions to mitigate the impact of whiteflies on agriculture. In this study we synthesize iron nanoparticles using neem leaves extract and characterize them using FTIR, zeta potential and Transmission electron microscopy. Three different concentration of iron nanoparticles were prepared (1000 ppm, 10000 ppm, 100000 ppm) for insecticidal bioassay. Mean percentage mortality of Bemisia tabaci (whiteflies) over a period of 7 days under different concentrations of FeONPs (*Azadirachta indica* nanoparticles) compared to a control

group. In case of FeONPs treatment groups, mortality increased significantly in all treatment groups compared to the control. Highest mortality obseved on 7th day at 100000 ppm. Hence the results suggested that FeONPs have promising potential as an alternative approach to conventional chemical pesticides for controlling whitefly populations, offering effective pest management with potentially fewer environmental impacts.

Keywords: Whitefly, Nanoparticles, Management, Insecticidal

ENVM-18 (Poster)

Bioprospecting Chitinolytic Bacteria from Insects

Ashish Potdar, Sneha Pandit and **Neeraja P. Dhole***
*neerajadhole420@gmail.com

Savitribai Phule Pune University, Pune, Maharashtra, (411007), India

Abstract: Aquatic insects are diverse and widely distributed carnivorous insects. Insects and small invertebrates form a major part of the food of these insects. As a result, invertebrate chitin is a major part of their diet. Extracellular digestion of chitin by gut microflora has been reported in several animals. So, in the present study we report screening and characterization of chitinolytic bacteria from the gut of adults of *Lethocerus indicus* and *Cybister japonicus*. TVC and TCC of *L. japonicus* hindgut were found to be$39.3*10^{-4}$ CFU/g and $41.5*10^{-2}$. Nine different chitinase producing strains namely, AP1, AP2, AP3, AP4, AP5, AP6, AP7, AP8, AP9 were isolated from the hindgut.TVC and TCC of *C. japonicas* foregut were found to be$35.7*10^{-3}$ CFU/g and $27.6*10^{-2}$. Seven different chitinase producing strains namely, PD1, PD2, PD3, PD4, PD5, PD6, PD7 were isolated from the foregut. Both primary (CZ/CS ratio: 1.065± 0.002) and secondary screening (enzyme activity: 4.523± 0.85 U/ml) from isolates of *L. indicus* showed AP6 as the most efficient isolate. While primary (CZ/CS ratio: 0.83± 0.21) and secondary screening (enzyme activity: 3.31± 0.297 U/ml) from isolates of *C. japonicus* showed PD3 as the most efficient isolate.The isolate AP6 was able to produce cellulase, urease, and esterase. whileisolate PD3 was able to produce cellulase and esterase. AP6 showed the highest growth at 45^0C, pH 6 and 8% of NaCl concentration. PD3 showed the highest growth at 45^0C, pH 8 and 6% of NaCl concentration. Results of molecular characterization showed strain AP6 as the closest relative of *Klebsiella oxytoca* with 99% similarity. While strain PD3 as closest to *Acenatobacter junii* with 100% similarity. Antibiotic susceptibility showed the AP6 to be erythromycin, nalidixic acid, doxycyclin, gentamycin resistant. Antibiotic susceptibility showed the PD3 to be erythromycin resistant.Among the tested substrates, the highest chitinase activities were seen by *K. oxytoca* AP6 on crab shells (1.127 ± 0.04), while *A. junii* PD3 on prawn shells().Among the substrates *K. oxytoca AP6* showed maximum (51.53%) degradation of CS and minimum (19.9%) degradation of CF. *A. junii* PD3 showed maximum (70.65%) degradation of PS and minimum (15.3%) degradation of CF.Results suggest the possible role of extracellular bacterial chitinases in the digestion of chitin containing food and may have a bearing in the evolution of the digestive system of aquatic insects. These findings also suggest the chitin degradation potential of bacteria from novel sources such as the guts of insectivorous animals. Further these bacteria can be employed for production of N-acetyl D glucosamine, bioethanol, single cell protein production

Keywords: *K. oxytoca*, Nalidixic acid, Chitinases, *L. indicus*

ENVM-19 (Poster)

Biodegradation of C.I. Acid Blue 113 Azo Dye using A Novel Endophytic Bacterium (*Brachybacteirum rhamnosum*) to Minimize the Pollution Problem in Industrial Wastes Water: An Eco-Friendly Approach

Narmadha Ramasamy, T. Senthilvelan and M. Kannan
narmadhar9059.sse@saveetha.com

Department of Computational Biology, SIMATS Engineering, Saveetha Institute of Medical and Technical Sciences, Saveetha University, Chennai (602105), Tamil Nadu, India

Abstract: Azo dyes are toxic and hazardous pollutants discharging from various dyes using industries in huge volumes such as textile, leather, pharmaceutical, paint, paper, and dye manufacturing. Discharging of huge

volume of wastewater containing dye wastes to the environment causes severe environmental pollution problems such as soil pollution, water pollution and air pollution. Long term disposal of dyes wastes to the land and water bodies causes soil infertility, affects the aquatic life of the organisms, animal health and human health leads to cancer, when it is absorbed by our body. Azo dyes are aromatic pollutants which is naturally resistant for biodegradation. Hence, the dye wastes should be treated before discharging in to the environment. Various techniques have been adopted for the treatment azo dyes wastes such as physical, chemical, physico-chemical, and biological methods, but these techniques are not effective and generates secondary sludge problems after treatment and required additional investment and treatment for the degradation of secondary sludge. Hence, effective, and alternative techniques required for the treatment of azo dyes wastes. Present study has focussed on treatment of azo dye wastes using endophytic bacterium. Seven different endophytic bacteria have been isolated from *Clausena dentata* plant for the decolourisation of azo dye. Among the organisms, *Brachybacteirum rhamnosum* has been completely degraded the azo dye more than 99% at pH 5.5, and temperature at 37^{o}C within 48 h duration. The degradation of azo dye has been confirmed by various analysis such as UV-vis spectrophotometer, FTIR, and HPLC. The phytotoxicity study has revealed that, the toxicity of the dye has been reduced after treatment by endophytic bacterium. The pollution load such as BOD, COD, TDS and TSS have been reduced after degradation. Overall observation from the studies, the endophytic bacterium is more potential organism for the treatment of various azo dyes wastes discharging from various industries.

Keywords: Azo dyes wastes; Biodegradation; Endophytic bacterium; HPLC; Toxicity study; and Pollution reduction

ENVM-20 (Poster)

Characterization of Lead-Tolerant Fungus Isolated from Plant Rhizosphere and its Potential for Lead Bioremediation

Shruti Singh[1,2] and Manoj Kumar[1,2*]
manojkumar@iitr.res.in

[1]*Environmental Toxicology Group, FEST Division, CSIR-Indian Institute of Toxicology Research (CSIR-IITR), Vishvigyan Bhavan, 31, Mahatma Gandhi Marg, Lucknow, Uttar Pradesh (226 001), India*
[2]*Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, Uttar Pradesh (201002), India*

Abstract: Lead (Pb) contamination in soil has become a major environmental concern in recent years. Using amendments to immobilize Pb in contaminated soil has emerged as a sustainable and cost-effective strategy to reduce Pb bioavailability. This study evaluates the efficacy of three fungal strains, Si1 (DSM 11827), Si2 (PTB299), and Si3 (West Bengal), isolated from distinct geographical locations, in biomineralizing and accumulating Pb, thus reducing Pb bioavailability in Pb-polluted soils. An Individual Level Physiological Profiling (ILPP) analysis of the fungal strains was performed to assess metabolic diversity and ecological potential for niche succession. The strain tolerance to Pb was examined on AMM agar plates and in broth with varying concentrations of $PbNO_3$. Phenol cotton blue staining was used to identify morphological changes in spores post-Pb exposure. Pb bioaccumulation was assessed via ICP-MS analysis and confirmed by Scanning Electron Microscopy/Energy Dispersive X-ray Analysis (SEM-EDAX). ILPP analysis revealed the metabolic diversity of Si3 (80.66%) > Si2 (48.39%) > Si1 (45.16%), with Si3 exhibiting the highest diversity. Mycelial growth was in the order of Si3 > Si2 > Si1, and Si3 tolerated up to 517.5 ppm Pb, compared to 207 ppm for Si1 and Si2. Spores of all strains survived at 207 ppm Pb, with slight increases in spore size at 41.4 ppm, 51.75 ppm, and 103.5 ppm Pb. Biomass analysis has shown no significant changes in biomass up to 207 ppm Pb for all strains. ICP-MS result indicates that Si1, Si2, and Si3 mycelia accumulated Pb up to 207 ppm at 40000 ppm, with SEM-EDAX revealing Pb accumulation on Si 3 fungal cell walls and inside fungus, comprising 11.45% by weight of Pb. Further, we check the impact of Si 3 on Pb remediation potential in rice plants. These findings provide the way for further advancements in fungi-based remediation of Pb-contaminated soil.

Keywords: Amendments, Scanning Electron Microscopy (SEM), ICP-MS, Individual Level Physiological Profiling (ILPP)

ENVM-21 (Poster)

Exploring the Potential of Psychrotrophic Microorganisms for Paddy Straw Degradation at Low Temperature

S.T.M. Aravindharajan, Livleen Shukla*, D Vijaysri, S.H. Manoj and Sandeep Kumar Singh
lshukla65@gmail.com

Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi (110012, India)

Abstract: The aim of this study was to investigate the enzyme production of psychrotrophic lignocellulolytic, silicolytic, and xylanolytic fungi at low temperatures. To achieve this, a series of enrichment, isolation, and screening steps were conducted, resulting in the isolation of twentyone fungi from cold-adapted regions, namely Balim, Gurdaspur, Punjab. In the qualitative screening at 15ºC, a total of thirteen fungal isolates were selected. These screened isolates were further subjected to quantitative estimation of different enzymes at three low temperatures (10, 15, and 20 ºC). The maximum enzyme production was observed in isolate LTF 7 for CMCase and LiP, in LTF 21 for FPase, in LTF 1 and 5 for xylanase, in LTF 13 for laccase, and in isolates LTF 16, 17, and 19 for MnP and silicase. Furthermore, based on the data, tolerance of low temperature was checked by radial growth measurement at 15ºC, resulting in 100% growth was attained by LTF 1, 7, 13, 16, 17, and 21 under 7 days of incubation. Survivability of those isolates also checked for adaptation in colder region through freeze thawing experiment, in which, LTF 13, 21, 2, 7 and 14 recorded maximum population in series of 20 days experiments. Outcome of these study not only indicated a valuable psychrotrophic paddy straw degrading strain but also offer meaningful evidence for further exploration of the microbial degradation mechanism in waste management at cold regions.

Keywords: Paddy straw, Psychrotrophic microorganisms, Low temperature, Lignocellulolytic degradation, Reese mineral medium

ENVM-22 (Poster)

Techno-Economic Strategy for Cultivation of Marine Green Algae *Picochlorum sp.* using Domestic Wastewater for the Production of Value-Added Products

Nitharsan Kirubakaran[1,2]*, Arunachalam Nagaraj[3], Rajakumar Sundaram[2], Muralitharan Gangatharan[1,3] and Prabaharan Dharmar[1,2]
nitharsan.k@bdu.ac.in

[1]*National Repository for Microalgae and Cyanobacteria (NRMC- Marine), Bharathidasan University, Tiruchirappalli, Tamil Nadu (620024), India*
[2]*Department of Marine Biotechnology, Bharathidasan University, Tiruchirappalli, Tamil Nadu (620024), India*
[3]*Department of Microbiology, Bharathidasan University, Tiruchirappalli, Tamil Nadu (620024), India*

Abstract: The utilization of microalgae for producing value-added products offers significant potential as a sustainable and eco-friendly practice. This study investigates the feasibility of outdoor mass cultivation of marine microalgae using domestic wastewater as a growth medium. The objective was dual: to produce valuable by-products and address wastewater management issues. A high lipid-producing marine microalgae strain *Picochlorum* sp. from the NRMC-M repository was selected and initial growth potential assessments were conducted under various nutrient inputs in controlled laboratory conditions. Subsequently, the selected microalgae were cultured in outdoor fibre tanks utilizing low cost seawater based medium (Control) and domestic wastewater. Growth performance, biochemical composition, and wastewater treatment efficacy were evaluated. Results demonstrated that outdoor mass cultivation of selected marine microalgae in domestic wastewater significantly enhanced biomass production, lipid content, photosynthetic pigment concentration, carbohydrate and protein levels compared to control conditions at outdoor setup. Significantly, the protein content doubled from 0.0189 g/L to 0.3916 g/L and the carbohydrate content rose from 0.2108 g/L to 0.432 g/L which is precursor for the lipid accumulation. Concurrently it showed an upsurge in total lipid content from 16% to 20%, indicating a favourable influence on lipid accumulation. The fatty acid profile indicates higher concentration of essential fatty acids than the controlled environment. The findings suggest that outdoor mass cultivation of marine microalgae using domestic wastewater is both economically viable and sustainable and

representing a promising strategy for sustainable resource utilization and environmental management in microalgal biotechnology.

Keywords: Urban wastewater; Mass cultivation; Microalgae; Nutrient input; Value added products

ENVM-23 (Poster)

Bioremediation and Detoxification of Xenobiotic Compounds (Heavy Metals and Pesticides) using Novel Bacteria

Phogat A[1] Kumari S[1,] Singh T[1], Gohel S[2], Prasad R[1] and Banerjee A[1]
anjaliphogat0@gmail.com

[1]*Amity Institute of Biotechnology, Amity University Haryana (122413), India*
[2] *Saurashtra University, Rajkot, Gujarat (360005), India*

Abstract: Globally, heavy metal and pesticide pollution of soil is a serious threat to human health and the environment and one of the major sources of xenobiotic compounds. Bioremediation is an eco-friendly approach to mitigate environmental pollution caused by hazardous substances such as pesticides and heavy metals. This study focuses on the bioremediation of chlorpyrifos, a widely used organophosphate pesticide, and the bio removal of heavy metals, emphasizing microbial and techniques. Sampling, isolation and screening for pesticide degrading and heavy metal removal micro-organism. Understanding the mechanism involved in the degradation of pesticide and heavy metals. Detection and characterization of bacterial enzymes involved in the degradation of chlorpyrifos and bio removal of heavy metal that is chromium, magnesium, and iron. Metagenomic study of enzymatic activity of bacterial strain once we get novel strain for bioremediation process.
Bacterial strains from pesticide- and heavy metal-affected soil in the industrial areas of Rohtak, Bahadurgarh, and Gurugram were isolated using nutrient broth media. The study locations are dump site of heavy metal industrial waste and other industrial waste as well as agriculture wastes. Screening for microbe which can uptake heavy metals consortia and chlorpyrifos. Serial dilutions of the sample were carried out ranging from concentration of 10-3 to 10-5 concentration in sterile distilled water. The concentrations 10-4 were spread plated onto sterile Nutrient agar plates supplemented with 500 ppm of chromium, iron, magnesium and chlorpyrifos each; these plates were then incubated for 24 hours at room temperature to obtain colonies of organisms that could be potentially degrading. Morphologically distinct colonies were further purified.
MTC (maximum tolerance concentration): Gradual increase in ppm from 500 to 2000 ppm by plate assay of both heavy metal and pesticide to check that upto 2000 ppm concentration can the organism isolated can uptake the toxic mixture. Once the MTC via plate and tube broth method was done it was observed isolate 9 showed the best growth. Morphological and Biochemical Analysis was performed to identify the bacteria. Then samples' proceeded for FTIR studies and Conspicuous peaks are shown in the FT-IR. More investigation into molecular methods like PCR and sequencing will identify certain strains of bacteria. This study is to isolate the potential microorganisms from the heavily contaminated soils from dump-site for pesticide and heavy metal bioremediation.

Keywords: Bioremediation; Pesticides; Heavy metals; Microbial bioremediation; Chlorpyrifos

ENVM-24 (Poster)

Effect of Increasing Sulfate Concentration on Fe^{2+} Ion Oxidation Kinetics by *Leptospirillum ferriphilum* Dominated Chemostat Culture

Shatakshi Tiwari[1], Sugandha Aachhera[1], Pradeep Verma[1]** and Chandra Sekhar Gahan[2*]
*sekhar.gahan@ggu.ac.in, **pradeepverma@curaj.ac.in

[1]*Department of Microbiology, School of Life Sciences, Central University of Rajasthan, Bandarsindri, Kishangarh, Ajmer, Rajasthan (305817), India*
[2]*Department of Biotechnology, Guru Ghasidas Vishwavidyalaya (A Central University), Koni, Bilaspur, Chhattisgarh (495009), India*

Abstract: Acidophilic chemolithotrophic iron oxidizing microorganism oxidize sulfide minerals leaching metals tolerating high sulfate concentrations. The reason for high sulfate is metal sulfide oxidation and H_2SO_4 addition

to maintain pH at 1.5 as Fe^{2+} ion oxidation is a proton (H^+) consuming reaction. Therefore, elevated sulfate concentration causes toxic effect on microbial Fe^{2+} oxidation. Present study on 16, 30 and 40 g/L sulfate ion as potassium sulfate investigated the effect of sulfate ion on Fe^{2+} oxidation kinetics of a *Leptospirillum ferriphilum* dominated chemostat culture. Chemostat studies for 16 and 30 g/L sulfate concentrations at dilution rates (D) of 0.032 h^{-1}, 0.041 h^{-1}, 0.068 h^{-1} and 0.028 h^{-1}, 0.034 h^{-1}, 0.041 h^{-1} respectively. The critical dilution rate (D_c) for 16, 30, 40 g/L sulfate concentration was 0.071 h^{-1}, 0.042 h^{-1} and 0.031 h^{-1} respectively, stating 40 g/L sulfate to be the toxic level in a chemostat. Measurable parameters of experiment at 16 and 30 g/L sulfate such as Flow rate (F), working volume (V), biomass concentration (X), Feed concentration (S_0) and Residual substrate concentration (S) were used to calculate maximum specific growth rate (μ_{max}), Substrate coefficient (K_s), Observed biomass yield (Y_{obs}), True biomass yield (Y_{true}) and Maintenance coefficient (m_s), Biomass productivity (P_X), Ferric productivity (P_S) and Specific ferrous utilization rate ($q_{Fe^{2+}}$) by linearizing Monod and Pirt Equation. Study showed stable μ_{max} at increasing sulfate and elevated K_s at 30 g/L sulfate. The Y_{obs} and m_s values increased with increasing sulfate concentration, whereby Y_{true} decreased. The microbes thrived at 16 g/ but not at 30 g/L sulfate due to jarosite precipitation. Hence the chemostat operated at lower D for 30 g/L than 16 g/L sulfate. Hence, chemostat can't be operated above 0.041 h^{-1} D for 30 g/L sulfate and above 0.031 h^{-1} D for 40 g/L sulfate for *Leptospirillum ferriphilum* dominated chemostat culture.

Keywords: Sulfate; *Leptospirillum ferriphilum*; Kinetics; Ferrous ion; Biomass

ENVM-25 (Poster)

Nitrite Transformation using Potential Microbial Consortium

Anne Bhambri[1,2], Santosh Kumar Karn[2] and Arun Kumar[1]
anne.bhambri26@gmail.com

Department of Biotechnology, Shri Guru Ram Rai University, Patel Nagar, Dehradun, Uttarakhand (248001), India
Department of Biochemistry and Biotechnology, Sardar Bhagwan Singh University, Balawala, Dehradun, Uttarakhand, (248161), India

Abstract: Biological nutrients removal efficiently receiving the attention in wastewater treatment. The presence of high concentration of ammonia, nitrite and nitrate has become problem in aquaculture. To avoid the environmental damages and ensure sustainable natural resources is challenging in the rapidly developing global aquacuture industries. In recent years, removal of nitrogen waste has become a key focus. Therefore, a safe, environment friendly and economically feasible way is very essential to treat the ammonia, nitrite and nitrate that is highly toxic and causes harmful effect on the aquatic ecosystem. In this study, the removal of high concentration of ammonia, nitrite and nitrate was determined by using nitrite-oxidizing bacteria (NOB 1 & NOB 2) along with the microbial consortium of both the strains at labscale and also at in-situ bioreactor level. The highest percentage of removal was shown by NOB 2 (99.80 %) as compares to NOB 1 (98.71 %) at an initial concentration of 3 mg/l whereas at the concentration of 6 mg/l, NOB 1 shown the highest percentage of removal i.e., (99.81 %) as compares to NOB 2 (99.58 %). Next, microbial consortium of NOB 1 and NOB 2 were used at lab-scale and found that the consortium of both the strains degrades ammonia (99.21 %) and nitrate forms (0.79 %) at the concentration of 6 mg/l. Further, in-situ transformation was carried out. Their growth was observed by colony forming unit (4.7 × 10 5CFU/ml) and found the transformation of ammonia (100 ± 4.5 %). Hence, this study proves that both the strains NOB 1 and NOB 2 are highly efficient in the removal of ammonia, nitrite and nitrate from aquatic system. Therefore, this work can be utilized for the treatment of ammonia, nitrite and nitrate wastewater treatment plants etc.

Keywords: Ammonia; Nitrate; Nitrite; Bacteria; Microbial consortium; Bioremediation

ENVM-26 (Poster)

Development of a Chemical Optode for the Detection of *Escherichia coli O157:H7* from Drinking Water

Bandita Panda and Sandip Kumar Dash*
*dashsandipkumar@gmail.com

Department of Zoology, Berhampur University, Ganjam, Odish (760007), India

Abstract: Gold (Au) NPs were synthesized from $HAuCl_4$, using whey water. The whey water was derived from a commercially procured milk following previously reported protocol. For the synthesis of Au NPs, 1 ml whey water was added to 2 ml 01 mM $HauCl_4$ and incubated at 80 °C and 100 RPM. The change in the color of the tube as well as its UV/Vis absorption spectra was observed at a regular interval of every 20 min right from the beginning. The conc. of precursors, reducing agent, time and temperature for the synthesis of NP were optimized. The NPs were recovered and characterized, using transmission electron microscopy, scanning electron microscopy (SEM), X-ray diffraction, Fourier transform infrared (FTIR) spectroscopy. The NPs were coated on a glass slide through dip coating along with optimization. The partial sequence of *eAe* gene of *E. coli 0157:H7* was PCR amplified through optimization and sequenced to design a 5'-SH-labeled complementary single stranded DNA probe against it. The 5'-SH probe was immobilized onto an Au-fabricated screen-printed carbon electrode through Au-S linkage, followed by hybridization with the single stranded genomic DNA isolated from *E. coli 0157:H7* as a complementary DNA. The fabrication, immobilization, and hybridization were characterized, using FTIR and SEM. Hybridization of the sensor with different conc. of the DNA was plotted to find the sensitivity and limit of detection. The stability of the electrode was also evaluated at room temperature.

Keywords: Biosynthesis; Biosensor; *Escherichia coli O157:H7*; Gold NP; Optode

ENVM-27 (Poster)

Eco-Friendly Co-Composting of Chicken Feathers with Cow Dung Using Keratinolytic Bacteria for Nitrogen-Rich Organic Fertilizer Production

Subhash Chand*, Sunita Devi, Kumari Manorma, Megha Sharma, Puneet and Parul Sharma
*subhashverma190@gmail.com

Department of Basic Sciences, College of Forestry, Dr YS Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh (173230), India

Abstract: The study aimed to explore the role of potent keratinolytic bacterial strains, including *Bacillus halotolerans* L2EN1, *B. cereus* N27, *B. cereus* N14, *B. megaterium* N35, and *B. halotolerans* DPE11, in the preparation of chicken feather compost (CFC) using chicken feathers (CF) and cow dung (CD) as substrates. Two experimental setups were employed: Set-I, with a keratinolytic bacterial consortium, and Set-II, without consortium, using five treatment combinations (T1 - CF only; T2 - 3CF:1CD; T3 - 1CF:1CD; T4 - 1CF:3CD; T5 - CD only), both in plastic pots and composting pits for a period of six months. Microbiological and physico-chemical analyses of CFC conducted at monthly intervals revealed that treatment T4 of Set-I exhibited the best microbiological (bacteria: 9.40 Log CFU/g; fungi: 4.20 Log CFU/g; actinomycetes: 3.49 Log CFU/g; enteric: 7.62 Log CFU/g; spore formers: 4.96 Log CFU/g; diazotrophs: 6.38 Log CFU/g; proteolytic bacteria: 7.98 Log CFU/g) and physico-chemical (pH: 7.53; temperature: 34.79 ºC; EC: 0.87 mmhos/cm; moisture: 45.10%; non-volatiles: 21.25%; volatiles: 78.75%; organic carbon: 45.68%; N: 7.02%; P: 0.68%; K: 2.06%; C:N ratio: 15.70) characteristics. In conclusion, co-composting CF (1 part) with CD (3 parts) using keratinolytic bacteria provides an eco-friendly approach to recycle CF waste into a nitrogen-rich organic fertilizer.

Keywords: Chicken feather compost; Keratinolytic bacteria; Nitrogen-rich fertilizer; Chicken feathers waste; Composting

ENVM-28 (Poster)

Antioxidant Activity of Phenolic Compounds Extracted from Rice Straw

Sujeeta[1*], Kamla Malik[1], Shikha Mehta[1] and Pushpa Dhillon[2]
*sujeetayadav12@gmail.com

[1]*Department of Microbiology,*
[2]*Department of Botany and Plant Physiology, College of Basic Sciences and Humanities,*
Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana (125004), India

Abstract: Agricultural waste especially rice straw is a serious problem in India. Utilization of these wastes through environmentally friendly approach is a very important issue. The objective of present study was to utilize rice straw into value-added products. The pretreatment of rice straw by alkaline (12%w/v NaOH) hydrolysis and the methanolic extract was used for the analysis of total phenolic compound (TPC), total flavonoid compound (TFC) and antioxidant activity. The extract exhibited strong antioxidant activity was measured by the 1,1-diphenyl-2-picrylhydrazyl (DPPH) radical scavenging method and 2,2′-azino-bis (3-ethylbenzothiazoline-6-sulfonic acid), and its IC50 value was 69.25 µg/ml and 34.25 µg/ml. The total phenolic compounds were found to be 160 mg Gallic acid equivalent (GAE) while total flavonoid content was 4.1mg Catechin equivalent (CE). Further, the surface characterisation of untreated and treated rice straw extract was analysed by X-Ray Diffraction (XRD), Fourier transform infrared spectroscopy (FTIR) and Scanning Electron Microscope (SEM). The structural characterization of extract was done using nuclear magnetic resonance (NMR). The research highlights the importance of promoting the commercial use of agricultural waste to maximize its nutritional benefits with low cost and reducing the amount of waste generated by human activities.

Keywords: Rice straw; DPPH; ABTS; NMR; XRD; SEM

ENVM-29 (Poster)

Isolation and Screening of Heavy Metal Resistant Bacteria from Different Industrial Sites

Swati[1*], Vinod Goyal[1] and Jagdish Parshad Jangra[2]
*swatiantil111@gmail.com

[1]*Department of Botany and Plant Physiology, CCS Haryana Agricultural University, Hisar, Haryana (125 004), India*
[2] *Department of Microbiology, CCS Haryana Agricultural University, Hisar, Haryana (125 004), India*

Abstract: Bioremediation is a fascinating field that harnesses the power of living organisms—like bacteria—to clean up environmental pollutants. Heavy metal pollution is a significant environmental concern, particularly in the industrial areas where metals like chromium, cadmium, arsenic, lead and mercury can accumulate to the toxic levels. Heavy metals/metalloids with density more than 5g/cm^3. These pollutants cause serious risks to human health and the environment. One promising solution is the use of heavy metal resistant bacteria for bioremediation. Bacteria can remediate heavy metal contamination through various processes like biosorption, bioleaching, biotransformation, intracellular accumulation etc. Our research explores the process of isolation and screening such bacteria from various industrial sites to check their resistibility towards chromium and cobalt. Samples were collected from contaminated soil across multiple industrial locations using selective media containing high concentrations of heavy metals, a variety of bacterial strains were isolated. These isolates were then screened for their resistance to different heavy metals through growth assays. The result revealed that microbial isolate with notable resistance to heavy metals. These strains exhibited potential for bioremediation application, offering a promising approach for detoxifying contaminated environment. In present work, we have isolated heavy metal resistant strains from Tata steel limited. Seven isolates were tested for heavy metal resistance on specific media supplemented with a concentration of 400 ppm of respective heavy metal. The promising bacteria were further tested for acid production.

Keywords: Bioremediation; Heavy Metals; Isolation; Screening; Bacteria

ENVM-30 (Poster)

Isolation and Characterization of Halophilic Microorganisms from Salt Affected Soil of Cauvery Command Area

Sushma N N[1]*, Suman Jayakumar Kankanwadi[2] and Asha N N[3]
*sushmannhnarayan@gmail.com

[1]*Department of Microbiology, College of Basic Sciences & Humanities*
Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana (125004)
[2]*Department of Microbiology, College of Basic Sciences & Humanities*
Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana (125004)
[3]*Department of Agricultural Microbiology, UAS Bangalore, College of Agriculture, V. C. Farm Mandya, Karnataka (571405), India*

Abstract: Salts are natural components of the soil, these salts are not harmful to crops at lower concentration, but their presence at higher concentration affects the growth and development of crops as well as soil health. The term "salt-affected soil" refers to soil having high concentration of dissolved mineral salts that reduce crop yield. The carbonates, chlorides, sulfates and bicarbonates of calcium (Ca^{2+}), magnesium (Mg^{2+}) and sodium (Na^{+}) make up the majority of the salts. Halophiles are diverse groups of extremophilic microorganisms that are well- adapted to harsh and hypersaline conditions, these microbes have unique cellular enzymatic machinery that allows them to thrive in extreme saline environments, hence the main objective of the study was to isolate and characterize the halophilic microorganisms from salt affected soils of Cauvery command area. The halophilic microorganisms were isolated from salt affected soils of Mandya, Maddur and Chamarajanagar of Karnataka under Cauvery command area having pH range from 8.5 to 10.2, EC value from 1 to 2.5 dS/m and characterized for salt tolerance and its plant growth promoting traits. Halophiles were isolated using Luria medium supplemented with different concentrations of NaCl (5%, 10%, 15%, 20%) by pour plate technique. Out of 65 isolates, four isolates namely, MDY 1A, MDR 4B, CRN 2A and CRN 5B tolerated upto 20% NaCl concentration. These isolates recorded higher ACC deaminase activity, proline accumulation, production of exopolysaccharide, siderophore, gibberellic acid and abscisic acid along with solubilization of phosphorus, potassium and zinc. These four isolates were subjected for molecular characterization on the basis of 16s rRNA sequencing and they were identified as *Halobacillus massiliensis, Staphylococcus edaphicus, Virgibacillus halophilus* and *Halobacillus dabanensis,* respectively.

Keywords: Characterization; Halophiles; Isolation; NaCl; Salt affected soils; Salt tolerance

ENVM-31 (Poster)

Enhancing Salt Stress Tolerance in *Oryza sativa* (Var. Swarna) through the application of *Streptomyces griseoincarnatus* RB7AG

Subhransu Sekhar Behera[a], Suchismita Nivedita[a], Pratyush Kumar Behera[b], Zahra Parwez[b], Seemon Giri[b], Sourav Ranjan Parida[b], Lopamudra Ray[a,b*]
subhransubiotech@gmail.com

[a]*School of Biotechnology, KIIT Deemed to be University, Bhubaneswar, Odisha, India*

Abstract: Plant growth promoters (PGPs) are natural fertilizers that boost plant growth. In this study, *Streptomyces* strain RB7AG was identified as a potential halotolerant growth promoter and its effects on rice plants under salt stress were evaluated. This strain thrived at NaCl concentrations up to 40mM (w/v), with optimal growth observed at 30mM, as indicated by cell growth, viability, and secondary metabolite production. Under salt stress, the strain remained viable and produced indolic chemicals and siderophores. Rice plants treated with this *Streptomyces* strain showed increased levels of proline and antioxidant enzymes such as superoxide dismutase (SOD), peroxidase (POD), and catalase (CAT), helping them cope with salt stress. Additionally, these plants exhibited enhanced root and shoot growth, suggesting a systemic tolerance mechanism. Formulations of the strain were developed using five organic and inorganic waste materials as carriers, and the viability of the propagules was monitored. Vermicompost and vermiculite formulations maintained the highest levels of viable bacteria after three months of storage.

Keywords: Plant growth promoters; *Streptomyces*; Salinity stress; Formulation; *Oryza sativa*; Reactive oxygen species

ENVM-32 (Poster)

Evaluating chromium-resistant bacteria for mitigating heavy metal pollution: Insights into their potential for sustainable remediation and phytoremediation

Simranpreet Kaur Natt[1]*, Priya Katyal[1], Sumita Chandel[2] and Pooja Manchanda[3]
*simmu_natt@yahoo.com

[1]*Department of Microbiology, College of Basic Sciences and Humanities, Punjab Agricultural University, Ludhiana, Punjab (141004), India*
[2]*Department of Soil Science, Punjab Agricultural University, Ludhiana, Punjab (141004), India*
[3]*School of Agricultural Biotechnology, Punjab Agricultural University, Ludhiana, Punjab (141004), India*

Abstract: Rapid urbanization and industrialization have severely impacted environmental health, particularly through heavy metal pollution in water resources. Industrial activities such as metal processing and electroplating have elevated heavy metal levels, particularly chromium. Conventional removal methods-physical, chemical and biological-often fall short due to environmental impact, cost, and inefficiency at low concentrations. This study explores the potential of chromium-resistant bacteria for bioremediation. Chromium-resistant bacteria were isolated from effluent and soil samples, with six isolates, including UN1 (*Alcaligenes faecalis*), LH1 (*Pseudomonas aeruginosa*) and positive control *Pseudomonas aeruginosa* MTCC 7812, showing high minimum inhibitory concentrations (MIC) and effective chromium reduction capabilities. Scanning electron microscopy (SEM) and Fourier Transform Infrared Spectroscopy (FT-IR) confirmed chromium accumulation in bacterial cells. qRT-PCR studies indicated significant up-regulation of the chromate reductase gene (*ChrR*) in UN1. Isolates displayed multi-antibiotic resistance and plant growth-promoting properties. In trials with *Gomphrena globosa*, plants inoculated with UN1 and LH1 showed enhanced growth and biomass under chromium stress. Inoculated plants also exhibited improved photosynthetic pigment content and reduced oxidative stress indicators. These findings suggest that bacterial isolates UN1 and LH1 are promising candidates for bioremediation of chromium-contaminated environments and could be integrated into phytoremediation strategies to mitigate heavy metal pollution and support environmental sustainability.

Keywords: Bioremediation; Chromium; Bacteria; *Gomphrena globosa;* Electroplating effluents; Phytoremediation

ENVM-33 (Poster)

Extremophiles and Extremozymes- Their Unique Biocatalyst Applications for Sustainable Development

Divya Mori[1] and Nikita Sinh Gohil[2*]
[*]nikitasinh.gohil@marwadieducation.edu.in

[1]*Department of Microbiology, Faculty of Science, Marwadi University, Rajkot, Gujarat, India*

Abstract: Microorganisms are a major component of biotechnological applications for industrial applications. Exhibit special metabolic and physiological adaptations. Extreme environmental factors that promote growth include high pressure, high temperatures, high salt, and extreme pH levels. Extremozymes have great potential in industrial biotechnology, including biocatalysis, medicines, biofuels, and bioremediation. They can function under severe temperature, pH, and salinity conditions. Biosurfactant is one potential source of surface-active compounds used in oil recovery, contaminated area bioremediation, and the creation of eco-friendly detergents and emulsifiers. Extremophile microbiomes play a critical part in the biorefining processes that convert lignocellulosic biomass into chemicals and biofuels. These extremozymes play a crucial role in pretreatment, saccharification, fermentation, and lignin valorisation, among other biorefining processes. Mining is one more significant industry that uses extremophiles and their enzymes. Using microorganisms, this procedure also referred to as bioleaching removes insoluble metal sulphides or oxides. Natural pigments called carotenoids are most frequently linked to the halophilic archaea and algae in extremophiles. There are extremophile microbiomes that are useful for industry: β-carotene, canthaxanthin, and bacteriorhodopsin. Extremophiles have potential in the medical domain as well. Their potential for the synthesis of antifungal, anticancer, and antibiotic medications is being investigated. Notably, the development of thermostable DNA polymerases from extremophiles has transformed molecular biology methods such as PCR (Polymerase Chain Reaction),

improving their accuracy for use in forensic and diagnostic applications. With the establishment of the 2030 Agenda for Sustainable Development, the United Nations captured and institutionalized these worldwide concerns. We examine the contributions extremophiles have made and will continue to contribute to the SDGs as we approach 2030.

Keywords: Extremophiles; Extremozymes; Biosurfactant; Biorefinery; Bio pigments; Sustainable Development Goals (SDGs)

ENVM-34 (Poster)

Assessing the Impact of IHBT-VHH4 PGPR on Heavy Metal Bioremediation and Plant Growth for Sustainable Agriculture

Priya Kaushal [1, 2] and Aparna Maitra Pati [1, 3*]
*aparna@ihbt.res.in

[1]*Biotechnology Division, CSIR-Institute of Himalayan Bioresource Technology, Palampur, (H.P.), India*
[2]*Department of Biotechnology, Guru Nanak Dev University, Amritsar, Punjab, India*
[3]*Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, Uttar Pradesh (201002), India*

Abstract: Pollution caused by heavy metals is considered as one of the most threatened abiotic stresses worldwide. Among all the heavy metals, lead (Pb) is one of the most hazardous environmental contaminants, posing long-term threats to soil health, water quality, and crop productivity. This study investigated the Pb bioremediation potential of IHBT-VHH4 bacterial strain. The results revealed that the IHBT-VHH4 strain tolerates upto 15mM of Pb stress and possess 96% Pb bioaccumulation efficiency. Moreover, it also maintained its plant growth promoting (PGP) attributes like phosphate solubilization, siderophore, and indole-3-acetic acid production under Pb stress. Furthermore, IHBT-VHH4 strain treated aqueous solution containing 15mM Pb (IHBT-W) also ameliorated the detrimental effects of Pb stress. Watering of rice seedlings with IHBT-W solution significantly decreased the Pb bioaccumulation in the rice plant and positively influenced the shoot, root length, and total roots as compared to the Pb stress plants (Pb-W). Besides rice crop, the biostimulant potential of IHBT-VHH4 strain has been explored over the marigold flower. Interestingly, bacterial inoculum treatment significantly improved the marigold seed germination by 60% as compared to control (after 7 days of treatment) under controlled conditions. Thus, our research underscores the remarkable Pb bioremediation and plant growth promoting potential of IHBT-VHH4, offering a promising avenue for improving soil health and productivity of commercial crops.

Keywords: PGPR; Heavy metal; Bioremediation; Bioaccumulation; Rice

ENVM-35 (Poster)

Batch Bioleaching of Zinc from Zinc Sulfide Concentrate using Adapted Microbial Culture of Iron Oxidising Microorganism

Sugandha Aachhera[1], Shatakshi Tiwari[1], Pradeep Verma[1**] and Chandra Sekhar Gahan[2*]
**sekhar.gahan@ggu.ac.in, *pradeepverma@curaj.ac.in

[1]*Department of Microbiology, School of Life Sciences, Central University of Rajasthan, Bandarsindri, Kishangarh, Ajmer, Rajasthan (305817), India*
[2]*Department of Biotechnology, Guru Ghasidas Vishwavidyalaya (A Central University), Koni, Bilaspur, Chhattisgarh (495009), India*

Abstract: This study investigates the bioleaching of sphalerite using an adapted microbial culture of iron oxidising microorganism dominated by Leptospirillum ferriphilum, with a focus on enhancing zinc leaching efficiency and reaction kinetics at increasing pulp densities. As an eco-friendly alternative to the conventional roasting-leaching-electrowinning (RLE) process, bioleaching is often limited by slow kinetics, particularly due to the formation of an elemental sulfur layer during the dissolution of polymetallic sulfides such as chalcopyrite, pyrite, and sphalerite. This sulfur layer acts as a diffusion barrier, hindering zinc dissolution from sphalerite. To address this limitation, the research evaluated the bioleaching of zinc sulfide flotation concentrate under non-controlled redox potential in batch mode. This study utilized adapted microbial consortia, dominated by

Leptospirillum ferriphilum, across various pulp densities in fed-batch mode, significantly improving zinc recovery. Results indicate the Zn recovery of 96%, 50%, and 55% at pulp densities of 2%, 7%, and 10% over 18, 26, and 40 days, respectively. Furthermore, leaching kinetics analysis implied that the leaching process was governed by an intermediate kinetic model. Field emission scanning electron microscopy (FE-SEM) and X-ray diffraction (XRD) analyses confirmed the formation of jarosite and elemental sulfur layer on sphalerite surfaces under mesophilic conditions.

Keywords: Bioleaching; Sphalerite; Iron-oxidizing microorganisms; Leaching kinetics

ENVM-36 (Poster)

Gibbago trianthemae: A potential plant fungal pathogen for management of hazardous weed *Trianthema portulacastrum*

Monika Chopra[1,2*], Madhu Choudhary[1], Vikas Kumar[2,3] and Manoj Singh[2]
*monika.17chopra@gmail.com

[1] *ICAR-Central Soil Salinity Research Institute, Karnal, Haryana, India*
[2]*Department of Bio-Sciences and Technology, Maharishi Markandeshwar University, Ambala, Haryana, India*
[3]*Department of Microbiology, IMS, UIB, Almaty, Kazakhstan*

Abstract: Weeds are one of the major yields limiting factor in crop production. *Trianthema portulacastrum* which also known as Horse purslane, Santhi, Santha, Black pigweed, Carpet weed, Hog weed, is considered to be one of the most troublesome weeds in various states of the country, causing yield reduction by 50-80%. Horse purslane is much branched, fast growing; prostate, succulent herb with ovate green leaves grows during June-November. Chemical herbicides are the most immediate solution for the management of horse purslane. However, the excessive use of chemical herbicides pollutes soil and ground water. The application of microbial herbicides can offer to mitigate the harmful effect of chemical herbicides on environment and soil health. This experiment was conducted at ICAR-CSSRI, Karnal and symptomatic leaves were collected from different fields. A total of three fungal pathogens namely, *Curvularia lunata*, *Exserohilum rostratum* and *Gibbago trianthemae* were isolated from the infected tissues on Potato dextrose agar (PDA). The sequences of all the three isolates were submitted to the NCBI and assigned with accession numbers i.e. PP053463 for *Curvularia lunata*, PPO57698 for *Exserohilum rostratum* and PP064127 for *Gibbago trianthemae.* In-vitro pathogenicity test was carried out to determine the virulence potential of all three isolates. *Curvularia lunata* is considered as non-pathogenic to horse purslane as it was failed to produce disease symptoms. The percent disease index for *Gibbago trianthemae* and *Exserohilum rostratum* was observed as 66% and 33% respectively. The inoculated pathogen was reisolated and found similar to the original isolate in cultural characteristics thus confirming the pathogenicity and completing the Koch's postulates. These findings may help to develop a commercial mycoherbicide for controlling a terrestrial weed of an agro-ecosystem using a novel biocontrol strategy by reducing the use of chemical herbicides.

Keywords: Biological control; Formulation; *Gibbago trianthemae;* Horse purslane; Mycoherbicide; *Trianthema portulacastrum*

ENVM-37 (Poster)

Novel Biosynthetic Secondary Metabolites from *Streptomyces sp.* LKIT: Potential Antimicrobial Agents for Healthcare Management

Sudhansu K Gouda[*], Khushbu Kumari, Ananta N. Panda[1], Lopamudra Ray, Dinabandhu Sahu[2] and Vishakha Raina[1]
sudhansukugouda@gmail.com

[1]*School of Biotechnology, Campus-11, Kalinga Institute of Industrial Technology-KIIT (Deemed University) Bhubaneswar, Odisha, India*
[2]*Institute of Bioresource & Sustainable Development, Imphal, Manipur (795004), India*

Abstract: Biosynthetic Gene Clusters (BGCs) are groupings of genes that work together to manufacture specific metabolites, many of which have bioactive potential present in bacterial genomes. These BGCs include

pathways such as non-ribosomal peptide synthetases (NRPSs) and polyketide synthases (PKSs) that generate distinct chemical structures. The modular enzymatic systems known as polyketide synthases (PKSs) and non-ribosomal peptide synthetases (NRPSs) are widely found in *Streptomyces* and are in charge of the manufacture of intricate secondary metabolites with practical applications in pharmaceutical and food industries.
In this study, we report the genome-based analysis of *Streptomyces* sp. LKIT, a Gram-positive, aerobic actinobacterium isolated from isolated from Loktak Lake, Manipur, India. Loktak Lake is a unique environment known for floating mats (Phumdi), being made up of a heterogeneous mass of soil and vegetation located in the northeastern region of India, an endemic region, and a hot spot for new microbial diversity. An integration of both genomics and chemical approaches was employed to explore the genomic insight of the strain LKIT displayed a collection of genes encoding for secondary metabolites, including those responsible for the biosynthesis of non-ribosomal peptides (NRPS) and polyketides (PKS) having an antimicrobial, anti-cancerous and antioxidant activity was identified. Our results suggest that *Streptomyces sp*. LKIT potential to produce low-cytotoxic bioactive compounds requires further testing to evaluate its potential for pharmacological applications.

Keywords: Biosynthetic Gene Clusters (BGCs); Non-ribosomal Peptide Synthetases (NRPSs); Polyketide Synthases (PKSs); *Streptomyces;* Secondary Metabolites; Anti-cancerous

ENVM-38 (Poster)

Metagenomic Profiling Reveals Unprecedented Microbial Diversity in Extreme Hypersaline-Alkaline Lakes of Rajasthan

Lekh Raj[1] and Shiv Swaroop[1]*
*shivswaroop@curaj.ac.in

[1]*Department of Biochemistry, School of Life Science, Central University of Rajasthan, Ajmer, Rajasthan, India*

Abstract: This pioneering study presents the comprehensive comparative metagenomic analysis of soil microbial diversity in two of India's extreme hypersaline alkaline lakes: Sambhar Salt Lake and Didwana Salt Lake in Rajasthan. Overcoming the challenges of these harsh environments by culture-independent methods to extract and analyse total DNA fragments from soil sediments, focusing on 16S rRNA gene amplicon-based sequencing. Our findings reveal an astonishingly rich microbial tapestry, with Proteobacteria dominating Didwana Lake (79.01%) and Firmicutes prevailing in Sambhar Lake (71.13%) at the phylum level and remarkably, uncovering a high abundance of previously unclassified species from the family Moraxellaceae (30.65%) in Didwana Lake and Flexus (45.72%) in Sambhar Lake. Employing advanced bioinformatics tools, in-depth analysis of operational taxonomic units (OTUs) and alpha diversity, providing an unprecedented census of these unique ecosystems. Our results demonstrate striking compositional differences between the two lakes and suggest specialized adaptations to their respective extreme conditions. This research provides crucial baseline data for monitoring these ecologically important yet vulnerable ecosystems in the face of climate change and anthropogenic pressures, which advances our understanding of microbial adaptation in extreme environments and opens new avenues for biotechnological applications. Identifying novel halophilic and alkaliphilic microorganisms could lead to breakthroughs in enzyme discovery for industrial processes and bioremediation strategies for contaminated saline environments.
Our work establishes the groundwork for further research into the functions of such extremophiles and how they can affect global biogeochemical cycles.

Keywords: 16S rRNA Gene sequencing; Didwana lake; Sambhar lake; Hypersaline-alkaline lakes; Metagenomics; Novel extremophiles

ENVM-39 (Poster)

Polyhydroxyalkanoate production by Sambhar Salt Lake haloalkaliphiles

Mamta*, Vishalakshi Bhanot, Shobham, Abhimanyu Kumar and Jitendra Panwar**
*mamtash1997@gmail.com, **drjitendrapanwar@yahoo.co.in

Department of Biological Sciences, Birla Institute of Technology and Science, Pilani (333031), Rajasthan, India

Abstract: Polyhydroxyalkanoates (PHAs), being both biobased and biodegradable nature is a great sustainable alternative to the synthetic plastics. Extremophiles such as haloalkaliphiles which can thrive in highly saline

and alkaline conditions holds great promise for PHA production under unsterile conditions. This study highlights the immense ability of haloalkaliphile isolated from hypersaline rhizospheric and non-rhizospheric soils of Sambhar Salt Lake. A total of 27 molecularly diverse bacterial isolates were selected based on BOX-PCR profiling out of 36 morphologically different bacterial isolates for screening their ability to synthesize PHA. Nile blue A fluorescent dye was used to stain the synthesized PHA granules. The synthesized PHA was quantified on the basis of (i) fluorescence intensity per bacterial cell, and (ii) percent PHA content in cell dry weight (CDW). The best PHA producing bacterial isolates (9) were molecularly characterized using 16S rDNA sequencing which were found belonging to three different genera i.e. *Bacillus*, *Priesta*, and *Halomonas*. The isolates belonging to genus *Halomonas* have shown significant proliferation, achieving higher CDW along with maximum PHA content up to ~63% without any optimization. To find out the possibility of their utilization at industrial level, growth dynamics studies were performed which indicated their PHA synthesizing potential under contamination-free environment. To check the monomer composition of extracted PHA, GC-MS/MS analysis was performed which confirmed the synthesis of polyhydroxybutyrate (PHB), the most abundant type of PHA having various applications in industrial and medical fields. These findings suggest that haloalkaliphilic bacterial isolates of Sambhar Lake holds substantial potential for large scale PHA synthesis in industrial settings. Our ongoing studies are focused on utilization of Response Surface Methodology (RSM) for optimizing various fermentation parameters to enhance the PHA production efficiency of best bacterial isolates.

Keywords: PHA; Haloalkaliphiles; Sambhar lake; Nile blue A; *Halomonas*; GC-MS/MS

ENVM-40 (Poster)

Antibacterial and Antibiofilm Activity of Sustainable Cabon Dots from Lignocellulosic Waste against Biofilm Producing Bacteria

Megha Mankoti, Sumer Singh Meena, Anee Mohanty*
*mohantya@nitj.ac.in

Department of Biotechnology, Dr B R Ambedkar National Institute of Technology Jalandhar G.T. Road Bypass, Jalandhar (144027), Punjab, India

Abstract: The biofilm forming bacteria are major contributors to biofouling in industrial, marine sectors and environmental systems leading to reduced efficiency of equipment, increased maintenance cost and energy consumption. The current research work highlights the sustainable approach to eliminate these biofilm producing bacteria which are mainly involved in biofouling. In this work, the biofilm producing bacteria were isolated from wastewater system to ensure practical application using Congo red method, microtiter assay, tube test and followed by their evaluation of biofouling potential. Subsequently, Carbon dots (CDs) from lignocellulosic biomasses and their mixture which are present abundantly in environment were synthesized in order to eliminate these biofilms. The synthesized CDs have demonstrated high antibacterial and antibiofilm activity against these isolated bacteria. Moreover, these CDs also showed broad spectrum antibacterial activity against different bacteria including *Staphylococcus aureus*, *Bacillus subtilis* and *Escherichia coli*. Therefore, the valorisation of lignocellulosic waste to CDs not only reduces negative impacts of these waste but also plays a crucial role in effective mitigation of biofilms and biofouling.

Keywords: Carbon dots; Lignocellulosic biomass; Mixture; Biofouling; Antibacterial; Antibiofilm

ENVM-41 (Poster)

Deciphering Microbial Diversity of Chumathang Geothermal Spring in Ladakh, India by High-Throughput Sequencing Method

Shalini Kumari[1,2*], Kumari Anu[1,2], Geetanjli Choudhary[1,2], and Sarita Devi[1,2]
*shalinii7890@gmail.com, shalini.ihbt21a@acsir.res.in

[1]*Biotechnology Division, CSIR-Institute of Himalayan Bioresource Technology, Palampur, Himachal Pradesh (176061), India*
[2] *Academy of Scientific and Innovative Research (AcSIR), Ghaziabad (201002), Uttar Pradesh, India*

Abstract: The Chumathang geothermal spring in Ladakh, India, offer a fascinating environment for microbiological research due to their unique and challenging conditions. This study aimed to comprehensively

characterize the bacterial and archaeal community structures, compositions, and networks in the water and soil of the geothermal spring using a culture-independent approach. The analysis revealed that 50% of bacterial phyla were present in the water samples, while 42.86% were found in the soil samples. Archaeal phyla accounted for 9.62% in water and 7.94% in soil. Additionally, the study identified unclassified phylum sequences, with 17.31% in water and 19.05% in soil, as well as unclassified bacterial phylum sequences, with 13.46% in water and 12.70% in soil. The most abundant bacterial phyla in the water samples were Firmicutes and Proteobacteria. While in the geothermal soil, Proteobacteria and Bacteroidetes were found to be the dominant phylum. The archaeal communities were primarily composed of Crenarchaeota in the soil and Euryarchaeota in the water. This study revealed the unexpected discovery of geographically distinct microbial communities uniquely adapted to the different geothermal water habitats along the Himalayan Geothermal Belt. The findings highlight the need for future research to explore the metabolic pathways of these microbial communities in extreme environments. Such studies will enhance our understanding of microbial metabolisms prevalent in these geothermal sites, which hold significant potential for biotechnological applications. Additionally, it will help to establish the connections between the microbial community composition and the physicochemical characteristics of the geothermal water and its surroundings.

Keywords: Geothermal spring, Himalaya, Extremophiles, Bacteria, Archaea, Metagenomics studies, Functional analysis

ENVM-42 (Poster)

Metagenomic Analysis of Microbial Communities of Alkaline Hot Spring in Panamik, Ladakh, India

Geetanjli Choudhary[1,2*], Kumari Anu[1,2], Shalini Kumari[1,2] and Sarita Devi[1,2]
*geetanjli291998@gmail.com

[1]*Biotechnology Division, CSIR- Institute of Himalayan Bioresource Technology, Palampur, Himachal Pradesh (176061), India*
[2]*Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, Uttar Pradesh (201002), India*

Abstract: Asian geothermal belts are known for their abundance of hot springs and the Himalayan Geothermal Belt is the most significant one. Ladakh, located in the Western Himalayas, is one of India's greatest frigid deserts and is notable for the manifestation of multiple hot springs. Microbial communities in hot springs at low elevations have been widely studied all over the world, although a very few investigations have been undertaken in these harsh environmental conditions. Hence, our current research aims to provide an in-depth analysis of the microbial diversity observed in the Panamik hot spring by high throughput sequencing techniques. Panamik is a remotely located geothermal site at 3200 m altitudes within the Nubra valley, Ladakh India. The taxonomic classification of high throughput metagenomic sequencing data for Panamik (hot spring) sample processed with KARAKEN2 database showed that the most dominating phylum was Proteobateria in water, sediment and soil samples. At the species level, *Acinetobacter baumannii*, *Dechloromonas aromatica*, and *Rhodopseudomonas palustris* were the most dominating species found in water, sediment and soil sample respectively. The functional categories such that KO, COG and NOG interpreted by using MG-RAST annotation pipeline to study the function profile of microbial community. Metagenomic studies of such distinct habitats are becoming progressively important in improving our understanding of microbial ecology and its implications in biotechnology.

Keywords: Ladakh; Panamik hot spring; Extremophiles; Western Himalayan; Metagenomic studies; Hotspring

ENVM-43 (Poster)

The Struggle for Survival: Exploring the Impact of Intraspecific Interaction between Sibling Colonies of *Bacillus cereus* MSM-S1

Kritika Prasad, Brinta Chakraborty and Tapas K Sengupta*
*senguptk@iiserkol.ac.in

Department of Biological Sciences, Indian Institute of Science Education and Research Kolkata Mohanpur, Nadia, West Bengal (741246), India

Abstract: Many bacterial species develop communities within their habitat where they interact with nearby members of the same or different species thus increasing their fitness to survive. Individuals of similar or different bacterial species may employ cooperative strategies to facilitate each other or may also compete for resources when they have overlapping niches or similar nutritional requirements. In the present study, we investigated the phenomenon of intraspecific interaction between sibling colonies of *Bacillus cereus* MSM-S1, isolated from soil. When spotted adjacent to each other on nutrient agar plates, the symmetry of the growing colonies altered during interaction with sibling colonies, leading to the formation of a distinct line of demarcation at the interacting zone of the two interacting colonies. This line of demarcation formed even when the colonies were spotted at varying distances. Confocal microscopic studies at different day points revealed alterations in the arrangement and morphology of peripheral cells at the interacting zone in comparison to the non-interacting zone and peripheral cells of colonies growing alone. Scanning electron microscopy revealed spore formation by the cells at the interacting zone. Interestingly, the cells at the interacting zone showed a reduction in the expression of quorum sensing related genes including its regulator *plcr* whereas increased expression of genes involved in sporulation including *spo0A, yqfd,* and chemotaxis response regulator, *cheY* was observed. These results suggest down regulation of quorum sensing network and upregulation of sporulation are parts of the survival strategy employed by the *Bacillus* cells to overcome the challenges of space and nutrient limitations while interacting with sibling colonies. Further studies are underway to understand the role of upregulation of chemotaxis response regulator, *cheY* and other contributing factors that prevent the interacting colonies from occupying each other's niche.

Keywords: *Bacillus*; Sibling rivalry; Quorum sensing; Chemotaxis; Sporulation

ENVM-44 (Poster)

A Step towards Sustainable Green Plastic Production from Algae to Approach a Clean Environment

Mayur Vala[1] and **Rachna Sharma[2]**
*rachsiffco@gmail.com

[1]*Department of Science, SMT Taramai Vartak Memorial Academy (CBSE) Virar, 401305*
[2]*Department of Science, Research Scholar, SMT Taramai Vartak Memorial Academy (CBSE) Virar, 401305*

Abstract: A recent study revealed that Vasai and Virar area of Mumbai witnesses about 8% rise in urbanization between 2004 and 2019, which is caused due to increase in pollution, depletion of ground water, and raise in plastic waste. Both these areas are near many water bodies that have algal blooms. In certain area, water bodies are covered with green carpet which is main reason of Eutrophication and results in mass dead bodies of aquatic life. This problem making microalgae is focused and made as resource for bio-plastic production method. From this perspective, the biodegradable plastic materials focus on creating a more sustainable and greener world with a smaller environmental imprint.

The research objective is to study the material characteristics to determine whether the algal biomass community can be used to produce bio plastics in newly identified environmentally friendly approaches, to solve the increased global plastic waste. This serious problem affects both marine life and humans as micro plastics can enter the food chain and cause many health impacts. So, we conclude this study to represent the biodegradable plastic & Eco-friendly material. It would balance ecosystem of earth and it would replace the plastic made up of fossil fuel. Biomass makes it possible to develop innovative, alternative solutions compared to conventional plastics.

Keywords: Microalgae; Culturing; Bioplastic; Eutrophication

ENVM-45 (Poster)

Exploring Airborne Algae from Coastal Regions: Biodiversity, Culturing, and Potential Applications

Mayur Vala[1] and Mona Kejariwal[2]
Mayurvala2399@gmail.com

[1]*Department of Botany, RD and SH National College Bandra West, Mumbai (400050), India*
[2]*Department of Botany, RD and SH National College Bandra West, Mumbai (400050), India*

Abstract: Airborne algae, commonly known as microalgae, are a significant but understudied component of the aerial environment. Despite their ecological importance and potential applications, there are limited research articles and review papers focusing on aerobiology. This study presents an innovative investigation of airborne microalgae in the Palghar district of the southern Baltic Sea, an area with a hot and humid climate conducive to the flourishing of algae. The research aims to identify and characterize the diversity of airborne algae in this coastal region and explore their potential applications.

The study employs the Petri-plate exposure method with BG11 or F2 or BBM media for air sampling to isolate and culture airborne algae. Various taxa such as *Chlorella*, *Nostoc Anabaena, Lyngbya*, and *Scytonema* have been identified during the primary screening. The selection of species for further research is based on abundance, economic importance, and ease of producing larger biomass.

Microalgae have been shown to produce diverse bioactive compounds, including lipids, polysaccharides, carotenoids, vitamins, phenolics, and phycobiliproteins. These compounds exhibit a wide range of activities, such as antibacterial, antifungal, antiviral, antioxidative, anticancer, neuroprotective, antiglycation, and bioplastic properties. Large-scale production of these bioactives could have significant implications for various applications.

Additionally, the study explores the potential role of airborne algae in cloud formation, the hydrological cycle, and Earth's climate. Harmful microalgae blooms can impact tourist areas near water bodies, where sunbathers may be exposed to harmful microalgae in high quantities during summer and rainy seasons.

This research emphasizes the need for a systematic approach to investigate airborne algae, including the establishment of protocols for sample collection, identification, and mass culturing. The findings highlight the biodiversity and sustainable practices of microalgae, offering opportunities to create a greener world with reduced environmental impact.

In conclusion, this study contributes valuable insights into the occurrence and significance of airborne algae, shedding light on their potential applications and their impact on the environment. It sets the stage for further research and development in utilizing airborne microalgae for sustainable solutions and bioactive compound production.

Keywords: Airborne algae; Microalgae; Aerobiology; Coastal regions; Biodiversity; Culturing

ENVM-46 (Poster)

Hypotheses to Decode Bacterial and Photocatalytic Degradation Mechanisms of LDPE

Rajalakshmi Sridharan and Veena Gayathri K*
*veenagayathri@stellamariscollege.edu.in

Department of Biotechnology, Stella Maris College (Autonomous), Affiliated to University of Madras, Chennai, Tamil Nadu, India

Abstract: Plastic garbage has to be treated effectively since it is a major environmental issue. The presence of plastic wastes in municipal solid waste even after segregation is less focused. Although there are several treatment processes, each has drawbacks of its own. Hence, Biodegradation and Photocatalysis of LDPE is highlighted in this study. Bacterial strains isolated from municipal solid wastes resulted in LDPE weight loss of 4.70 ± 0.45%, 2.32 ± 0.30%, 0.62 ± 0.04%, 1.00 ± 0.51%, and 1.27 ± 0.36% by *Staphyloccocus hominis, Lysinibacillus massiliensis, E. coli* and *Pseudomonas stutzeri* after 60 days incubation. The degradation was further confirmed by FTIR, GC-MS, TG-DSC and SEM analysis. The FTIR and GC-MS analysis confirmed the oxidation of the LDPE C-C backbone. Based on the GC-MS chromatogram, the degradation mechanism of five

LDPE degrading bacterial strains were hypothesized. The photocatalysis of LDPE was performed using bacterial and chemical synthesized CuO nanoparticles resulted to be monoclinic, with band width of 1.49 eV and 1.48 eV. The size of the nanoparticle was 16 to 38 nm (bacterial synthesized) and 50 to 70 nm (chemical synthesized). The photocatalysis performed for 300 hours with 25 hours interval resulted in LDPE weight of 20.46 ± 0.73% and 19.44 ± 0.83% respectively. The degradation was further confirmed using FTIR, GC-MS, TG-DSC and SEM analysis. The breakdown of LDPE polymer with free radical generation was hypothesized to predict the breakdown of the polymeric chain.

Key words: LDPE; Biodegradation; Photocatalysis; Weight loss; Degradation mechanism

ENVM-47 (Poster)

Green Synthesis of CUI Nanoparticle from *Ixora Coccinea* Flowers as a Photocatalyst in Ciprofloxacin Degradation

Dhanya. K.S, Hadhija Noora and Veena Gayathri K*
*veenagayathri@stellamariscollege.edu.in

Department of Biotechnology, Stella Maris College (Autonomous), Affiliated to University of Madras, Chennai, Tamil Nadu, India

Abstract: Green nanotechnology is a developing branch of science that emphasizes on how living cells use biological processes to produce nanoparticles. For the production of metal and metal oxide nanoparticles, green synthesis provides an excellent substitute to conventional techniques. These biological agents play the dual roles of capping and reducing agents by stabilizing the nanoparticles and accelerating the reduction process. The biocompatibility and environmental compatibility of nanomaterials are improved through their biosynthesis from plant phytochemicals. The study focusses on the analysis of the green synthesis of copper nanoparticles from *Ixora coccinea* flowers. The synthesized nanoparticles were characterized using XRD, UV-DRS, FT-IR, SEM and TEM analysis. The prepared copper iodide nanoparticles synthesized from *Ixora coccinea* flower extracts exhibited photocatalytic activity of the degradation of antibiotics. Maximum degradation of the antibiotic ciprofloxacin was seen in a concentration of 30mg/L at 120th minute with a degradation percentage of 64.35%. From this study, it can be concluded that CuI NPs synthesized from *Ixora coccinea* extract are promising in the remediation of environmental pollution from antibiotics.

Keywords: Green synthesis; Nanoparticles; Degradation; Ciprofloxacin

ENVM-48 (Poster)

Analysis of HDPE Degradation using Putative Bacterial Strains Isolated from Municipal Solid Waste in Tamilnadu

Monisha B, and Veena Gayathri K*
*veenagayathri@stellamariscollege.edu.in

Department of Biotechnology, Stella Maris College (Autonomous), Affiliated to University of Madras, Chennai, Tamil Nadu, India

Abstract: High-density polyethylene (HDPE) is a potential source of environmental pollution. The main objective of our research was to assess the efficiency of bacterial strains isolated from municipal solid waste, in Chennai in the degradation of HDPE sheets without any physical or chemical pre-treatment. The biodegradation of HDPE was determined by evaluating weight loss % every 10 days of intervals over 200 days and the morphological changes of the HDPE sheets were analyzed using SEM. Among all the 11 isolates of HDPE-degrading bacterial strains, the isolates BFOT3, SRBK4, and SRBK3 achieved the maximum weight loss percentage of 15.56% ± 0.000115, 13.79%± 0.000115, 11.50%± 0.000115. Weight loss of HDPE film after inoculation of bacterial strains in MSM medium indicated that it was capable of utilizing HDPE as a sole source of carbon. The changes in the presence of functional groups and the metabolite formation of alkanes, phenol, alcohol, and esters during the process of HDPE degradation were analyzed using FT-IR and GC-MS analysis.

The thermal analysis of the control and bacteria-treated HDPE sheet was analyzed using TGA DSC. The results affirmed that the bacterial strains isolated from the municipal solid waste were capable of degrading HDPE sheets efficiently proving its suitability for future environment-friendly degradation studies.

Keywords: Pollutants, Municipal solid waste, HDPE, Degradation

ENVM-49 (Poster)

Degradation of Congo Red using Bacterial Biofilm

Barkha Verma* and Soham Chattopadhyay
*phdbe10051.23@bitmesra.ac.in

Department of Bioengineering and Biotechnology
Birla Institute of Technology, Mesra, Ranchi, Jharkhand (835215), India

Abstract: Rapid industrialisation, urbanisation, and technological revolution have facilitated the accumulation of many dangerous compounds in the environment. Water pollution is a significant problem caused by different dye sectors. It is responsible for giving birth to many diseases and premature deaths of organisms. Untreated dye discharged into aquatic systems degrades the quality of land, soil, etc. The colony of microorganisms produces enzymes that carry out dye bioremediation by breaking down synthetic dyes. Physical and chemical treatments are conventionally used to remedy hazardous textile dyes. There are several limitations to physical and chemical techniques, which biological approaches can overcome. Among several methods, biofilm-based bioremediation has recently popular for controlling water pollution caused by azo dyes. Biofilm is a collection of single or mixed microbial cells attached to living or non-living surfaces with the help of extracellular polymeric substances, known as EPS. EPS consists of protein, lipids, nucleic acid, etc. The growth of biofilm includes four stages: reversible, irreversible, maturation (EPS production) and dispersion/detachment. Two lab isolates, *Pseudomonas aeruginosa* and *Bacillus subtilis,* produced EPS, indicating the biofilm formation by both strains, which helped in the decolourisation and breakdown of the toxic Congo red dye. An increase in biofilm growth by *P. aeruginosa* and *B. subtilis* was observed. A complete degradation was observed in static conditions. A UV-Vis spectral analysis was used to measure the decolourisation percentage. So, we can summarize that the present study provides a direction for the effective degradation of Congo red dye into less harmful components using eco-friendly and economical strategies.

Keywords: Biofilm; EPS; Bioremediation; Decolourisation; *Pseudomonas, Bacillus*

ENVM-50 (Poster)

Isolation of BHET Hydrolase Producing Fungi to De-Polymerise Polyethylene Terepthalate

Sheetal Gola, Anjali Panchal and Deepansh Sharma*
*deepanshsharma@gmail.com

Department of Life Sciences, J.C. Bose University of Science and Technology, YMCA, Faridabad, Haryana (121006), India

Abstract: The increasing use of plastic has led to a significant environmental challenge due to the vast amounts of waste, particularly from PET (polyethylene terephthalate), commonly used in bottles. During the hydrolysis of PET, Bis (2-hydroxyethyl) terephthalate (BHET) and mono-2-hydroxyethyl terephthalate (MHET) are produced as intermediate products. These intermediates further break down into terephthalic acid (TPA) and ethylene glycol (EG). Although enzymes like PETase and MHETase have been well-studied for their roles in the depolymerization of PET and MHET, research into BHET hydrolases is still limited. Developing these enzymes is essential for addressing the challenge of TPA and EG accumulation.
Understanding the microbial utilization and degradation of BHET is crucial for advancing PET bio-upcycling. In this study, a BHET-degrading fungal strain from the genus *Cladosporium* was isolated and identified. This strain demonstrated the ability to use BHET as its sole carbon source, thus contributing to its depolymerization.

Additionally, the strain was screened for the production of BHET hydrolases, including lipases, which are capable of breaking down the BHET structure.
This research offers a promising microbial approach by utilizing an indigenous fungal strain to tackle the problem of heterogeneous product formation, thereby advancing the upcycling of PET.

Keywords: BHETase; MHETase; Bioremediation; De-Polymerization; Cutinases

ENVM-51 (Poster)

Characterization of Culturable and Non-Culturable Rhizospheric Bacterial Communities from *Dactyloctenium Aegyptium* Capable of Phytoextraction of Chromium from Tannery Waste

Pratishtha Sharma and Ram Chandra*
*prof.chandrabbau@gmail.com

Department of Environmental Microbiology, Babasaheb Bhimrao Ambedkar University, Lucknow, Uttar Pradesh (226025), India

Abstract: Tannery waste is the major source accountable for environmental chromium (Cr) pollution. This study has focused on culturable and non-culturable rhizospheric bacterial communities' analysis from *Dactyloctenium aegyptium* growing on disposed Cr-rich tannery waste at CETP, Unnao. The research employed a comprehensive approach to assess bacterial diversities, their potential of plant growth-promoting attributes for phytoextraction of Cr, and the plant's hyperaccumulation potential. *Shewanella putrefaciens, Alcaligenes phenolicus, Serratia marcescens, Brucella anthropic, Bacillus cereus*, and *Gallionella ferruginea* were isolated and identified as culturable bacteria. The abundant unculturable phyla of Proteobacteria, Actinobacteria, Firmicutes, Bacteroidota, etc. were detected in the rhizospheric sludge through Metagenomic analysis. The metagenomic analysis revealed the taxa and functional genes associated with chromium resistance and diverse enzymatic pathways supporting metal accumulation and reduction. Concurrently, physicochemical analysis showed that the fresh sludge is alkaline (8.55 pH) and contains high amounts of Cr (6403.16 ppm). The organic compounds like Resorcinol, Dibutyl phthalate, Benzeneacetamide, Benzoic acid, Octadecanoic, etc. were detected in fresh sludge through Gas chromatography-mass spectrometry (GC-MS). After 55 days of plant growth, sludge exhibited an acidic nature (6.57 pH) with reduced Cr concentrations (1787.5 ppm), and the organic constituents were either degraded or new metabolic compounds were formed. Techniques like Transmission electron microscopy (TEM), Scanning electron microscopy (SEM), and ICP-MS were used to determine the distribution and bioaccumulation patterns of heavy metals in the plant tissues. The analyses confirmed the propitious phytoremediation capabilities of *D. aegyptium*. The findings render a basis for the development of enhanced and efficient bacterial-assisted phytoremediation techniques dealing with the weed plants and associated rhizospheric bacterial communities holistically.

Keywords: Benzeneacetamide; Scanning Electron Microscopy (SEM); Transmission Electron Microscopy (TEM); ICP-MS

ENVM-52 (Poster)

Response Surface Methodology for Optimization of Biodegradation of Chlorpyrifos

Sunanda* and Shashwati Ghosh Sachan**
*phdbe10053.19@bitmesra.ac.in, **ssachan@bitmesra.ac.in

Department of Bioengineering and Biotechnology, Birla Institute of Technology, Mesra, Ranchi, Jharkhand (835215), India

Abstract: Extensive pesticide use is negatively disturbing the environment and humans. Pesticide bioremediation with eco-friendly techniques bears prime importance. This study evaluates the bioremediation of chlorpyrifos in soil using indigenous microbes, isolated from rice agricultural fields. 7 bacterial isolates obtained from soil collected from the agricultural fields of Jahanpur, and Chuttu were screened for chlorpyrifos

degradation. Amongst the screened isolates, SS5003 showed maximum chlorpyrifos degradation (87.01%) after 12 days of incubation at 37℃. Central composite design (CCD) was employed for further optimization taking into account five important variables temperature, pH, the initial concentration of chlorpyrifos, inoculum size and nutrient availability. Growth curve and degradation study under optimized conditions confirmed that the microbe can improve the biodegradation potential. SS5003 effectively degraded chlorpyrifos and can successfully be used for bioremediation of chlorpyrifos-contaminated soils.

Keywords: Chlorpyrifos; Degradation; Microorganism; Optimization; Pesticide

ENVM-53 (Poster)

Assessment of Degradation Potential of Fungal Isolate for Bio Fertilizer Production from Different Agriculture Waste

Kirti, **Adhisha Dahiya** and Namita Singh*
*namitasingh71@gmail.com

Lab No. 202, Microbial Biotechnology, Department of Biotechnology, Guru Jambheshwar University of Science and Technology, Hisar, Haryana (125001), India

Abstract: With the increasing population and diminishing agricultural land, developing bio fertilizers from agricultural waste, which contains lignocellulosic biomass, using fungal consortia developed in the microbial Biotechnology laboratory department of Biotechnology provides a sustainable solution. This approach enhances soil fertility and crop yields, addressing both food scarcity and efficient land use. The study aimed to produced biofertilizers from rice husk, mixed plant leaves, and peels to improve soil fertility and support sustainable crop yields. Rice husk, peels, and plant leaves were inoculated with microbial consortium and allowed to degrade for 30 days. Post-degradation measurements were taken to assess cellulose, hemicellulose, lignin degradation, and NPK content increase. This study also investigates the functional groups, surface morphology, and elemental composition of a sample using various analytical techniques. Fourier Transform Infrared Spectroscopy (FTIR) was employed to identify and characterize the functional groups present in the sample. Scanning Electron Microscopy (SEM) was utilized to examine the surface morphology, providing insights into the texture and structure of the sample. Energy-Dispersive X-ray Spectroscopy (EDX) was used for elemental mapping, revealing the presence and distribution of various elements within the sample. The combination of these techniques offers a comprehensive understanding of the sample's chemical and physical properties. In conclusion, the study successfully demonstrated the potential of fungal consortia to transform agricultural waste into valuable biofertilizers. This approach not only enhances soil fertility and crop yields but also offers a sustainable solution to the challenges of food scarcity and diminishing agricultural land. The findings underscore the viability of using agricultural waste as a resource for eco-friendly agricultural practices, contributing significantly to sustainable farming and efficient land use.

Keywords: Agriculture waste; Lignocellulosic biomass, Biofertilizer; Microbial consortium

ENVM-54 (Poster)

Biocontrol Rhizobacteria Enhances the Growth and Yield of Wheat (*Triticum aestivum*) against Phytopathogenic Fungi

Poonam S. Ingle** and Ajaykumar G. Jadhav*
*akgjadhav@gmail.com, **poonamingle222@gmail.com

Department of Microbiology, Government Institute of Science, Aurangabad, Maharashtra (431004), India

Abstract: Plant growth promoting rhizobacteria (PGPR) promotes plant growth amongst them some help in survival in stressful conditions.
In present studies, plant growth-promoting rhizobacteria (PGPR) isolated from Rhizospheric soil collected from Chhatrapati Sambhajinagar, Maharashtra (19°55'00.3" N,75°18'48.1" E) W859+PM. These were characterized

for PGPR attributes are Indole acetic acid, Phosphate solubilization, Ammonia production, Zinc solubilization, and Hydrogen cyanide. Further, the antifungal potential of the bacterial isolates such as, *Pseudomonas aeruginosa, Bacillus licheniformis, Bacillus amyloliquefiens, and Streptomyces mutabilis* and evaluated for antifungal potential against phytopathogenic fungi.
The growth pattern obtained in dual culture-confirmed antifungal potential against 7 phytopathogenic fungi they are *Curvularia lunata, Chaetomium globusum, Phomopsis sp., Alternaria alternata, Fusarium oxysporum, Macrophomina phaseolina, Sclerotium rolfsii.*
The current study aimed to identify the survival of bio-control bacteria with antifungal activity against 7 different phytopathogens and assess their growth-promoting activity in wheat crop conditions.

Keywords: Plant-growth-promoting Bacteria; Phytopathogens; Wheat seeds

ENVM-55 (Poster)

Development, Optimization, and Metagenomic Study of PHE-degrading Consortia: Insight into the Functionality

Suryakant Panchal and Namita Singh*
*namitasingh71@gmail.com

[1]*Lab No. 202, Microbial Biotechnology Laboratory, Department of Bio and Nano Technology, Guru Jambheshwar University of Science and Technology, Hisar, Haryana (125001), India*

Abstract: Phenanthrene ($C_{14}H_{10}$) abbreviated as PHE, is a three-benzene ring bearing angular LMW PAH. It is used as a raw substance for the manufacturing of certain drugs, dyes, explosives, and phenanthrenequinone. It is enlisted among 16 PAHs priority pollutants by the US EPA. It is a human skin photosensitizer, a mild allergen. It is widely used as a model PAH for various research purposes due to its peculiar molecular structure with K and bay-region. This studies proved that mixed bacterial cultures e.g., bacterial consortium can efficiently biodegrade high concentration of PHE. This study depicts the comparison of species diversity of two different PHE degrading consortia NS-PAH-2015-HSR-4 & NS-PAH-2015-PNP-5 developed from petrochemical contaminated sites of the auto market, Hisar, and petrochemical contaminated sites near IOCL refinery, Panipat, respectively. Both places are approximately 120 kilometer radially apart and located in the province of Haryana (India). The 16S rRNA metagenomic analysis showed, in each consortium, phylum Proteobacteria and class Gammaproteobacteria were prominent taxa at respective taxonomic ranks. The dominating abundance of unclassified species of the genus Stenotrophomonas and unclassified species of the genus Pseudomonas in NS-PAH-2015-HSR-4 and NS-PAH-2015-PNP-5, respectively; suggested them as the key player species in PHE degradation. Shannon-Wiener index (*H'*) is a measure of species diversity in an ecological community, where its' high value denotes rich species diversity and low value denotes less diversity. The higher value of *H'* of NS-PAH-2015-HSR-4 (2.52) than NS-PAH-2015-PNP-5 (2.43) represents its more species diversity. And, it is also supported by the higher number of OTUs of NS-PAH-2015-HSR-4 than NS-PAH-2015-PNP-5. Another metric, Pielou's evenness index (*J'*) measures the evenness of species in the ecological community. A zero value of Pielou's evenness index represents no evenness, whereas a value of one represents complete evenness (Smith and Wilson 1996). The almost equal value of Pielou's evenness index (*J'*) of NS-PAH-2015-HSR-4 and NS-PAH-2015-PNP-5 (i.e., 0.44 and 0.43, respectively), represent almost same species evenness. The OTUs in NS-PAH-2015-HSR-4 and NS-PAH-2015-PNP-5 were observed 285 and 273, respectively.

Keywords: Phenanthrene; PAH; Shannon-Wiener Index; Pielou's Evenness Index; Consortium

ENVM-56 (Poster)

A Study to Enhance Algal Biomass Production through Strategic Bioprocess Optimization of Initial Inorganic Carbon Concentration, Inorganic Nitrogen Concentration and Initial Biomass Concentration

Shiba prasad Kar[*], Sumit Kumar Mondal[**] and Anirban Das Gupta[***]
*shibaprasad0625@gmail.com; **sumitmondal196@gmail.com; ***dasgupta.anirban42@gmail.com

Department of Biotechnology, The Neotia University, South 24 Parganas, West Bengal (743368), India

Abstract: One of the main driving forces for anthropogenic climate change in the twenty first century has been the over utilization of fossil fuels leading to production of greenhouses gases particularly carbon dioxide. Carbon dioxide is a source of inorganic carbon that can be captured by the action of photosynthesis by photoautotrophic organisms including microalgae. Therefore, microalgae can play a critical role in climate change mitigation by carbon capture and sequestration. Furthermore, microalgal biomass can be also used for biofuel production, a rich source of renewable energy. To this end, microalgae can be grown in the presence of bicarbonate, a source of dissolved inorganic carbon at the physiological pH of microalgae. Moreover, nitrate is a source of inorganic nitrogen which is imperative for microalgal growth and biomass production. Additionally, the inoculum size that is the initial biomass concentration also plays a critical role in biomass production. In the current study, strategic optimization tools have used to simultaneously optimize all three parameters to maximize biomass production of microalgae namely *Chlorella* sp. An optimized dose of inorganic carbon in the form of sodium bicarbonate, inorganic nitrate in the form of sodium nitrate and initial biomass concentration has been determine to obtain optimum biomass, photosynthetic pigment production, and associated growth parameters. Central composite design method has been used for optimization process in the current study.

Keywords: Microalgae; Fossil fuel; Inorganic carbon; Inorganic nitrogen; Carbon capture; Biomass

ENVM-57 (Poster)

A Study to Develop a Single Chambered Photobioreactor for Strategic Wastewater Treatment Coupled with Microalgal Biomass Production

Sumit Kumar Mondal[*], Shiba Prasad Kar[**] and Anirban Das Gupta[***]
*sumitmondal196@gmail.com; **shibaprasad0625@gmail.com; ***dasgupta.anirban42@gmail.com

Department of Biotechnology, The Neotia University, South 24 Paraganas, West Bengal (743368), India

Abstract: The over utilization and overexploitation of natural resources particularly water resources have led to widespread environmental degradation and damage to the natural ecosystems. Domestic sewage is the single largest form of waste water in the world and effective and rapid treatment of waste water is therefore the imperative need of the hour. To this end, a single chambered photobioreactor has been designed and developed in this study to treat waste water rapidly and efficiently using microalgae. Furthermore, the microalgal biomass can be harvested and used for bioenergy production. The focus of the current study has been to design and develop an effective strategy for wastewater treatment using microalgae namely *Chlorella* sp. with bench scale photobioreactors. Standard water quality parameters namely biochemical oxygen demand, dissolved oxygen, pH, fecal coliform count, ammonium concentration has been analysed to determine the rate and extent of wastewater purification. Additionally standard growth parameters including microalgal biomass production, photosynthetic pigment production have been analysed to determine the rate and extent of microalgal biomass production. The results of the study revealed after Day 6 of reactor operation, the waste water was adequately treated resulting in more than 60-70% BOD removal, more than 90% fecal coliform removal, high DO concentration and high algal biomass production. Therefore, the current study revealed that an effective integrated strategy can be developed for wastewater treatment coupled with microalgal biomass production.

Keywords: Wastewater; Microalgae; Sewage; Biochemical Oxygen Demand, Dissolved oxygen, Fecal coliform

ENVM-58 (Poster)

Comparative Study of Phytoremediation Potential and Culturable Bacterial Communities of *Cannabis sativa* and *Eleusine Indica* Growing on Distillery Sludge for Eco-Restoration of Polluted Sites

Mohd. Zobair Iqbal and Ram Chandra*
*prof.chandrabbau@gmail.com

Department of Environmental Microbiology, Babasaheb Bhimrao Ambedkar University, Lucknow, Uttar Pradesh (226025), India

Abstract: The study examines the comparative phytoremediation potential of two potential plant species, i.e., *Cannabis sativa* and *Eleusine indica*, growing on sugarcane molasses-based distillery sludge, a major source of complex organometallic pollutants. The dominant bacterial communities growing within the rhizospheric region of these plants were isolated and characterized for their PGPR attributes. Seven bacterial species were isolated from *C. sativa*, among which three potential bacterial species were characterized based on 16S rRNA sequencing, they are *Bacillus thuringenesis* (PP963487), *Bacillus cereus* (PP963486), *Burkholderia cepacia* (PP962515). Similarly, six bacterial species were isolated from *E. indica*, among which three potential bacterial species were characterized based on 16S rRNA sequencing, they are *Pseudomonas putida* (PP956925), *Bacillus subtilis* (PP956913), *Achromobacter denitrificans* (PP956932). The GC-MS analysis of fresh sludge revealed the presence of major organic compounds like Thiopene, 2-butyloctanol, Cyclodecasiloxane, Silane, Callitrisic acid, etc. In addition, the fresh sludge showed high concentrations of Iron (2356.4±0.181), Copper (856.76±0.022) Manganese (198.32±0.010) Magnesium (342.8±0.462) Calcium (359.7±0.617), etc. The sludge obtained after the growth of *C. sativa* and *E. indica* showed a reduction in physicochemical parameters. GC-MS analysis also showed the disappearance of some of the organic compounds. However, *C. sativa* showed a greater reduction in physicochemical parameters and concentration of organic contaminants and heavy metals compared to *E. indica.* The research revealed that compared to *E. indica, C. sativa* was more efficient in metal accumulation in biomass and contaminant degradation. This study's findings may be used to develop a phytoremediation tool for the eco-restoration of polluted sites.

Keywords: *Cannabis sativa; Eleusine indica;* GC-MS analysis; Rhizospheric region

ENVM-59 (Poster)

Toxicity of Pollutant-Adsorped Polyethylene Microplastics on Zooplanktons with Artemia as a Model Organism

Aiswarya, K. P., R. Karthika and S. Rajakumar
kodairaj@gmail.com

Department of Marine Biotechnology, Bharathidasan University, Tiruchirappalli, Tamil Nadu, India

Abstract: Microplastics being tiny can get incorporated into the marine food chain, through primary consumers or zooplanktons. The study conducted in *Artemia salina* a model organism for toxicity studies showed decreased hatching rate and mortality. The lethal concentration (LC50) showed lethality between 200 to 300 µl of Zinc pyrithione (ZnPt), an anti-foulant used in marine paints, in the studies conducted with microplastics, ZnPt adsorbed microplastics and ZnPt along. After 24 to 48 hrs, the Zinc pyrithione was able to kill 50% of the *Artemia salina*. The *Artemia* exposed to only polyethylene microplastics has shown comparatively lower toxicity but caused physical damage if it has been microplastics. In the experiment with combined microplastics and Zinc pyrithione, the results varied from expectation of offering higher toxic effects to lower compared with only Zinc pyrithione exposure. The reason is assumed to be the selective adsorption of ZnPt by microplastics the culture medium. *Artemia* was affected by the underdevelopment of appendages, lower motility, the collapsed digestive tract and retarded photo tacticity.

Keywaords: Microplastics, Zinc pyrithione, *Artemia salina,* Selective adsorption

ENVM-60 (Poster)

Characterization of the Lipid and Fatty Acid Composition in Marine Cyanobacteria

Selvapriya, S.*[1], G. Muralitharan[2] and S. Rajakumar[1]
priyaselvam1919@gmail.com

[1]*Department of Marine Biotechnology, Bharathidasan University, Tiruchirappalli, Tamil Nadu (620024), India*
[2]*National Facility for Marine Cyanobacteria, Bharathidasan University, Tiruchirappalli, Tamil Nadu (620024), India*

Abstract: The cyanobacterium is an oxygen-consuming, photosynthetic autotroph that is classified as a gram-negative and is one of the most common and ancient life forms. Cyanobacteria are important worldwide primary producers that provide major contributions to the biogeochemical cycles of carbon, oxygen, and nitrogen. Marine forms are superior to all other creatures in terms of their high surface-to-volume ratio, wide range of adaptation, and ease of scaling from lab to industrial size bioreactors. In addition to repository strains from the National Repository for Microalgae and Cyanobacteria (NRMC)-Marine, Bharathidasan University, Trichy, the current endeavor focuses on surveying and screening potential marine cyanobacteria from Tamil Nadu& southern east coast for improved lipid synthesis. The novel isolates were recognized by both molecular and morphological methods. A total of 27 marine cyanobacteria were screened for lipid content; of them, 17 strains were newly isolated isolates from a recent study conducted on Tamil Nadu & south east coast. Out of the 27, four marine cyanobacteria were found to have a maximum lipid content of 15% or more, making them classified as high lipid yielders. The largest amount of lipid found in 17 maritime cyanobacteria was 10%. The combined lipid, biomass productivity, and FAME Profile were investigated in the study with regard to the production of biodiesel.

Keywords: Marine Cyanobacteria, Survey and Isolation, Lipid

ENVM-61 (Poster)

Biofermentation of Human Serum Albumin using E. coli as Host and its Biotechnological Applications

Priya Payla and Ashima Sharma*
*ashimasharma@jcboseust.ac.in

Department of Life Sciences, J.C. Bose University of Science and Technology, YMCA, Faridabad, Haryana (121006)

Abstract: Human serum albumin is a 66.5kDa, globular, monomeric, single chain non-glycosylated, multidomain, heart shaped therapeutic protein having half-life of 19 days. It contains 17 disulfide bonds. It is the most abundant protein which play important role in maintaining oncotic pressure transport hormones, fatty acids and drugs etc. However, the shortage of and safety issues arises from using the plasma derived HSA. Hence, there arises the need of downstream processing of rHSA. The E. coli derived rHSA found to be equivalent to the pHSA in terms of functional, biochemical and biophysical properties. E. coli appears to be the efficient, safe and cheaper compared to the othern expression hosts. But recovery of this large protein from the E. coli is quite difficult due its production as insoluble inclusion bodies in the cytosol of E. coli. It has various biotechnological applications like drug therapeutic strategies, in cell growth and productivity, in nanotubes, bio chromatography for analysis of drug binding affinity with target molecules, used for the identification of protein markers, have good ligand binding property to transported the molecules and drugs to the target site, others are ligand trapping, fusion proteins, bioimplants, surgical adhesives. E. coli is the most convenient host for rHSA production. It is genetically and physiologically well- characterized organism which grows rapidly and reaches high cell density rate using cheaper and simpler substrates as compared to other hosts. The fermentation batch culture of E. coli is much greater than other hosts. Several physiological activities are optimized to enhance the production of functional protein. Despite of having numerous advantages, E. coli have some limitations. In the reducing environment of the cytosol of E. coli, the expressed rHSA forms aggregates which leads to inclusion bodies. It is very difficult to recover the functional protein in its native state from these inclusion bodies. The recovery of rHSA in its functional form is the multistep process. It involves production of vector containing gene of interest

using RDT and it is followed by insertion and expression of gene in E. coli cell. Then, using different techniques like chromatography, SDS gel electrophoresis, western blotting etc, the expressed protein is harvested and purified. Finally, the functional and clinical activities are checked before its use.

Keywords: Rhsa, E.coli, SDS gel electrophoresis, Western blotting

ENVM-62 (Poster)

Microbial Utilization of Fish Scales for Protease Production and Chitin Extraction

Neha Kumari* and Shashwati Ghosh Sachan
*1994nkneha@gmail.com

Department of Bioengineering and Biotechnology Birla Institute of Technology, Mesra Ranchi, Jharkhand (835215), India

Abstract: Fisheries significantly contribute to the food and pharmaceutical industries by providing essential nutrients such as protein, omega-3 fatty acids, vitamins, and minerals. However, the rapid expansion of the global fish industry, which produced 214 million tonnes in 2020 (FAO 2022), has resulted in a considerable increase in fish waste, including whole fish, scales, viscera, bones, and skin, leading to serious environmental challenges. Improper disposal of this waste in water bodies or landfills can deteriorate water quality and produce harmful leachate-containing toxic compounds that threaten aquatic life and human health. Traditional methods of fish waste degradation, such as physiochemical processes, are both expensive and environmentally harmful. In contrast, microbial degradation offers a more sustainable and cost-effective alternative. this study investigates microbial degradation as a more sustainable and cost-effective alternative. Twenty bacterial isolates were obtained from soil samples at fish waste dumping sites and employed a zero-waste approach where the broth is utilized as an enzyme source and the solid residue as crude chitin. Primary screening for protease production involved observing halo zones on skim milk agar plates and identifying 10 proteolytic isolates. These were further assessed for gelatinase activity, with 7 showing positive results. Secondary screening was performed based on protease activity. The solid residue were analysed using XRD, FESEM, EDAX, TGA, and DSC characterization of crude chitin. The bioactive products resulting from this process hold potential applications in cosmetics, food, and pharmaceutical industries, offering an environmentally friendly solution to fish waste management.

Keywords: Environment; Microbial degradation; Fish scales; Bioactive compounds; Zero waste; Untreated waste

ENVM-63 (Poster)

Unravelling Fipronil Biodegradation using *Pseudomonas* sp. FIP_A4: Multiomics Approaches

Anjali Jaiswal* and Suresh Kumar Dubey
*anjalijaiswal@bhu.ac.in

Molecular Ecology Laboratory, Department of Botany, Banaras Hindu University, Varanasi, Uttar Pradesh (221005), India

Abstract: Fipronil is a phenylpyrazole used to eradicate insects that have become resistant to conventional pesticides. Although it reduces the significant losses caused by insect attacks on agriculture, its continued use causes it to accumulate across numerous environmental niches and causes harmful consequences. One efficient bioremediation technique is the biodegradation of pesticides into less harmful compounds. This work uses multi-omics techniques to thoroughly examine the fipronil degradation kinetics and pathways in a native bacterial isolate, *Pseudomonas* sp. FIP_A4. Soil microcosm study revealed ~87% of the fipronil degradation in 40 days. The first stage of degradation can be mediated by proteins related to cytochrome P450 monooxygenase and enoyl-CoA hydratase, which share 30% sequence similarity with dehalogenase detected in the genome. Subsequent breakdown was caused by differential enzyme expression of dioxygenase, decarboxylase, and

hydratase, as demonstrated by proteome analysis. Fipronil metabolites were found in the presence of strain FIP_A4 metabolome analysis, corroborating the suggested degradation pathway. Molecular docking and molecular dynamic simulation modelling demonstrated sufficient binding and favourable stability in the complex between the enzyme and each identified metabolite. This work offers a groundbreaking report on genes/enzymes involved in the breakdown of fipronil and the formation of several metabolites during the degradation of pollutants. The results of this investigation have the potential to significantly impact the advancement of efficient techniques for the bioremediation of soil contaminated with fipronil.

Keywords: Fipronil, Soil-microcosm, Degradation pathway, Genomics, Proteomics, Metabolomics

ENVM-64 (Poster)

Isolation and Identification of Polyhydroxybutyrate (PHB) Producing Bacterial Species Isolated from Soil Samples of Ujjain

Sheeba Khan[a] and Rekha Khanna[a*]
drkhanna107@yahoo.com

[a] *Department of Zoology, Govt. Madhav Science College, Ujjain, Madhya Pradesh, India*

Abstract: Poly-3-hydroxybutyrate (PHB) is a biodegradable copolymer belonging to the polyhydroxyalkanoate (PHA) family, known to accumulate within the intracellular granules of bacteria when exposed to carbon rich and nitrogen-limiting conditions. This study aimed to isolate PHB-producing bacteria from diverse sources of Ujjain soil sample using E2 media by the serial dilution method. Confirmation of the strain's PHB production capability was conducted through Sudan Black B plate flood assay and staining. The identified colonies were transferred to E2 agar plates containing Nile Blue A for specific staining of PHA granules. Upon incubation, blue fluorescent colonies were observed under UV transilluminator, indicating positive PHB production. Subsequently, the isolated strain underwent morphological, biochemical, and molecular (16S rRNA sequencing) characterization and phylogenetic analysis identified the organism as TG1. This research underlines the significance of isolating local PHB-producing bacteria, offering potential solutions for sustainable, eco-friendly biodegradable plastic alternative to traditional, petroleum-based plastic production through microbial fermentation processes.

Keywords: Polyhydroxybutyrate, PHA, Sudan Black B, Nile Blue A, 16S rRNA sequencing, UV transilluminator

ENVM-65 (Poster)

Production of BHETase Hydrolases for Depolymerization of PET

Nishu Yadav, Prashant Kumar and Deepansh Sharma*
*deepanshsharma@gmail.com

Department of Life Sciences, J.C. Bose University of Science and Technology, YMCA, Faridabad, Haryana (121006)

Abstract: One of the most used plastics is PET, a hydrolysable C-O polymers that make up the spine. PET accounts for 9-10% of plastic produced globally, with an annual production of 70 million tons. Reusing plastic is essential to reduce resource depletion and substituting environmentally harmful practices in the establishment of a clean and sustainable plastic economy. Plastic degrading microbes have opened up new avenues for biotechnological plastic degradation and bio-upcycling. PET trash can be managed alternatively through the biosynthesis of reclaimed monomers, such as ethylene glycol (EG) and terephthalic acid (TPA) by microbial depolymerization of PET, resulting in reduced emission of CO2. Hydrolytic microbes and enzymes are well known for degradation of PET to bis(2-hydroxyethyl) terephthalate (BHET) and mono(2-hydroxyethyl) terephthalate (MHET) using PETase, cutinase, esterase, carboxylesterase, while BHET and MHET can be further degraded to TPA and ethyl glycol. Using compost soil samples from different locations, bacteria were isolated and screened for BHETase hydrolases activity. The identification was done using 16SrDNA gene

sequence analysis using search tool BLAST. The alignment results of the 16S rDNA sequences showed that strain DSP1 is a member of genus *Pseudomonas*; Strain DSP2 is a member of the genus *Bacillus* and DSP3 is a member of the genus *Stenotrophomonas* and DSP3 formed a consistent cluster with *Stenotrophomonas* sp. CanR-49. (Accession no: KT580655.1; similarity 98%).

Keywords: BHETase, MHETase, Bioremediation, De-Polymerization, Cutinases

ENVM-66 (Poster)

Phenotypic and Genetic Insights into ESBLs, Carbapenemase-Producing, and Biofilm-Forming Gram-negative Bacteria in the Hospital and Domestic Wastewater of Aligarh City

Nikita Chaudhary* and Iqbal Ahmad**
*nikitachaudhary20014@gmail.com, **ahmadiqbal8@yahoo.co.in,

Department of Agricultural Microbiology, Faculty of Agricultural Sciences, Aligarh Muslim University, Uttar Pradesh (202002) India

Abstract: This study focuses on identification and characterization of Gram-negative bacteria isolated from the hospital and domestic wastewater samples in Aligarh city, with emphasis on biofilm-forming ESBLs and metallo-beta-lactamases (MBLs) producers.

A total of 117 bacterial isolates were obtained using nutrient agar, EMB and SS agar medium. AST by disc diffusion was conducted to evaluate resistance profiles. Phenotypic and PCR-based method, were used for detection of ESBL, Carbapenamase, and MBLs production/genes. Biofilm structures of strong biofilm formers were visualized using SEM and CLSM. MIC of biofilm-forming ESBL-producing isolates against selected antimicrobials (ampicillin, cefotaxime, ceftazidime, cefepime, and meropenem) was determined using standard guidelines. Further, the production of MBLs was assessed through mCIM/eCIM method. P.C.R was employed to detect resistance genes, NDM-1 and SHV genes and those bearing NDM and SHV genes, were identified by partial 16S rRNA gene sequence analysis.

Results revealed (92.30%) of strains were resistant to multiple drugs (≥3). Highest resistance was against ampicillin (100%) followed by ceftazidime (68.37%), cefotaxime (67.50%) and lowest against gentamicin (12.82%). Of MDR strains, 64.10% demonstrated moderate to strong biofilm formation while 35.89% were weak biofilm formers. β-lactamases activity was observed in 58.97% of isolates due to ampicillin production. Among β-lactamase-positive strains, 56.41% were ESBL positives. The MIC analysis exhibited high resistance levels towards ampicillin and β-lactam antibiotics(8≥1024µg/ml). PCR-based detection of genes revealed 8(53.33%) SHV and 9(60%) NDM-1 genes in the selected MDR isolates. Isolates were tentatively identified as E coli (37.60%), Klebsiella (14.52%), Citrobacter (4.27%), Pseudomonas (7.69%), Salmonella (10.25%), Shigella (18.80%) and Proteus (6.83%). Selected 09 MDR strains were confirmed as E. coli (06), Klebsiella pneumoniae (01), Pseudomonas aeruginosa (01), Salmonella sp(01), Shigella sp,(03), Citrobacter sp(01) and Proteus sp(01) by partial 16SrRNA gene sequence analysis.

This study highlights alarming prevalence of ESBL, MBL-producing and biofilm-forming Gram-negative bacteria in hospital and sewage /wastewater of Aligarh. These findings emphasize need for stringent wastewater treatment and monitoring strategies to mitigate the risk posed by MDR bacterial pathogens.

Keyboard: MDR bacterial pathogens, 16S rRNA gene sequence analysis, Carbapenamase, β-lactamase-positive strains

ENVM-67 (Poster)

Computational Screening of Photoprotective Compounds from Polar Psychrophilic Cyanobacteria

Vinotha K[1,2*], Rajakumar S[2], Muralitharan G[1] and D. Prabaharan[1,2]
*microvino95@gmail.com

[1]*National Repository for Microalgae and Cyanobacteria (NRMC- Marine), Bharathidasan University, Tiruchirappalli, Tamil Nadu (620024), India*
[2]*Department of Marine Biotechnology, Bharathidasan University, Tiruchirappalli, Tamil Nadu (620024), India*

Abstract: The cyanobacterial existence in diverse ecological niches from polar to desert climate is due to the structural diversification coupled with metabolism and environmental plasticity. This study evaluates the Arctic and Antarctic psychrophilic strains and the metabolic properties. Vulnerability of sunlight is a deleterious ecological factor, which is damaging to be photosynthetic systems of cyanobacteria. Copious facts have demonstrated that UV radiation is harmful to cyanobacteria. This prokaryotic photosynthetic, ubiquitous organism is an immense source of photoprotective compounds. Six strains from National Repository for Microalgae and Cyanobacteria, were screened for the UV-absorbing pigments namely, mycosporine like amino acids (MAAs) and lipid soluble pigment Scytonemin. On the whole, 20 target ligand were docked on the active site of the protein which is responsible for melanoma cancer to elucidate the binding affinity. Finally, two drug targets showed a better binding score when compared with Dabrafenib Mesylate (-10.4 kcalmol^{-1}) the known inhibitor for the melanoma cancer. These findings may develop a photoprotective compound from cyanobacteria as early anti-cancer drug therapeutics. Skin sensitivity and permeability of selected photoprotective compounds emphasize applicability in sunscreen formulation. With rising demand for natural sunscreens, polar prokaryotes serve as a rich source of photoprotective agents. Beyond its ecological role as sunscreens, MAAs have potential applications in cosmetics as UV blockers, cell proliferation activators and therapeutic agents, making them valuable for commercial use.

Keywords: Psychrophiles, Cyanobacteria, UV-B radiation, Mycosporine-like amino acid, Scytonemin, HPLC, Docking, ADMET properties

ENVM-68 (Poster)

Isolation and Characterization of Cadmium Tolerant Plant Growth Promoting Rhizobacteria

Shreya Verma and Manishi Tripathi*
*manishitripathi@csjmu.ac.in

Department of Microbiology, School of Life sciences and Biotechnology, CSJM University Kanpur, Uttar Pradesh (208024), India

Abstract: Heavy metal contaminations are major environmental issues which directly obstruct the global plant production. Among metals, cadmium is top most toxic heavy metal possess threat to food chain safety and human health. Prior causes of cadmium stocking in the soils are mining, industrial emissions, burning of fossil fuels and others. Their uptake in plant resists them by inhibiting the fixation of carbon and photosynthetic activities. Therefore, the present study was carried out to isolate, identify, and characterize the Cd-resistant bacteria stains from the contaminated soils of agricultural fields near thermal power of Tanda Ambedkarnagar, Uttar Pradesh. Twenty-one bacterial strains were isolated and were screened for Cd resistance. The tolerant strains RRS-1, RRS-2, RRS-4, RRS-5, RRS-6, RRS-7 and SRL-3 were grown on Nutrient Agar plate supplemented with Cd as Cadmium chloride stock ranging between 50 µg ml-^{1} to 1000 µg ml-^{1} . The results showed that the strains RRS-1, RRS-2, and RRS-4 are capable to grow invitro up to 1000 µg Cd ml-^{1} , whereas RRS-5, RRS-6, RRS-7 and SRL-3 can grow up to 600 µg Cd ml-^{1}. Based on morphological, biochemical, and molecular characteristics RRS-4 was identified as *Pseudomonas Aeruginosa* CS-17. This strain also showed plant growth-promoting (PGP) characteristics such as the production of Siderophore, IAA, HCN, Ammonia, Phosphate solubilization etc. PGP traits of isolated Cd resistant rhizobacterial strain indicated the strains could be useful as potential phytostimulators, biofertilizers, and stress ameliorators in achieving sustainable

agriculture. The identified Cd-resistant bacterial strain may be used to develop bacterial consortia for the remediation of heavy metal contaminated soil.

Keywords: PGPR, Heavy metal, Rhizobacteria

ENVM-69 (Poster)

Phycoremediation and Lipid Synthesis Using Marine Microalgae: Exploring Mixotrophic Growth with Diverse Carbon Sources and Effluent Waters

Vivek, N[1,2*], K. Nitharsan[1], D. Prabaharan[1], L. Uma[1], G. Muralitharan[1,3] and T. Sivasudha[2]
*vivek.n@bdu.ac.in

[1] *National Repository for Microalgae and Cyanobacteria - Fresh Water & Marine (NRMC – F & M), Bharathidasan University, Tiruchirappalli, Tamil Nadu (620024), India*
[2]*Department of Environmental Biotechnology, Bharathidasan University, Tiruchirappalli, Tamil Nadu (620024), India*
[3]*Department of Microbiology, Bharathidasan University, Tiruchirappalli, Tamil Nadu (620024), India*

Abstract: Microalgae, as eukaryotic photosynthetic organisms, exhibit diverse applications in wastewater treatment, phytoremediation, lipid production and CO_2 sequestration, offering significant environmental benefits. The rapid growth and adaptability make microalgae suitable for addressing various environmental challenges. This study investigates the mixotrophic growth and lipid production of two marine microalgae strains, *Chlorella vulgaris* BDUG 91771 and *Picochlorum* sp. BDUG 100241, using different carbon sources at 10mM concentration (glucose, sucrose, sodium acetate, glycerol, ethanol and sodium bicarbonate) and effluent waters diluted with sea water (ossein effluent, sugarcane molasses effluent). In the strain *Chlorella vulgaris* BDUG 91771, glucose proved to be an excellent carbon source for enhanced biomass, pigments, and protein production, while *Picochlorum* sp. BDUG 100241 showed effective growth and enhanced metabolite production with glycerol as the carbon source. Cultivating the above strains in ASN III medium with various carbon sources and effluent dilutions (10%, 25%, 50%, 75%), and biomass production, lipid yield, and the effectiveness of effluent utilization for phycoremediation and biofuel production were assessed. The non-sterile effluents at lower dilutions resulted in a notable 10% increase in lipid production compared to the control. The results demonstrate that non-sterile effluents, particularly at lower dilutions, can significantly enhance lipid production while maintaining high biomass yields. The integrated approach of using microalgae for effluent treatment and biofuel production not only supports environmental remediation but also promotes sustainable bioenergy generation. The results highlight the potential of marine microalgae as a viable candidate for next-generation renewable energy solutions

Keywords: Phycoremediation, Marine microalgae, *Chlorella vulgaris, Picochlorum* sp

ENVM-70 (Poster)

A Study on Prevalence of Resistance Genes and Pathogenicity Markers among ESBL Producing *Enterobacteriaceae* Focusing *Klebsiella pneumoniae*

Vikar Ahmed, Syed Ahmed Rizvi and Qazi Mohd Rizwanul Haq*
*qhaque@jmi.ac.in

Department of Biosciences, Jamia Millia Islamia, New Delhi, India

Abstract: Excessive use of antimicrobials in healthcare and agriculture has led to the development of antimicrobial resistance, a serious global health issue. Drug resistant *K. pneumoniae* is one of the leading urinary tract infections (UTIs) causing pathogen. This present study highlighted the high prevalence of multidrug resistance genes among ESBL producing bacterial isolates focusing *Klebsiella pneumonia* from different aquatic environments in Delhi NCR, India. The collected samples were spread on amoxicillin-clavulanic acid (2:1) amended Klebsiella-Selective Agar Base plates for the selection of resistant *Klebsiella*

pneumoniae followed by preliminary phenotypic testing through Kirby-Bauer's disc diffusion test. Out of total 178 bacterial isolates, 119 were found to be resistant for amoxicillin-clavulanic acid (AMC 20/10 µg/ml) and phenotypic resistant bacteria were further streaked on EMB agar plates and 56 bacteria displaying green metallic sheen were neglected. The remaining non-metallic sheen bacterial isolates were processed for MALDI-TOF MS based identification and 33, 17, 7 and 3 were confirmed to be *Klebsiella pneumonia, E. coli, Citrobacter freundii,* and *Enterobacter hormaechei* respectively. A single isolate of each *Enterobacter bugendensis, Enterobacter kobii and Hafnia alvei* were also detected. Furthermore, the identified isolates were screened for Extended spectrum β-lactamase (ESBL) production by phenotypic disc confirmatory test (PDCT) and 28 were found to be ESBL positive. Molecular analysis of ESBL positive isolates through PCR based amplification showed the presence of *bla*CTX-M, *bla*TEM, *bla*SHV, *bla*NDM-1, *bla*OXA-48 like, *bla*CMY in 17, 28, 19, 17, 18 and 20 isolates respectively. Moreover, other resistance genes such as *qnrA, qnrB, qnrS, tetA* and *tetB,* mobile genetic elements (*intI-1, intI-2* and *sul-1)* and virulence associated genes (*fimH, iuc, mrkD,* and *ecpA)* were also detected.

Key words: Aquatic environment, ESBL, MALDI-TOF MS, *K. pneumonia,* PCR, *bla*CTX-M, Virulence genes

ENVM-71 (Poster)

Sample Preparation Strategies for Extraction of Microbial Protein from Diverse Environmental and Clinical Matrices for Downstream Proteomic Analysis

Veer Vikram Prakash* and Syed Imteyaz Alam
*vikram.cimap20a@acsir.res.in

Biotechnology Division, Defence Research and Development Establishment, Gwalior, Madhya Pradesh, India

Abstract: Pathogens and toxins are known to be detrimental for human health since time immemorial. Possible nefarious applications of some of these infectious agents and toxins have gained prominence in the recent past. The accurate identification and characterization of biological agent from a wide range of complex matrices, which includes those from the environmental and clinical settings, are necessary for the mitigation of biological emergency and implementation of relevant medical countermeasures. One of the major confounding elements in the identification of such microbes is the complexity of environmental and clinical samples with an array of interfering substances and inhibitors for downstream assay. Efficiency of bacterial protein extraction from these complex milieus (e.g. soil, sand, surface, body fluids etc.) is likely to improve pathogen identification and characterisation using downstream proteomic technologies.

Here, we describe methods for extraction of bacterial protein from non- proteinaceous (glass, plastic, metal, wood laminate, talcum powder and sand) and proteinaceous (plasma and blood) matrices spiked with bacterial agent for intended downstream mass spectrometry based analysis. Optimised methods for total bacterial protein extraction from these diverse matrices, was used to determine expected LOD for downstream proteomic analysis. In order to address scenario-centric challenges, effect of environmental conditions (time lapse, temperature, humidity, sunlight) on recovery of total bacterial protein from surfaces spiked with bacterial agent was also studied. Surface swabbing from different surfaces was analysed for comparison of swab types and surfaces with respect to efficiency of protein extraction. In-matrix lysis was found to yield more protein from sand and talcum powder.

The bacterial protein extraction methodologies optimised here for diverse matrices and the effect of environmental parameters on extraction efficiency provide insight for developing verification methodologies in biological emergencies.

Keywords: Sample preparation, Protein extraction, Bacterial pathogens, Proteomic analysis, Biodefence, Bioverification

ENVM-72 (Poster)

Indigenous Microbial Isolation for Chlorpyrifos Remediation of Contaminated Field Soils of Parbhani, Maharashtra

Sandeep Kumar Singh[1*], Livleen Shukla[1**], Suaad Khadeeja[1], Brijesh Kumar Mishra[1], Aravindharajan S.T.M[1], Vijayashree D[1], Dolamani Amat[1] and Ajay Kumar[2]
*sandeepksingh015@gmail.com; **lshukla65@gmail.com

[1]Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi (110012), India
[2]Amity Institute of Biotechnology, Amity University, Noida, Uttar Pradesh (201313), India

Abstract: Chlorpyrifos (O,O-diethyl O-3,5,6-trichloro-2-pyridyl phosphorothioate), a widely used organophosphate pesticide, poses significant environmental challenges due to its persistence in soil and potential toxic effects on non-target organisms, ecosystems, and human health. The half-life of chlorpyrifos, commonly referred to as DT50, can range from weeks to several months, depending on environmental conditions such as temperature, soil type, and microbial activity. This extended persistence raises concerns about soil and water contamination, as well as bioaccumulation in food chains. Bioremediation, a process that utilizes microorganisms to degrade harmful contaminants, has emerged as a promising solution to mitigate chlorpyrifos contamination in soil. Through natural microbial processes, specific bacteria, fungi, and other microorganisms metabolize chlorpyrifos into less non-toxic compounds. This approach is environmentally friendly, cost-effective, and sustainable compared to traditional chemical or physical remediation techniques. The success of bioremediation is influenced by various factors, including microbial diversity, environmental conditions, and the presence of nutrients. Optimizing these factors can significantly reduce the DT50 of chlorpyrifos in soil, accelerating the degradation process and minimizing its ecological impact. The current study aimed to identify possible microorganisms from highly contaminated soil collected from Maharashtra as potential bioremediation agents of pesticide residues. Total 20 bacterial and 38 fungal species isolated from chlorpyrifos contaminated soil by enrichment culture technique. The growth response and degradation of chlorpyrifos by the isolates in MSM broth supplemented with 0.25-1.0% chlorpyrifos was monitored periodically upto 30 days of incubation. The course of the degradation process was studied using high-performance liquid chromatography. The results showed that the chlorpyrifos degrading fungal and bacterial strain had the potential to degrade the pesticide-contaminated agricultural soils even without addition of nutrients. The remediation of chlorpyrifos represents a critical step towards sustainable land management, enabling the detoxification of contaminated soils while preserving ecosystem health and reducing risks to human populations.

Keywords: Chlorpyrifos, Remediation, Pesticide, Degradation process, Contaminated soil

ENVM-73 (Poster)

Streptomyces Mediated Synthesis of Silver Chitosan Nanocomposite for Antibiofilm Applications

Subhransu Sekhar Behera**, Smaranika Pradhan*,** Seemon Giri, Pratyush Kumar Behera, Zahra Parwez and Lopamudra Ray
*smaranikapradhan710@gmail.com

Abstract: The green synthesis of chitosan-silver nanocomposites (CS-AgNC) represents a promising approach in nanobiotechnology, emphasizing eco-friendly production and multifunctional applications. This study details the green synthesis of silver nanoparticles (AgNp) using a sustainable method with *Streptomyces griseoincarnatus* RB7AG. These AgNp were subsequently integrated with chitosan to create a chitosan-silver nanocomposite (CS-AgNp), with its properties characterized by UV-visible spectroscopy and dynamic light scattering (DLS). UV-visible spectroscopy confirmed the successful synthesis of the nanocomposite, while DLS provided insights into its size distribution and stability. The antibiofilm potential of CS-AgNp was assessed against mixed bacterial biofilms of *Staphylococcus aureus* and *Escherichia coli*. Notably, at the highest concentration tested (300 µL/mL), CS-AgNp exhibited significant antibiofilm activity, markedly reducing biofilm metabolic activity. This was further validated by fluorescence imaging, which visually confirmed the diminished biofilm formation. These results highlight the potential of CS-AgNp as a potent antimicrobial agent against mixed bacterial biofilms, with important implications for treating biofilm-associated infections.

Additionally, the mechanistic insights into its antibiofilm action lay the foundation for future research on innovative antimicrobial strategies.

Keywords: Antimicrobial, Biofilm, *E. coli*, Green synthesis, Silver-chitosan nanocomposite, *Staphylococcus aureus*

ENVM-74 (Poster)

Chitosan as a Dietary Supplement: Evaluating its Effects on Zebrafish Physiology and Development

Zahra Parwez, Subhransu Sekhar Behera, Seemon Giri, Pratyush Kumar Behera, Smaranika Pradhan and Lopamudra Ray
zahra.parwez@gmail.com

Abstract: In this study, zebrafish (*Danio rerio*) are used to examine the effects of varying doses of chitosan on innate immunity parameters, immune-related gene expression, and growth performance. 50 fish with a mean weight of 1.25 ± 0.1 g were provided and randomized to be put in five aquariums with five distinct treatments. For 12 weeks, zebrafish were given either a control diet or a control diet supplemented with varying feed i.e. Control (only fish feed), synthesized chitosan, commercial chitosan, Synthesized chitosan + fish feed; commercial chitosan + fish feed. After the feeding trial, growth performance, immune-related gene expression (interleukin 1 beta [il1b], Lysozyme [lyz], tumor necrosis factor-alpha [tnf-alpha]), and innate immunological markers (total immunoglobulin, total protein, and alkaline phosphatase activity) were assessed. Examining immunological markers in zebrafish given synthesized chitosan + fish feed showed a significant ($P < .05$) increase in weight gain, total protein, and total Ig compared to other treatments. According to gene expression studies, the same fish group showed a considerable elevation ($P < .05$) of the lyz and tnf-alpha genes but no significant improvement in iL-1 expression. The current findings showed that chitosan doesn't have any beneficial effects on its own but when combined with fish feed, the diet then benefits zebrafish innate immunity parameters and associated gene expression.

Keywords: Chitosan, Fish feed, Gene expression, Growth, Immunity, Zebrafish

ENVM-75 (Poster)

Evaluating Biogas Production Potential of Cattle Dung Supplemented with Tea Waste under Batch Digestion

Mansi Phogat, Shikha Mehta, Kamla Malik, Pragati and Raj Bala
*mansiphogat1999@gmail.com

Department of Microbiology, COBS&H, CCS Haryana Agricultural University, Hisar, Haryana (125004), India

Abstract: The development and utilization of renewable energy resources have become fundamental components of sustainable global energy policies in an effort to limit the usage of fossil fuels. Renewable energy sources include biomass such as plant and animal materials, biodegradable municipal waste, kitchen waste, agricultural residue and energy crops. Tea is one of the most consumed plant-based beverages in the world. On an estimation, 18-20 billion cups of tea are consumed daily around the world which results into tremendous tea waste production. If the waste is not degraded properly, it can leach into water bodies causing pollution. So, recycling techniques such as composting, fermentation, silage production and anaerobic digestion can be used for bioconversion of tea waste into valuable products. In the present study, biogas production from tea waste and cattle dung was studied under laboratory conditions by making several combinations (T1-T8). Maximum weekly biogas production was observed in treatment – T7 (Cattle dung + tea waste @ 30%) with a range of 4.5 to 19.9 liters/week followed by treatment – T8 (Cattle dung + tea waste @ 35%) in which weekly biogas production was found in the range of 4.4 to 19.7 litres/week. Similarly, maximum cumulative biogas production (93.4 litres) was observed in treatment – T7 (Cattle dung + tea waste @ 30%) under batch digestion. Thus, utilizing tea waste to produce valuable products presents a compelling example for effective waste management

which also promotes sustainable economic growth, thereby unlocking both environmental and economic benefits.

Keywords: Anaerobic digestion, Biogas, Cattle dung, Renewable energy, Tea waste

ENVM-76 (Poster)

Microbial Enrichment of Press Mud as Valuable Bio Manure and Rooting Media for Sugarcane

Akshaya A
akshayaarulazhagan2000@gmail.com

Tamilnadu Agricultural University, Tamil Nadu, India

Abstract: Press mud (PM), a by-product of alcohol distillation from the fermentation of sugar cane molasses, poses challenges due to its large production volume and high organic matter content, making it unsuitable for direct disposal into water bodies or lands. Therefore, there is a need to treat PM microbially to transform into usable manure by reducing its heavy metal toxicity and make it to fit for crop cultivation. A pot culture experiment was conducted to nutritionally enrich the decomposed pressmud (DPM) with liquid formulation of four different Microbial inoculants consortia developed using the standard bioinoculants viz., *Azospirillum brasilense, Azotobacter chrococcum, Bacillus megatherium* (PSB), *Pseudomonas chlororaphis* (ZSB), *Paenibacillus mucilaginosus* (KRB) along with native yeast from spent wash.Findings revealed that microbial inoculants consortia MC2 (Azospirillum + PSB+ ZSB+ KRB+ Spent yeast) enriched pressmud (EPM) showed highest level of all nutrients in the decomposed pressmud i.e. nitrogen, potassium and phosphorous level increased twice and thrice from the initial level. Additionally, microbial enrichment positively influenced the levels of the secondary nutrients also namely, the Ca, Mg, and other micronutrients while slightly reducing heavy metal concentrations. The pH is not affected by enrichment of pressmud and electrical conductivity (EC) decreased over time, indicating successful enrichment fit for using as manure. The population load of the microbial inoculants recorded ranged 10^6 to 10^8 per g from Initial to final stage of the enrichment period. This enhanced microbial activity accelerated the nutrient levels. Hence, the microbial consortium MC2 proved to be highly effective in enriching the nutrient status of the decomposed press mud and to use as bio manure for crop cultivation. In addition, this MC2 consortia enriched pressmud also showed comparatively better performance as rooting media for germination of sugarcane bud under portray nursery condition tested along with sand and composted coirpith recorded 92 % and 85 % germination respectively. This study underscores the importance of selecting appropriate rooting media to maximize germination success. Sand is often more readily available and cheaper than composted coir pith, reducing input costs for farmers. Additionally, using Soil + EPM (enriched pressmud) not only enhances germination but also improves soil fertility, potentially lowering the cost on chemcical fertilizers, thus making a cost-effective and sustainable alternative.

Keywords: *Azospirillum brasilense, Azotobacter chrococcum, Bacillus megatherium* (PSB), *Pseudomonas chlororaphis* (ZSB), *Paenibacillus mucilaginosus* (KRB), Enriched pressmud

ENVM-77 (Poster)

Genomic Insights and Taguchi-Based Optimization of Culture Conditions for Enhanced Alkaline Protease Production by *Streptomyces barkulensis* RC1831

Pratyush Kumar Behera*, Zahra Parwez, Seemon Giri, Subhransu Sekhar Behera, Suchismita Nivedita, Ananta Narayana Panda, Himadri Tanaya Behera and Lopamudra Ray
*pratyushbehera80@gmail.com

School of Biotechnology, KIIT Deemed to be University, Bhubaneswar, Odisha, India

Abstract: This study presents whole genome sequence (WGS) analysis of *Streptomyces barkulensis* RC1831 for identification of various alkaline protease genes. The culture conditions were optimized for enhanced production

of alkaline protease (AP) enzyme by RC1831. The WGS analysis was carried out by bio informatics tools such as RAST, KEGG, KAAS, and BLASTx. It revealed the presence of 10 genes that are responsible for the enzyme production. Multiple sequence alignment showed a high sequence identity with M24 family serine protease followed by subtilisin-like serine protease. Optimum conditions for enhanced protease production were 37°C, pH 11, casein 1% (W/V), dextrose 0.5% (W/V), urea 0.5% (W/V), tryptophan 1% (W/V), 1mM Mn^{+2}, Tween-80 1% (V/V) in LB medium and an incubation time of 72 hours. Out of the 10 alkaline protease genes, 2 genes expressed significantly according to the activity observed during optimization processes i.e., M24 family, Mn^{+2} dependent metalloprotease and Ca^{+2} dependent subtilisin-like serine protease. Furthermore, the AP enzyme was remarkably stable in the presence of various cofactors (Metal ions) and surfactants, indicating its potential for industrial applications under diverse conditions.

Keywords: *Streptomyces* RC1831, Alkaline protease, Industries, Whole genome, Optimization, Taguchi method

ENVM-78 (Poster)

Unveiling the PHA Production Potential of *Streptomyces* Species: Screening, Optimization, and Molecular Characterization

Seemon Giri*, Pratyush Kumar Behera, Zahra Parwez, Smaranika Pradhan, Subhransu Sekhar Behera and Lopamudra Ray
*giriseemon@gmail.com

Abstract: Polyhydroxyalkanoates (PHAs) are a group of biodegradable polymers synthesized by various microorganisms to serve as intracellular energy storage compounds. Due to rising environmental concerns associated with petroleum-based plastics, PHAs have attracted significant attention as a sustainable alternative. Bacteria such as *Ralstonia eutropha* and *Pseudomonas* species are well-studied and commercially utilized for PHA production. However, the genus *Streptomyces*, traditionally recognized for its extensive production of antibiotics and other secondary metabolites, has recently emerged as a promising but relatively underexplored candidate for PHA biosynthesis. In this study, 20 *Streptomyces* isolates were obtained from soil sediments collected from Chilika Lake in Odisha, India, and were qualitatively screened for polyhydroxybutyrate (PHB) production using a medium containing Sudan Black B stain. Among the 20 isolates, *Streptomyces chitinivorans* (RC1832), identified through 16S rRNA sequencing, was the highest PHB producer, outperforming other positive isolates. The optimized conditions such as temp (37℃), pH (7.5), carbon (Sucrose), and nitrogen source (wheat bran) significantly influence PHA yield as simple carbon sources are easily metabolized by *Streptomyces*, leading to higher PHA yields, and also nitrogen limitation triggers the redirection of carbon flux towards storage compounds like PHAs whereas complex substrates require specific enzymatic breakdown before utilization. Under optimized conditions, the RC1832 strain produced 2.408 g/L of PHA. The purity and molecular weight of the extracted PHAs were typically assessed using Fourier-transform infrared (FTIR) spectroscopy

Keywords: Biodegradable polymers, Characterization, Microbial biosynthesis, Optimization, Polyhydroxyalkanoates (PHAs), *Streptomyces*

ENVM-79 (Poster)

Biodegradation of Pesticides and Bioremoval of Heavy Metals: A Metagenomic Approach

Singh T[1]*, Kumari S[1], Phogat A[1], Gohel S[2], Prasad R[1] and Banerjee A[1]
*aks.tanvi28@gmail.com

[1]*Amity Institute of Biotechnology, Amity University Haryana (122413), India*
[2] *Saurashtra University, Rajkot, Gujarat (360005), India*

Abstract: Bioremediation is an eco-friendly approach to mitigate environmental pollution caused by hazardous substances such as pesticides and heavy metals. This study focuses on the bioremediation of chlorpyrifos, a widely used organophosphate pesticide, and the bioremoval of heavy metals, emphasizing microbial and

phytoremediation techniques.Sampling, isolation and screening for pesticide degrading and heavy metal removal micro-organism. Understanding the mechanism involved in the degradation of pesticide and heavy metals. Detection and characterization of bacterial enzymes involved in the degradation of chlorpyrifos and bio removal of heavy metal that is chromium, magnesium, and iron. Metagenomic study of enzymatic activity of bacterial strain once we get novel strain for bioremediation process.
Screening for microbe which can uptake heavy metals consortia and chlorpyrifos. Serial dilutions of the sample were carried out ranging from concentration of 10-3 to 10-5 concentration in sterile distilled water. The concentrations 10-4 were spread plated onto sterile Nutrient agar plates supplemented with 100 ppm of chromium, iron, magnesium and chlorpyrifos each, these plates were then incubated for 24 hours at room temperature to obtain colonies of organisms that could be potentially degrading. Morphologically distinct colonies were further purified.
MTC (maximum tolerance concentration): Gradual increase in ppm from 500 to 2000 ppm by plate assay of both heavy metal and pesticide to check that upto concentration can the organism isolated can uptake the toxic mixture. Once the MTC via plate and tube broth method was done it was observed isolate 9 showed the best growth. Morphological and Biochemical Analysis was performed to identify the bacteria. FTIR, GCMS and ICPMS analysis has been completed. Results will be obtained shortly. After confirmation of degradation by analytical method 16sRrna will be proceeded for identification of bacteria.
This study is to isolate the potential microorganisms from the heavily contaminated soils from dump-site for pesticide and heavy metals bioremediation.

Keywords: Pesticides, Heavy Metals, Microbial bioremediation

ENVM-80 (Poster)

Prevalence of Antibiotic Resistance among Enteric Bacteria Isolated from Industrial Wastewater in Aligarh City

Zia Islam*, Shirjeel Ahmad Siddiqui, Iqbal Ahmad
*ziaislam919@gmail.com

Department of Agricultural Microbiology, Faculty of Agricultural Sciences, Aligarh Muslim University, Aligarh, Uttar Pradesh (202002), India

Abstract: The emergence and spread of antibiotic-resistant bacteria in the environment through poorly treated wastewater is a potential threat to human and animal health. Analysis of antibiotic-resistant pathogenic bacteria circulating in the local environment requires continuous monitoring. The present study aims to determine the prevalence of antibiotic-resistant enteric bacteria from wastewater discharge in the drainage of meat and lock industries in Aligarh city. UP.Wastewater samples were collected from Jan to March 2024. The viable bacterial count on EMB agar varies from 2.3 x 10^4 (CFU/mL) to 7.9 x 10^5 (CFU/mL). Lactose fermenting and non-fermenting colonies were randomly selected from each sample plate and subjected to antibiotic resistance profiling using standard methods. A total of 70 isolates bacterial isolates were tested for drug susceptibility, the maximum incidence of resistance was observed against vancomycin (82.57%) followed by ampicillin, colistin, tetracycline, erythromycin, sulfadiazine, cefixime, cefazolin, aztreonam, ceftazidime, cefepime, imipenem, streptomycin, and least resistance was observed against prulifloxacin (5.71%). Among 30 MDR strains phenotypic detection of ESBL production was recorded among 56% of the isolates while only 13.3% of isolates could produce carbapenemases. These MDR isolates developed strong biofilms *in vitro* on 96-well microtiter plates indicating intrinsic ability to tolerate antibiotics and survive under stress environments.
The preliminary investigation of wastewater findings demands the proper treatment of wastewater before releasing it into the environment. Further, these MDR strains can easily spread resistance genes to other bacteria and may be transmitted to humans through various ecological modes of transmission.

Keywords: Antibiotic Resistance, Industries, Wastewater, Biofilm

ENVM-81 (Poster)

Microalgae-Bioenzyme Formulation: A Revolutionary Solution for Wastewater Treatment

Sukhmanjot Kaur[1*], and Urmila Gupta Phutela[1,2]
*skaurghatoura@gmail.com

[1]*Department of Microbiology, PAU Ludhiana, Punjab (141004), India*
[2]*Department of Renewable Energy Engineering, PAU Ludhiana, Punjab (141004), India*

Abstract: Due to the critical issue of water resource depletion, wastewater treatment is indispensable for the well-being of all living beings. Conventional wastewater treatment facilities, due to their high energy consumption and significant cost in construction and operation, pose a challenge, especially in lower-middle-income countries. The present research is dedicated to the physicochemical and microbiological characterization of wastewater, coupled with biological treatment involving a microalgae (*Spirulina platensis*)-bioenzyme formulation to elevate water quality. A revolutionary microalgae-bioenzyme-based formulation solution has been devised for the economical and eco-friendly remediation of domestic wastewater. Wastewater analysed from the oxidation pond of Punjab Agricultural University, Ludhiana and treated with varying concentrations of microalgae, bioenzyme, and their combinations (ranging from 2.5% to 5% v/v). The efficacy of these formulations was evaluated by collecting wastewater at 5 days intervals for 30 days. Results indicate that the microalgae-bioenzyme (2.5%) formulation treatment resulted in a more substantial reduction in BOD (70%), COD (35%), pH (13%), and Electrical conductivity (29%) of the wastewater. However, reduction of Heavy Metals also observed viz. Lead, Selenium, Zinc, Sodium, Phosphorus, Magnesium, Iron. Additionally, the microalgae-bioenzyme (2.5%) formulation exhibited the maximum reduction in wastewater parameters and heavy metal concentration, showcasing its increased efficiency in wastewater treatment, and paving the way for potential utilization in irrigation and domestic activities.

Keywords: Bioremediation, Wastewater, Microalgae, Bioenzyme, Heavy metals, Irrigation

ENVM-82 (Poster)

Assessment of Low-Density Polyethylene Degrading Efficiency of Selected Indigenous Bacterial Isolates from Polluted Soil and Standardization of Physiological Condition for its Biodegradation

Rahul Khatik[*] and Afuwale C.D.
*khatikrahulrahul@gmail.com

P.G. Dept. of Microbiology, Smt. S. M. Panchal Science College, Talod, Gujarat, India

Abstract: Low-density polyethylene (L.D.P.E.) is highly recalcitrant and is accumulated fast in environment due to two reasons. First is it's high production and use second is it's resistance to degradation. This study focuses on the biodegradation of LDPE strips with the help of indigenous bacterial strains, isolated from dumping sites having polyethylene polluted soil. The initial isolation, screening and enrichment was done by using mineral salt medium (MSM) with LDPE as sole source of carbon. The screening of isolates was based on their ability to utilize LDPE as a primary carbon source. During *in vitro* degradation, three isolates PD-10, PD-11, and PD-12 showed the highest degradation. The increase in bacterial growth and weight loss of LDPE in the medium, were recorded in terms of measurement of turbidity and loss of LDPE weight at regular time intervals respectively. The degradation efficiency was assessed by two methods. On solid medium, the clear zone surrounding the LDPE strips and weight loss in liquid medium was recorded by gravimetry analysis. The observation was done for 30 days and reading was taken at the interval of every 5 days. The standardization of physiological conditions for the biodegradation of L.D.P.E. involves optimizing environmental factors to enhance microbial breakdown of this persistent plastic. Two Indigenous isolates RB3 and RP1, are used to evaluate their potential in degrading LDPE under controlled conditions. Key physiological parameters, including temperature, pH, inoculums size, substrate volume and carbon source and nitrogen source are optimized for maximum plastic degradation efficiency.

Key words: L.D.P.E, Recalcitrant, Biodegradation, Gravimetry, Physiological conditions, Indigenous isolates

ENVM-83 (Poster)

Sample Preparation Strategies for Extraction of Microbial Nucleic Acid from Environmental Matrices for Downstream Genomic Analysis

Snehasri Motamarry* and Syed Imteyaz Alam
*snehasrimotamarry@gmail.com

Biotechnology Division, Defence Research and Development Establishment, Gwalior, Madhya Pradesh, India

Abstract: There are a few infectious agents that can be potentially used for clandestine applications resulting in biological emergency and disease dissemination. This includes various toxins, infectious agents, and microbes that are known to spread easily and have high morbidity and mortality. Accurate identification of such biological agent from clinical and environmental matrices is of paramount importance for implementation of medical countermeasures. Complexity of sample (e.g. soil, sand, surface, body fluids etc.) is one of the major confounding elements in the identification of such microbes. Efficient methodologies for the extraction of nucleic acid from these complex milieus are likely to improve pathogen identification and characterisation using downstream genomic technologies.

In view of the above, sample preparation strategies were optimised for extraction of microbial nucleic acid from diverse matrices [surfaces (glass, plastic, metal, and wood laminate), sand, talcum powder] for downstream genome analysis. Effect of environmental conditions (time lapse, temperature, humidity, sunlight) on recovery of total nucleic acid from surfaces spiked with bacterial agent was also studied to address scenario centric challenges. Nucleic acid from different matrices was extracted by swabbing from surfaces using different swab types and in-matrix lysis from sand, talcum powder. Among the four surfaces, metal exhibited relatively poor recovery of DNA. Scenario centric challenges (effect of field conditions, moisture, and temperature) were addressed for the extraction of bacterial nucleic acid from surfaces. LOD was determined for assess the amenability of extracted DNA from different matrices for downstream PCR analysis.

The methodologies of NA extraction from diverse surfaces, sand, and talcum powder optimized here and the effect of different environmental factors on these methodologies are likely to provide critical insight for the response to biological emergencies and deliberate release of pathogens.

Keywords: Sample preparation, Nucleic acid extraction, Bacterial pathogens, Genomic analysis, Biodefence, Bioverification

ENVM-84 (Poster)

Biodegradation of PVC Film by Fungus- *Lasiodiplodia theobromae S*train RAH19

Sumit Kumar Polley and Swapan Kumar Ghosh*
*gswapan582@gmail.com

Molecular Mycopathology Lab, Biocontrol and Cancer Research Unit, PG Department of Botany, Ramakrishna Mission Vivekananda Centenary College (Autonomous), Rahara, Kolkata, West Bengal (700118), India

Abstract: Today's world plastic pollution has been identified as a global issue. So, we need to manage plastic wastes effectively and, in this purpose, we can use fungi for plastic biodegradation. Waste plastics were collected from different places of North 24 Paragana and those waste plastics were used to isolate plastic eating fungi. One isolated fungus was identified as *Lasiodiplodia theobromae* strain RAH19 (both morphological and molecular identification with ITSs marker). The whole genome sequence of the fungal isolate was also done and raw data was submitted in the SRA database of NCBI and its accession number is PRJNA1071518. Total genome length of the fugus was 52.89 Mb, total number of contig/scaffold 296/3476, total number of gene was 20376 and Percentage of GC content was 55.21%. We also evaluated its plastic (PVC film) degradation efficiency by weight loss method and observed 7.14 % weight loss of PVC film within 30 days, by this fungus in liquid minimal mineral medium. Treated PVC films under both light microscope and scanning electron microscope showed deformation and pores. In search of PVC film biodegradation mechanism, treated PVC film was analysed by FT IR and it revealed that the chemical changes were occurred at peak number 1672.7 cm^{-1} that denoted for ketones. ESI-MS data also supported its PVC film biodegradation ability. We performed lipase, catalase and peroxidase enzyme estimation assay by UV-Vis spectrophotometer and found that good amount of lipase, catalase and peroxidase enzymes were secreted by this fungus. We tested for two adhesins i.e.; PR1 and

mucilage and observed good activity of both adhesins for attachment to plastic surface. In conclusion, this fungus is one promising PVC plastic degrader and it may be used in plastic waste management.

Keywords: Biodegradation, Whole genome, *Lasiodiplodia theobromae*, PVC film, Weight loss, Adhesin

ENVM-85 (Poster)

Soil Nutrient Augmentation through Degradation of the Poultry Feathers using Keratinase Producing Isolate *Bacillus cereus* H16

Priyanka Bumbra and **Babita Khosla**
babitakhosla@gmail.com

Department of Environmental Science, Maharshi Dayanand University, Rohtak, Haryana, India

Abstract: Poultry feathers consist of over 90% proteins primarily keratins are posing significant environmental challenges due to their recalcitrant nature and very slow degradation. The enzyme assisted microbial degradation of keratins is a beneficial alternative to convert waste into value added products. The present study explores the usage of keratinolytic bacteria *Bacillus cereus* H16 isolated from poultry waste dump site to enhance feather decomposition and produce nutrient-rich compost.
The composting of chicken feathers in soil was performed during the winter (October 2021 - December 2021) and summer (March 2022 - May 2022) seasons. The experiments varied four different concentrations of chicken feathers: 2.5%, 5.0%, 7.5%, and 10% (w/w) of whole feathers mixed into pots containing 2 kg of soil each, using a complete randomized design. The treatment sets were divided into sterile and non-sterile sets. Among the different treatments- the nonsterile set with keratinolytic bacteria *B. cereus* H16 showed 62.10% and75.25% feather degradation in the winter and summer season respectively. The presence of natural decomposers in non-sterile conditions, combined with keratinolytic bacteria *B. cereus*, significantly improved the degradation of chicken feathers in soil. The mineralization of feathers enriched the soil with essential macronutrients as carbon (up to 0.82%), nitrogen (up to 0.210%), and phosphorus (up to 9.61 µg/gm). The increase in enzyme activities like dehydrogenase, cellulases, acid phosphatases and keratinase indicated a thriving rhizospheric micro-fauna supporting nutrient cycling and enhancing soil fertility. Consequently, degradation of chicken feathers by *B. cereus* H16 can lead to more efficient recycling of the feather waste, reducing environmental pollution and improving soil health.

Keywords: Keratin, Poultry waste, Composting, Soil nutrients, *Bacillus cereus*

ENVM-86 (Poster)

Comparative Evaluation of *Drosophila melanogaster* and *Drosophila simulans* Larva against Environmental Chemicals

Nisha Khan[1], Usha Rani[1], Veer Bhan[1*] and Anish Khan[2,3]
*veerbhan79@rediffmail.com; *veerbhan.uiet@mdurohtak.ac.in

[1]*Department of Biotechnology, University Institute of Engineering and Technology, Maharshi Dayanand University, Rohtak, Haryana (124001), India*
[2]*Centre for Biotechnology, Maharshi Dayanand University, Rohtak, Haryana (124001), India*
[3]*Department of Biotechnology, Chaudhary Ranbir Singh University, Jind, Haryana (126102), India*

Abstract: *Drosophila* genus comprises of ~1600 species but *D. melanogaster* (DMG) is most-common fly that is present on fruits thus it's known as fruit-fly/vinegar-fly. Unlike, *D. simulans* (DSI) are also closely related to DMG but morphologically have distinct feature. As compared to DSI, DMG is consideration to be progression modified to decaying, overripe/fermented fruits that released huge quantity of ethanol (EtOH), acetic-acid (AA), methanol (MeOH) and ethyl-acetate (EtOAc) chemicals. We explored survival rate of DMG and DSI larva at various concentrations (ranges 2-10%) of EtOH, AA, MeOH and EtOAc. Further, inhibitory-concentration 50 (IC_{50}) was calculated and compare tolerance power+susceptibility of both larva of DMG & DSI against EtOH, AA, MeOH and EtOAc. Firstly, a highly statistically significant (p<0.01) difference was observed between survival rate of DMG and DSI larva against 10% of EtOH (37.4 *vs.* 25.1%), AA (34.9 *vs.* 23.2%), MeOH (32.5

vs. 19.9%) and EtOAc (26.9 *vs.* 17.6%), respectively. Secondly, IC_{50} values of larva of both flies were found statistically significant ($p<0.01$) at 10% EtOH (DMG: 5.8-6.8 *vs.* DSI: 3.9-5.0%) and EtOAc (DMG: 3.8-4.8 *vs.* DSI: 2.3-3.6%). Thus, we found a descending order of IC_{50} values as EtOH>AA>MeOH>EtOAc for both flies larva. Survival rate+sensitivity pattern had EtOH>AA>MeOH>EtOAc in order but mortality+resistivity pattern had EtOH<AA<MeOH<EtOAc in order. To considering DMG and DSI larva's have diverse habitats, ecological, physiological/morphologically difference, hence present study also support it due to susceptible, tolerable larva of DMG than DSI against environmental chemicals like EtOH, AA, MeOH and EtOAc.

Keywords: Chemicals; Comparative; *Drosophila melanogaster; Drosophila simulans;* Larva

ENVM-87 (Poster)

Microbial Solutions to Azo Dye Pollution: Exploring Bacterial Biodegradation in Liquid Medium

Monu Sharma[*]**,** Sonu Sharma, and Raman Kumar
*monusharma311998@gmail.com

Department of Biosciences and Technology, Maharishi Markandeshwar (Deemed to be University), Mullana, Ambala, Haryana (133207), India

Abstract: Azo dyes, widely used in textile and other industries, contribute significantly to environmental pollution due to their recalcitrant and toxic nature. This study investigates the biodegradation potential of specific bacterial strains in the removal of Acid Orange 7 and Acid Red 9 dyes from liquid media. Utilizing bacterial isolates capable of degrading these dyes, we achieved high removal efficiencies, with the degradation process optimized for pH, temperature, and dye concentration to enhance efficacy. Experimental results demonstrated that the bacterial strains could decolorize Acid Orange 7 and Acid Red 9 at removal percentages exceeding 90% under optimal conditions, showcasing an eco-friendly and efficient solution for treating dye-laden wastewater. The study's findings underscore the potential of microbial bioremediation in addressing azo dye pollution and offer a sustainable alternative to conventional physicochemical treatment methods. Further exploration of metabolic pathways and genetic mechanisms involved in dye degradation may expand the applicability of these bacterial strains in large-scale wastewater management.

Keywords: Azo dye degradation, Biodegradation, Bacterial decolorization, Acid Orange 7, Acid Red 9, Wastewater treatment

ENVM-88 (Participate only)

Bioremediation of Polyaromatic Hydrocarbon-Polluted Sewage Sludge Soil Employing a Bacterial Consortium and Phytotoxicity Evaluation

Gulfishan Khan[1]**,** Anshul Tiwari[2,4], Devendra K Patel[2,4] Sadasivam Anbumani[3,4] and Natesan Manickam[1,4]*
*nmanickam@iitr.res.in

[1]*Environmental Biotechnology Laboratory, Environmental Toxicology Group, FEST Division. CSIR-Indian Institute of Toxicology Research, Vishvigyan Bhawan, 31 Mahatma Gandhi Marg, Lucknow, Uttar Pradesh (226001), India*
[2]*Analytical chemistry Laboratory, Analytical Sciences and Accredited Testing Services, ASSIST Division, CSIR-Indian Institute of Toxicology Research, Vishvigyan Bhawan, 31 Mahatma Gandhi Marg, Lucknow, Uttar Pradesh (226001), India*
[3]*Ecotoxicology Laboratory, REACT Division, CSIR-Indian Institute of Toxicology Research, CRK Campus, Lucknow 226008, Uttar Pradesh, India*
[4]*Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, Uttar Pradesh (201002), India*

Abstract: A consortium of five distinct bacterial strains was evaluated for their ability to biodegrade multiple PAHs present in sewage sludge under microcosm-based studies, besides determining their contamination. The

sludge samples were collected during pre- and post-monsoon seasons from three different waste water treatment plants (WWTPs) from Lucknow (Bharwara), Kanpur (Jajmau) and Prayagraj (Naini) locations. Among the sixteen PAHs prioritized by USEPA and EU, fifteen of them were found except fluorene in both the seasons. Overall, the UHPLC analysis revealed that the lowest concentration was 1.75 ng/g of benz(k)fluoranthene and the highest was 5415.59 ng/g of indeno(1,2,3-cd) pyrene in sludge soil. Further, to our surprise the concentration ranges of PAHs found in both the seasons were comparable as post-monsoon expected yield less concentration owing to some wash-off. Indeno(1,2,3-cd) pyrene was found in high concentrations both in dry and wet samples perhaps owing to its multiple origin of contaminations. A bacterial consortium comprised of *Stenotrophomonas maltophilia* IITR87, *Ochrobactrum anthropi* IITR07, *Microbacterium esteraromaticum* IITR47, *Pseudomonas aeruginosa* IITR48 and *Pseudomonas mendocina* IITR46 were employed for PAHs bioremediation in the sludge following microcosm studies. In 20 days, 65-70 % of PAHs were remediated and it was noticed that low molecular weight PAHs such as naphthalene, phenanthrene and pyrene showed enhanced degradation, as revealed by UHPLC analysis. The bioremediated samples showed significant reduction in phytotoxicity using the germination of plants, wheat (*Triticum aestivum*), black chickpea (*Cicer arietinum*) and mustard (*Brassica juncea*) and contaminated soil had inhibitory effects on growth. The results obtained comprehensively suggests a possible remediation option for PAH-contaminated sludge preventing their further contamination into other environmental compartments.

Keywords: Sewage treatment plant, Polyaromatic hydrocarbons, Bacterial consortium, Bioremediation, Microcosm, Phytotoxicity

ENVM-89 (Poster)

Optimization, Characterization and Application of Keratinase Obtained from *Chryseobacterium indologenes*

Tejas S. Hazari*, Ulhas K. Patil and Jayashri J. Bhuktar
tejashazari123@gmail.com

Microbiology Department, Institute of Science, Chhatrapati Sambhajinagar, Maharastra (431120), India

Abstract: The exponential increase of agricultural and animal husbandry leads to generation of excess pressure on environmental issues. The increased production of agro-industrial waste, including keratinous waste from the poultry processing farms, leather industry and slaughterhouse is major problem. It was documented that the daily accumulation of waste reached 5 million tons around the world. Efficient management of the keratin through recycling into value-added products is of major focus all over the world. Microbial keratinases are versatile proteases assisted with efficient biodegradation of keratinous material. The global keratin market size was valued at USD 1.4 billion in 2021 and is expected to expand at a compound annual growth rate (CAGR) of 6.2% from 2022 to 2030 (Grand View Research).

In this view, a keratinase secreting *Chrysobacterium indologenes* was investigated in this study. The physicochemical (using KOH, NaOH, formic acid and cyclohexane) treatment on keratin was found to improve the utilization of keratin by keratinase secreted by *Chrysobacterium indologenes*.

The protease activity of enzyme obtained from *Chryseobacterium indologenes* strain was optimized for the physical parameters of pH and temperature. The effect of metal ions and inhibitors was assessed over the enzyme produced by *Chryseobacterium indologenes.*

The combined approach of physicochemical and enzymatic processing of keratin is the sustainable solution to attain the issue. The keratin hydrolysate obtained by the suggested technique will be utilized for organic fertilizer, animal feedstuff, and biogas production. The efficiently recovered functional peptides and amino acids could be useful in the cosmetics industry. Furthermore, the techniques will contribute to lowering the burden of keratin in the environment.

Keywords: Keratin, Keratinase, Biodegradation, *Chrysobacterium indologenes*

FIM-1 (Oral)

Investigating Gene Expression of Cold Shock Proteins under Different Stress Conditions

Evieann Cardoza and **Harinder Singh***
*harinder.Singh@nmims.edu

Department of Biological Sciences, Sunandan Divatia School of Science, NMIMS University, Vile Parle (West), Mumbai, India

Abstract: There are nine cold shock proteins (csps) in E. coli, whereas one to three is commonly found in other bacterial systems. These proteins are highly similar, but only some have been shown as cold shock response proteins. Are they really cold shock proteins, or do they have other roles? Based on this assumption, the current project was aimed at checking csp expression patterns under different stresses. Expression of csps in response to oxidative and heat stress will be presented here, which can help in assigning different functional roles to those csps where either role is not defined or insufficient information is available.

Keywords: Cold shock proteins, Stress response, Gene expression, qPCR, *E. coli*

FIM-2 (Oral)

Investigation And Characterization of Multi Species, Drug-Resistant, Biofilm forming Food-Borne Pathogens and Safe Intervention Strategies

Abhishek Kaushik* and Neetu Kumra Taneja
*abhikaushik2796@gmail.com

Department of Basic and Applied Sciences, National Institute of Food Technology Entrepreneurship and Management, Sonipat, Haryana (131 028), India

Abstract: Microbial food contamination is a global food safety and public health concern. Unsafe food causes 600 million foodborne diseases and 420,000 deaths worldwide. According to the Centre for Disease Control and Prevention (CDC), biofilms are responsible for approximately 65 percent of all microbial illnesses. Biofilms are microbial consortia embedded inside a self-produced matrix that adheres to solid surfaces or forms on the liquid-air interface and imparts antimicrobial resistance and protection against adverse conditions. This study characterized the multispecies biofilm forming ability of AMR (Antimicrobial resistance) foodborne isolates Escherichia coli EMC17 and Salmonella typhimurium SMC25. Biofilm forming potential of single and multi-species food-borne pathogens was evaluated using Crystal Violet assay, total biomass production and Fluorescence microscopy. Antimicrobial susceptibility of both strains was evaluated using MIC antibiotic strips. Total bacterial counts reached up to 7.29 $\log_{10}$ CFU/cm^2 for E. coli EMC17 and 5.95 log CFU/cm^2 for S. Typhimurium SMC25 in dual-species biofilm state. E. coli EMC17 were found to be resistant towards 46% antibiotics while S. Typhimurium SMC25 was found to be resistant against 38% antibiotics. For the efficient microbial intervention, a plant-based derivative (Quercetin) and class I preservatives (Malic acid/ Citric acid) were used against these AMR foodborne pathogens by Checker-Board assay (Synergy Test). Thus, the result shows that, a plant-based derivative (Quercetin) in combination with class I preservatives (Malic acid/ Citric acid) can be used as a potent alternative of antibiotics against these pathogens and a better approach against these pathogens unlike antibiotics in terms of food safety and human health.

Keywords: Mix-species biofilms, Food Safety, Anti-microbial Resistance (AMR), Intervention

FIM-3 (Oral)

Valorization of Guar Gum for Generation of Prebiotic Mannooligosaccharides: Production Optimization, Characterization, Purification and Bioactive Properties

Suresh Nath* and Naveen Kango
*sureshnath.3592@yahoo.com

Dr. Harisingh Gour Vishwavidyalaya, Sagar, Madhya Pradesh (470003), India

Abstract: Mannans are the polymers of mannose linked together by β-1, 4 glycosidic bonds and occur both as structural and storage polysaccharide in plants. Some of the commercially produced mannans include guar gum, locust bean gum, konjac gum, etc. Mannans are hydrolyzed into mannose and mannooligosaccharides by mannanases, which are glycosyl hydrolases. Endo-β-mannanases have multifarious applications and are used in paper bleaching, nutritional additives, laundry detergents, and the tertiary recovery of petroleum. In the present study, various mesophilic and thermophilic fungi were screened for endo-β-mannanase and accessory enzyme production. *Aspergillus niger* ATCC 26011, an endo-mannanase-producing fungus, was cultivated on copra meal, a low-value mannan-rich agricultural waste. The response surface approach was used to optimize endo-mannanase production. Under statistically optimized conditions, a 2.46-fold increase in β-mannanase production (10028.9 U/gds) was obtained. Purified endo-mannanase (*ManAn*) had an apparent molecular weight of ~47 kDa and the highest specific activity of 110.15 U/mg with guar gum (GG). *ManAn* had optimum activity at 80°C and pH 5.0 making it a thermostable and acidophilic enzyme. The present study demonstrated the optimized production, purification, and characterization of endo-β-mannanase from *A. niger* ATCC 26011. Later, its utilization for mannooligosaccharides generation from GG is demonstrated. Purification and multiscale characterization of partially hydrolyzed guar gum is also performed. The prebiotic effect, antioxidant potential, tolerance assay to gut conditions, and biofilm formation are also evaluated. Lastly, the short-chain fatty acid analysis and its antagonistic effect on enteropathogens are also analyzed.

Keywords: β-mannanase, Mannooligosaccharides, *Aspergillus niger*, Guar gum

FIM-4 (Oral)

Biomimetic Nanoparticles Influence *Listeria monocytogenes* Communication to Reduce Virulence and Biofilm forming Properties

Vaibhav Bharat Rokade[1*], Abhishek Kumar[2], Lalit Pratap Singh[2], Raghu HV[1] and Shilpa Vij[1]
*vaibhav191991@gmail.com

[1]*Dairy Microbiology Division, ICAR-National Dairy Research Institute, Karnal, Haryana (132001), India*
[2]*Animal Biotechnology Division, ICAR-National Dairy Research Institute, Karnal, Haryana (132001), India*

Abstract: *Listeria monocytogenes* are ubiquitous and present in the environment and persist in food processing areas for long periods in various harsh environments, resulting in biofilms on surfaces. The existence of niches in facilities frequently causes contamination of food products and leads to potential human health threats. Our study aimed to counter *Listeria monocytogenes* growth and their pathogenicity with the help of green synthesised magnesium oxide nanoparticles (G-MgO NPs). The nanoparticles were characterised, and MIC was determined against *Listeria monocytogens* cells. The treatments of G-MgO NPs at MIC and sub-MIC were given to analyse an antivirulence property using a hemolysis assay and phospholipase activity. The biofilm-forming ability of Listeria with nanoparticles was determined using a crystal violet assay, motility and EPS production. The nanoparticles were synthesised, and FE-SEM evaluated the size of 37 nm with spherical shapes. The G-MgO NPs minimum inhibitory concentration (MIC) ranged from 3.12mg/mL to 6.25mg/mL for strains of *Listeria monocytogens,* which reduced the cell's growth by 2 to 3 log CFU/mL in the BHI medium. Hemolysis virulence was reduced by 50-55% in treated Listeria strains as compared to the untreated strains. The phospholipase C lecithinase enzyme activity was reduced to 2-6 U/mL, followed by no lecithinase activity on egg yolk agar medium treated with G-MgO NPs. The Listeria strains showed significantly ($p<0.001$) less biofilm development at MIC after 48 hours with control. Exopolysaccharide products were reduced by 20 %,

and motility showed a 60% reduction at 25ºC for 48 hours. Further, gene expression analysis showed that nanoparticles at MIC concentrations significantly down-regulated the expression of virulence (*prfA, hly*, *plcA* and *plcB*) and Quorum sensing genes (*agrA*, *agrC*, and *agrD*). This study presents a green approach for low-cost nanoparticle synthesis and their ability to counter Listeria virulence.

Keywords: *Listeria monocytogenes,* MIC, Quorum sensing genes, Antivirulence, Nanoparticle

FIM-5 (Oral)

Physicochemical Properties of Honey from Different Agro-Climatic Zones of Haryana

Manoj Kumar Jat, Sunita Yadav and Harish Kumar
nitharwal84@gmail.com

*Department of Entomology, College of Agriculture, CCS Haryana Agricultural University, Hisar, Haryana (125*004), India

Abstract: Honey is a natural sweetest produced by bees from floral nectar, known for its rich flavor and health benefits. Its antimicrobial properties, antioxidants and nutrients make it valuable in both culinary and medicinal uses. The study evaluated the physicochemical properties of honey from three agro-climatic zones (Zone-I, II, III) of Haryana. A total of 22 honey samples were collected from bee keepers or Government/University apiary analyzed for moisture content, sugar composition (glucose, fructose and sucrose), acidity, proline content and specific gravity. Significant variation was observed across the samples. The highest moisture content (20.80%) was recorded in the Sirsa-I sample, while the lowest (16.20%) was found in Yamunanagar-III. Total reducing sugars ranged from 66.89% to 81.93%, Yamunanagar-III sample showing the highest value. Sucrose content varied between 1.17% and 3.89%, with Hisar-I displaying the highest. The glucose: fructose ratio ranged from 0.98 to 1.47, with Sirsa-II exhibiting the highest ratio. Specific gravity values, affecting honey consistency, were between 1.39 and 1.51. Acidity was within acceptable limits, ranging from 0.04% to 0.15%. Fructose and glucose content showed considerable variation, with the highest fructose level (45.58%) in Mahendragarh-I and the highest glucose level (40.79%) in Yamunanagar-III. Proline content, an indicator of honey freshness, varied widely from 188.31 to 5629.63 mg/kg. While most samples met the Food Safety and Standards Authority of India (FSSAI) quality standards, a few samples from Zone-II was found positive in Fiehe's test. Overall, the study confirms the quality of honey from different agro-climatic zones in Haryana for consumption and export.

Keywords: Physicochemical, Export, Honey, Haryana

FIM-6 (Oral)

Characterization of a Novel Thermo-Acidophilic L-Asparaginase of *Pseudomonas aeruginosa* CSPS4 And its Applicability in Acrylamide Degradation in Starch-Based Food Products

Digvijay Verma
digvijay.udsc@gmail.com

Department of Environmental Microbiology, School of Earth, and, Environmental Sciences Babasaheb Bhimrao Ambedkar University, Lucknow, Uttar Pradesh (226025), India

Abstract: L-asparaginase (EC 3.5.1.1) finds applications in starch-based food industries for degrading acrylamide (a carcinogen). Acrylamide is usually generated during the deep frying of starch-based food products when sugar and asparagine react. A bacterial isolate *Pseudomonas aeruginosa* CSPS4 showed l-asparaginase activity. Enzyme production was achieved using the 'One Variable at a Time' (OVAT) approach followed by purification using the precipitation method. Purified l-asparaginase was observed as a single band of molecular weight ~35 kDa on SDS-PAGE gel. On characterization, the purified l-asparaginase (wild-type) showed optimum temperature at 60°C under an acidic pH of 6.0 which categorizes this enzyme as thermo-acidophilic type along with fair stability at higher pH as well as temperatures to make it a suitable enzyme for industries. These properties also make this enzyme novel as compared to the other asparaginases of *Pseudomonas*-type. Purified asparaginase was assessed for acrylamide gel inhibition properties at varying concentrations. Besides,

a significant amount of ammonia (464 ± 1.23 nM/min in 30 min) was also liberated from fired potato chips in the presence of l-asparaginase over the control group. The l-asparaginase gene of the CSPS4 strain was cloned, expressed, and, characterized which corroborates the enzyme's characteristics from the wild-type. Molecular dynamics (MD) simulation unveiled its structural insights at higher temperatures. Therefore, l-asparaginase of *P. aeruginosa* CPS4 exhibits potential for its applicability in starch-based food industries.

Keywords: L-asparaginase, *Pseudomonas aeruginosa,* Acrylamide degradation, Starch-based food industries, Thermophilic enzymes

FIM-7 (Oral)

Isolation of Probiotic Microorganisms with Antimicrobial and Bacteriocin Activity from Fermented Pearl Millet Porridge

Jamuna Elumalai*, Srividhya Srinivasan, V. Vijayageetha, Shibi Sebastian, R.Neelavathi, Arul Selvi and S. Thiruvarassan
*jamunae@tnau.ac.in

Abstract: Millet is acknowledged as the sixth most significant cereal. This grain exemplifies a fundamental food source for individuals with lower socioeconomic status. Millet is nutritionally comparable to other cereal grains and has beneficial effects on health. Pearl Millet (*Pennisetum glaucum*) is the predominant variety of millet cultivated globally, constituting 46% of the total millet production. The present work was focused on isolation of probiotic isolates from fermented pearl millet porridge. Microorganisms such as *Lactobacillus, Leuconostoc, Pediococcus*, and yeast, which are primarily involved in fermentation, were extracted from naturally fermented pearl millet porridge, resulting in a total of 25 isolates. The isolates were chosen based on their probiotic characteristics, such as their ability to tolerate acid and bile, their sensitivity to antibiotics, and their antimicrobial and bacteriocin activities. The acid-tolerant isolates were additionally assessed for their ability to tolerate bile. Isolates LA1 and LA8 demonstrated the capacity to grow in the presence of 0.4% oxgall at pH levels of 3, 4, and 5. The antibiotic sensitivity assay indicated that the isolates LA1 and LA8 exhibited resistance to antibiotics such as novabiocin, amikacin, piperacillin, streptomycin, oxacillin, as well asbacitracin. The antimicrobial activity of the lactobacilli isolates against pathogenic microorganisms was assessed, and the isolates LA1 and LA8 exhibited the highest level of antimicrobial activity against *Bacillus subtilis, Staphylococcus sp, Salmonella sp, Corynebacterium sp, and E. coli,* with inhibition zones measuring 22, 14, 12, 10, and 12 mm, respectively for LA1, and 17, 12, 13, 10, and 12 mm, respectively for LA8. The bacteriocin activity of the lactobacilli isolates against pathogenic microorganisms revealed that isolates LA1 and LA8 exhibited the highest level of bacteriocin activity against *E. coli, Salmonella sp, Bacillus subtilis, Corynebacterium sp, &Staphylococcus sp*. The *invitro* growth study of the 4 isolates was done at different pH and temperature conditions; it was found that the growth of LA1, LE1, and Y2 was optimum at 30 and LA8 at 37^{o}C. The optimum pH for the growth of LA1, LA8, and LE1 was 5, and pH 6 for Y2. From this study, LA1, LA8, LE1, and Y2 were identified as probiotic isolates. They were characterized and identified as *Lactobacillus brevis*LA1, *Lactobacillus fermentum*LA8, *Leuconostoc mesenteroides*LE1, *Saccharomyces cerevisiae*Y2.

Keywords: Acid and bile tolerance, Probiotics, Antimicrobial activity Bacteriocin activity, *Lactobacillus*, *Leuconostoc*, *Saccharomyces,* Antibiotic sensitivity

FIM-8 (Oral)

Bioprospecting Sourdough Fermentation for the Alleviation of Irritable Bowel Syndrome (IBS)

Richa Arora* and Kritika Jain
*richaarora@pau.edu

Department of Microbiology, Punjab Agricultural University, Ludhiana, Punjab (141004), India

Abstract: Out of several functional gastrointestinal disorders (FGIDs), irritable bowel syndrome (IBS) leads to change in bowel habits, abdominal pain, diarrhoea and inflammation in the intestines. It is not life threatening but greatly affects the quality of life (QOL) owing to the consumption of high FODMAP (Fermentable oligosaccharides, disaccharides, monosaccharides and polyols) diet. The present study was carried out with the

objective to produce type II sourdough bread with lower FODMAP content using a novel yeast PAU-Y1 as starter for sourdough fermentation. The type II sourdough bread was found to have low pH (4.49) and high total titrable acidity (TTA) as 0.5 mL of 0.1 N NaOH used to reach the pH of 8.5, thereby, imparting palatable sourness alongwith low total sugars (0.22 %). Furthermore, freshly prepared the sourdough bread was found to have higher antioxidant activity and lower phytic acid content as compared to Baker's yeast bread. In addition to this, the type II sourdough bread was found to have desirable textural, color and volatilome profile. On organoleptic analysis, the sourdough bread scored higher for various attributes viz. appearance, color, mouth feel and overall acceptability. Thus, the present study highlights the promising potential of novel yeast PAU-Y1 for reduction of FODMAP content in foods and alleviation of IBS symptoms. However, further studies on clinical trials and upscaling would be required for exploitation of this novel starter culture at commercial scale.

Keywords: Sourdough fermentation, FODMAPs, Functional Gastro-Intestinal Diseases, IBS

FIM-9 (Oral)

Metabolome analysis of traditional Kombucha and its nutraceutical properties

Katyal P
drpkatyal@pau.edu

Department of Microbiology, Punjab Agricultural University, Ludhiana, Punjab(141004), India

Abstract: Kombucha is a millennial beverage with great potential due to its functional claims and is prepared by fermentation of sweetened tea with Symbiotic Culture of Bacteria and Yeast (SCOBY). Physiochemical properties of the finished productdepend upon tea and sugar concentration, percentage of inoculum, fermentation days and incubation temperature. Various studies have been conducted to improve the flavour and nutritional profile of the Kombucha by blending with different fruits and vegetables. In the present study, traditional kombucha was prepared using the conditions pre-optimized in our laboratory (i.e. black tea - 5g/L and sugar - 80 g/L, inoculum level – 5%, incubation temperature - 25 ^{O}C and incubation period of 7 days) and its untargeted metabolome analysis was carried out using GC-MS approach. Further, blending of black carrot juice in Kombucha was evaluated to enhance its physicochemical properties, nutritional properties and sensory qualities. Selected blend of black carrot blended Kombucha with maximum antioxidant activity and sensory scores as suggested by Response Surface Methodology (RSM) were juice concentration - 20% and spices mixture - 1%. Comparison of black carrot blended product with Kombucha revealed an increased antioxidant activity from 72.84 to 84.36% and total polyphenolic content from 72.67 to 99.02 mg/100mL.

Keywords: Kombucha, metabolome, SCOBY, black carrot, fermentation

FIM-10 (Oral)

Saccharification and Isomerization Studies using Actinobacteria

Tannu Kushwah[1*] and Sheetal Bhasin[2]
*tanukushwah1234@gmail.com

[1]*Banasthali Vidyapeeth, Tonk, Rajasthan, India*
[2]*Maharaja Ranjit Singh College of Professional Sciences, Indore, Madhya Pradesh, India*

Abstract: The natural reserve consisting of immense potential for biocatalysis was tapped to solve environmental issues. An extremely adaptive group of heterogenous microorganisms, the Actinobacteria were employed for the production of cellulase and glucose isomerase. Saccharification of cellulosic material was done by cellulase produced by submerged and solid-state fermentation technology using *Streptomyces sp. SA19*. The production ability was checked by assaying FPase and CMCase. Solid state fermentation process yielded better cellulase production with FPase activity of 5.53 U/g and CMCase activity of 5.95U/g. This was aimed to facilitate the disposal by saccharification of ever accumulating agro-residue in the agricultural field in current Indian scenario. Biotransformation of the argo-residue shall not only solve the disposal issue but also give rise to useful products which can be employed in the production of further value-based products. In this investigation we used the glucose released from saccharification for the production of fructose. Isomerization of glucose into fructose was carried out by glucose isomerase produced using *Streptomyces sp. T.S.A.KP.* Solid state

fermentative process proved better for the production of glucose isomerase also with the yield of 13.44 U/g as compared to 11.93 U/ml by submerged fermentation method. Saccharification of CMC yielded 12.86µg/ml. of glucose which was isomerized to 9.22 µg/ml of fructose yielding 71.69 % isomerization. Significantly high isomerization efficiency of the enzyme makes it a very suitable candidate to be picked up for industrial and biotransformation processes.

Keywords: Actinobacteria, Cellulase, Fermentation, Saccharification, Isomerization, *Streptomyces*

FIM-11 (Oral)

Thermal Inactivation of *Salmonella* during Manufacturing of High Milk Protein Cookie Baking Process

Arshdeep Singh, Conor Hunt, Drushya Ramesh and **Lakshmikantha H. Channaiah***
lchannaiah@missouri.edu

Division of Food, Nutrition & Exercise Sciences, University of Missouri, Columbia, MO-65211, USA

Abstract: *Salmonella*'s thermal resistance can be significantly impacted by the food matrix. A study was conducted to evaluate the thermal inactivation of *Salmonella* during high milk protein (HMP) cookie baking process. Two independent high milk protein cookie baking process experiments were conducted to compare the thermal inactivation parameters (*D*- and *z*-values) of selected *Salmonella* serovars in cookie dough made with flour and whey protein concentrate (WPC80). Unbleached bread flour was mist inoculated with 3-serovar *Salmonella* cocktail and used to prepare two different cookie doughs. In control dough, equal parts of inoculated and non-inoculated flour (totaling 140g) were used along with butter, brown sugar, skim milk powder, pasteurized eggs, vanilla extract, water, salt, and sodium bicarbonate. For high protein cookie dough, 70 g each of inoculated flour and WPC80 were mixed along with other ingredients to obtain HMP cookie dough. To determine D and *z* values of *Salmonella*, four regular TDT (Thermal Death Time) disks and one T-type disk filled with freshly prepared inoculated dough were used at three target dough temperatures (55, 58, and 61°C). At pre-determined sampling times, the TDT disks were removed from the hot-water bath and placed in the ice-water bath. The samples were enumerated for remaining *Salmonella* using injury recovery media. Linear regression graphs were plotted to determine the D and *z* values of *Salmonella* in cookie dough. The D-values for *Salmonella* in control and HMP cookie dough at 55, 58, and 61°C were 41.17±3.12, 14.2±0.25, 5.6±1.15 min; and 49.25±3.03, 26.1±1.23, 10.1±1.13, respectively. The *z*-values for control and HMP cookie dough were 6.9±0.44 and 7.9±1.14°C, respectively. The study demonstrates that low water activity coupled with an increase in protein content increases the thermal resistance and survivability of *Salmonella* in HMP cookies.

Keywords: *Salmonella,* Heat resistance, High milk protein cookie, *D* and *z* values

FIM-12 (Poster)

Isolation and Characterization of Glucose Oxidase Enzyme from Fungal Source: Towards Enhanced Production

Pinakin Dhandhukia[1*], Heena Asfak Khan[1] and Janki N Thakker[2]
*pinakin.dhandhukia@vvwusurat.ac.in

[1]*Department of Microbiology, School of Science and Technology, Vanita Vishram Women's University, Athwagate, Surat, Gujarat, India*
[2]*Department of Biological Science, P D Patel Institute of Applied Science, Charotur University of Science and Technology (CHARUSAT), Changa, Anand, Gujarat, India*

Abstract: Glucose oxidase (GOD) is a crucial enzyme that catalyzes the oxidation of β-D-glucose to produce d-glucono-δ-lactone and hydrogen peroxide. Its wide-ranging applications, from glucose sensing to food preservation, have made it an enzyme of significant industrial interest. This study aimed to investigate the potential of various fungal species for GOD production and to characterize the enzyme's properties. A screening of 19 fungal isolates revealed *Aspergillus niger* and *Penicillium* spp. as the most promising producers. Partial purification of GOD from these fungi yielded specific activities of 9.502 U/ml and 7.50 U/ml, respectively.

Biochemical characterization indicated optimal enzyme activity at a temperature of 45°C and a pH of 5.2. Kinetic analysis using Michaelis-Menten kinetics revealed that *Aspergillus niger* exhibited a lower Km (3.95 mM) and a higher Vmax (0.734 U/ml) compared to *Penicillium* spp. These results suggest that *Aspergillus niger* is a more efficient GOD producer with a higher affinity for glucose. The findings of this study highlight the potential of *Aspergillus niger* as a superior source of GOD for various applications. Its high enzyme activity, favorable kinetic properties, and ability to operate under optimal conditions make it a promising candidate for industrial-scale production of GOD. Further research on optimizing GOD production and purification from *Aspergillus niger* could lead to the development of more efficient and cost-effective enzymatic processes.

Keywords: Sensor, Glucose estimation, Kinetics, Partial purification, Isolation, Screening

FIM-13 (Poster)

Fructosyltransferase Production by *Bacillus stercoris* S1 Isolated from *Stevia rebaudiana* for the Biocatalytic Conversion of Sucrose into Oligosaccharides

Puneet[1] and **Neha Gautam[2]***
*gautamneha@yspuniversity.ac.in

[1,2]*Microbiology Research Laboratory, Department of Basic Sciences, Department of Food Science and Technology*
Dr Y S Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh (173230), India

Abstract: *Stevia rebaudiana* was exploited to isolate Fructosyltransferase enzyme producing bacteria. In total 07 bacterial isolates were isolated. Preliminary screening to select FTase producers was done by Triphenyl Tetrazolium Chloride plate assay. The bacterial isolate S1 was selected as it exhibited maximum zone of hydrolysis (22 mm). Quantitative screening was done in terms of transfructosylating activities. Isolate S1 exhibited 50.06 U/ml. Fructosyltransferase producer was identified by morphological, biochemical techniques followed by 16S rRNA gene technique. The Fructosyltransferase producing potential of *Bacillus stercoris* is being reported for the first time in the present investigation. Fructosyltransferase production of *B. stercoris* S1 was enhanced by optimization of inoculum size, incubation time, temperature, pH of medium, carbon source concentration by following one variable at time method. Maximum Fructosyltransferase activity 119.55 U/ml was recorded in nutrient broth supplemented with 60 % sucrose at 72 h with an optimized pH of 6.0 at 40 °C. Partial purification of FTase was achieved by ammonium sulphate precipitation at 30-60%. FTase titres after partial purification were 161.25 U/ml with specific activity 497.68 U/mg, purification fold and recovery percent 1.73 and 73.6 % respectively. Partially purified FTase were found active in a temperature range 30^{0}C to 80^{0}C and in pH range of 5.0 to 9.0. FTase was found stable at -20^{0}C for 45 days. The results obtained showed that the *B. stercoris* S1 represents a promising source for FTase enzyme that can be efficiently utilized for FOS production.

Key words: Fructosyltransferase, Prebiotics, Fructooligosaccharides, *Bacillus stercoris*, Characterization

FIM-14 (Poster)

Rheological Study of Modified Guar Gum Cross-Linked with Nano Material for Gelling Agent Fracturing Fluid Application

Shishram Chahar[1*], Banwari Lal[1,] Sivakumar Pandian[2], C Paul Jeyaseelan[1], K Nanthakumar[1], Veeranna Channashettar[1], Sunil Kumar[1] and Mukesh Yadav[1]
*shishram.chahar@teri.res.in

[1]*Environmental and Industrial biotechnology department, TERI, New Delhi (110003), India*
[3] *Department of Petroleum Engineering, School of Energy Technology, Pandit Deendayal Energy University, Gandhinagar, Gujarat (382426), India*

Abstract: The biopolymer demands are increasing in the oil and gas sector due to its eco-friendly nature. There are so many types of biopolymers which are using in the petroleum industry to enhance the viscosity, YP, PV,

Gel strength, and mud fluid rheological performance. The xanthan gum, poly-anionic cellulose HV-LV, guar gum, carborymethyl guar gum, carboxymethyl hydroxypropyl guar gum, hydroxypropyl guar gum, carboxymethyl cellolose HV-LV, biopolymers are mostly using for drilling fluid applications. The study aims to investigate the rheological conditions of the gelling agent biopolymer and its stability at HTHP well conditions. The modified guar gum (CMHPG-GO) cross-linked with graphene oxide Nano material to enhance the thermal stability of the fluid. We used a standard industry rheometer, Viscometer and aging cells to perform the rheological test of the modified biopolymer. The experiments were designed with developed biopolymer and comparing with different grades of HPG and CMHPG which are available in the market. The prepared cross-linked (CMHPG-GO) and other biopolymers (HPG, CMHPG) were weighed of w/v-0.6% and hydrated in RO water with 3% KCL solution to analyse the rheological properties of the fluid. The prepared fluid were followed the American petroleum standards and set the temperature with 140 ° C temperature, 100 psi pressure and 100 1/s shear rate. Then, the same procedure with same quantity was tested with the range of the temperature between 24±2 to 140 ° C. The experimental results showed that the viscosity of the biopolymer is more stable with developed cross-linked (CMHPG-GO) biopolymer, and the other HPG and CMHPG were degraded when temperature rises. The stability of biopolymers is more pronounced in RO and DI water compared to normal water, with salt percentage and cross linkers playing significant roles. Crosslinkers in KCL fluid rheology cause viscosity changes.

Keywords: Apparent viscosity, Biopolymer, Crosslinking, *Cyamopsis tetragonoloba*, Graphene oxide, High temperature, Plastic Viscosity, Rheology, Yield value

FIM-15 (Poster)

Modulating Permeability and Metabolic Efficiency: Unlocking the Industrial Potential of Bacterial Microcompartments

Komal Timane[1,2]* and Chiranjit Chowdhury[1,2]*
c.chowdhury@ncl.res.in

[1]*Biochemical Sciences Division, CSIR-National Chemical Laboratory, Dr. Homi Bhabha Road, Pune, Maharashtra (411008), India*
[2]*Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, Uttar Pradesh (201002), India*

Abstract: Bacterial microcompartments (MCPs) are enzymatic cores encased in semi-porous protein shells resembling viral capsids, found in 45 bacterial phyla. These protein-based organelles encapsulate critical enzymes within selectively permeable protein shells, creating confined biochemical environments that localize reactions and improve catalytic performance. These organelles optimize metabolic pathways by channeling intermediates to downstream enzymes and isolating toxic or volatile compounds. MCP shells are mainly composed of 5-10 BMC-domain proteins, forming hexameric subunits with 6-fold symmetry. Crystal structures reveal central pores in these subunits, likely affecting flux properties. The permeability properties of the shell proteins play a crucial role in regulating the flow of substrates and products in and out of the compartment, making BMCs ideal for optimizing multi-step biochemical processes.
MCPs improve product yield and purity by selectively transporting metabolites, minimizing toxic intermediates and unwanted reactions. They can be tailored to enhance microbial tolerance to harsh conditions by isolating reactions within the compartments. However, lack of comprehensive understanding of function of the diverse array of shell protein pores hinders the effective use of MCPs as customizable protein containers in diverse applications like in industrial microbiology and Metabolic Engineering etc. In our present research, we aim to explore the essential functions and permeability properties of shell proteins found in bacterial microcompartments, specifically focusing on well-known microcompartment such as the 1, 2-propanediol utilization (Pdu) microcompartment of *Salmonella*. To achieve this, we employ a structure guided mutagenesis of shell proteins and analyzing their impact on bacterial growth, enzyme activity and the transport of different metabolites across the bacterial microcompartment shell by HPLC. Continued research will pave the way for engineering a tailor made nanobioreactor with customized permeability properties, enabling the fine-tuning of metabolic fluxes for specific industrial applications.

Keywords: Bacterial microcompartments, Industrial microbiology applications, Shell protein permeability

FIM-16 (Poster)

Functional Potential of *Toddy*, a Traditional Fermented Palm Beverage of India: an *in-silico* Metagenomics Study

Souvik Das* and Jyoti Prakash Tamang
*svkstpp95@gmail.com

Food Microbiology and Omics Laboratory, Department of Microbiology, Sikkim University (A Central University), Tadong, Gangtok, Sikkim (737102), India

Abstract: *Toddy* is a popular refreshing palm beverage of different provinces of coastal and inland India, produced from the fresh saps of various palm trees through uncontrolled spontaeneous fermentation. Natural microflora modulates the fresh sap into a sparkling white beverage with numerous functional and bio-active attributes. In our study, ONT-Nanopore based shotgun metagenomics and UHPLC based metabolomics were applied to decipher the entire microbial profile that actually orchestrate the bio-functionalities through the production of a numerous number of primary and secondary metabolites. Meta-taxonomic analysis revealed a balanced interplay between bacteria (94.48%) and eukaryotes (3.38%), where *Leu. mesenteroides*, *Leu. citreum*, *Lb. helveticus*, *Lpb. plantarum*, *Lactococcus lactis*, *A. malorum*, *Gluconobacter japonicus*, *Gluconacetobacter liquefaciens*, *Fructobacillus durionis*, *Zymomonas mobilis* and yeasts *Saccharomyces cerevisiae*, *Hanseniaspora uvarum* and *Hanseniaspora guilliermondii* were found to drive the fermentation while maintaining a significantly positive co-existence. PCoA analysis based on Bray-Curtis index demonstrated the similarities and dissimilarities among the samples explaining the geographical influence, one of the key factors in any natural fermentation. KEGG (58.92%) and COG (41.08%) annotated predictive functional pathways justified the exact role of each of the microorganisms during the course of fermentation; these predicted profiles include biosynthesis of ethanol, acetic acid, butanoate, linalool, staurosporine, prodigiosin, folic acid, riboflavin and other basal level pathways which were either product centric or fermentation centric. Predictive analyses were further reconfirmed through untargeted metabolomic analysis where a number of primary metabolites and secondary metabolites with anti-microbial, anti-cancer, anti-tumor, anti-diabetes, anti-obesity, anti-inflammatory, anti-neuro degenerative and immuno-modulatory properties were detected. Lastly, the detection of CRISPR arrays (n=23; 23.69 bp ± 4.28) and absence of any major AMR genes among the major microbial communities confirm the addition safety of the drink for the consumption.

Keywords: *Toddy*, Spontaneous fermentation, Shotgun metagenomics, Metabolomics, Immuno-modulators, Bio-activities

FIM-17 (Poster)

Optimization of Xylanase Enzyme Activity using Response Surface Methodology

Monika sri S, Vinuthana V H and Sivakumar Uthandi
*monikasenthil138@gmail.com

Biocatalysts Laboratory, Department of Agriczultural Microbiology, Tamil Nadu Agricultural University (TNAU), Coimbatore, Tamil Nad (641003), India

Abstract: Xylanases are glycosidases mainly responsible for the hydrolysis of β-1,4 linkages in xylan. The production of thermostable xylanase by a newly isolated *Aspergillus fumigatus* PFS1 was optimized by one factor at a time (OFAT) and response surface methodology (RSM) approaches. The present study aimed to optimize the critical parameters that affect the xylanase activity. Various physical parameters like inoculum load, temperature, and pH, as well as nutritional parameters like carbon and nitrogen source, were optimized. Through this optimization process, the most significant factors affecting the xylanase activity were determined. The optimal conditions were 5 discs of inoculum load, pH 5, 40 °C, beef extract as 1g.L^{-1} nitrogen source, and 4% wheat bran as a carbon source. The optimized conditions enhanced the yield of xylanase from 445.49 ±19.00 IU mL^{-1} to 624.56 ±11.54 IU mL^{-1} and the model's efficacy was indicated by the R^2 value of 0.98.

Keywords: Submerged fermentation, Temperature, Xylanase, Response surface methodology, Optimization

FIM-18 (Poster)

Incidence and Virulence Characterization of the Emerging Pathogen *Cronobacter* Spp. in Seafood Sold in Fish Markets of Mumbai

Deeksha Bharti, B.B. Nayak, Sanath Kumar H. and Manjusha L.*
*manjusha@cife.edu.in

FRHPHM Division, ICAR-Central Institute of Fisheries Education, Versova, Mumbai, Maharashtra (400061), India

Abstract: *Cronobacter* is an emerging pathogen, that has gained importance due to its association with neonatal infections like meningitis, necrotizing enterocolitis, and septicemia, with case fatality rates of 40-80%. The infections occur in all age groups, though with less severe complications in adults. They are gram-negative, facultatively anaerobic, motile and non-spore forming rods belonging to Enterobacteriaceae family. The pathogen has been isolated from a variety of food and food ingredients, however, the study on their association with seafood is still lacking. In the present study, 75 seafood samples were screened, including 25 fresh finfish, 25 shellfish and 25 dried fish samples, out of which, 24 (32%) samples were found to harbour *Cronobacter* spp. The isolation was carried out using nine media combinations of enrichment and selective isolation media, and 44 isolates were identified as *Cronobacter* spp. based on biochemical tests and PCR. Of these, 21 (47.72%) were isolated from dried fish, 19 (43.18%) from fresh finfish and 4 (9.09%) from shellfish samples. The 16srRNA and ITS sequencing confirmed 20 isolates to be *C. sakazakii* and 24 as *C. malonaticus*. The confirmed isolates were further analyzed for putative virulence and virulence associated genes such as, *hly*, *cpa*, *sip*, *sod*, *ompA*, *ompX*, *zpx* and *fliD*. All isolates were found to be positive for *ompA*, *ompX*, *fliD* gene, while negative for *sip*, *sod*, *hly*, and *zpx* gene, however, 18 isolates showed amplification of *cpa* gene. Overall, this study reports the contamination of seafood by *Cronobater*, which shows a high incidence in dried fish samples, indicating its ability to survive in dried and dehydrated foods.

Keywords: *Cronobacter*, Seafood, Virulence, Dried fish

FIM-19 (Poster)

Lactiplantibacillus plantarum mediated millet-rice fermentation for folate fortification antipathogenic and anti-inflammatory effects

Priyadarshini Pratikshya Nayak and Sandeep Kumar Panda*
*sandeeppanda2212@gmail.com, *sandeep.panda@kiitbiotech.ac.in

School of Biotechnology, Kalinga Institute of Industrial Technology (KIIT) Deemed to be University, Campus 11, Patia, Bhubaneswar, Odisha (751024), India

Abstract: The objective of this study was to optimize a novel *Lactiplanti bacillus plantarum*-mediated fermentation process for optimum folate retention, using finger millet (*Eleusine coracana* L.) and rice as substrate. Optimization was attained through response surface methodology (RSM) and validated by artificial neural network (ANN) analysis. The optimal conditions determined for the process was 2% bacterial inoculum (2.43×10^8 CFU/mL), and a fermentation duration of 6 hours. Under the condition, the developed formulation had a folate content of 182.58 µg/100g. The fermented millet formulation exhibited the following biochemical characteristics: reducing sugar, 2.100 ± 0.087 mg/g; protein, 4.31 ± 0.22%; pH, 3.87 ± 0.02; total phenolic content, 11.617 ± 0.21 mg GAE/100g; lactic acid concentration, 21.44 ± 0.10 mg/mL; and DPPH radical scavenging activity, 65.38 ± 0.481%. The formulation exhibited anti-pathogenic efficacy against *Salmonella enterica* serovar Enteritidis, a common causative agent of foodborne illness. The immunomodulatory properties of the formulation were evaluated using the human macrophage cell line THP-1 derived from *ex-vivo* human peripheral blood mononuclear cells. The formulation was found to significantly enhance (~ 72%) the production of the anti-inflammatory cytokine interleukin-10 (IL-10), suggesting a potent modulatory effect on macrophage polarization. Concurrently, it could effectively reduce the secretion of key pro-inflammatory cytokines, interleukin-1 beta (IL-1β), and tumor necrosis factor-alpha (TNF-α), by ~ 55% and ~ 60%, respectively. These findings indicate that the novel folate fortified formulation not only exerts an elevated folate level in the food

substrate but also has direct antimicrobial action and modulates the inflammatory response, potentially offering dual therapeutic benefits.

Keywords: Finger millets, Fermentation, Response surface methodology, Folate fortification Artificial Neural networking, Anti-inflammatory

FIM-20 (Poster)

Evaluation of Microbial Quality of Masmin from Lakshadweep, India

Mohammed Ihzan M.P., Sanath Kumar H., Layana P., Fathima Salam and Nayak B.B
sandeeppanda2212@gmail.com, sandeep.panda@kiitbiotech.ac.in

Fish Processing Technology, FRHPHM Division, ICAR- Central Institute of Fisheries Education, Off yari road, Panch marg, Andheri west, Mumbai, Maharashtra (400061), India

Abstract: Masmin is a cooked, smoke-dried traditional product of Lakshadweep, India, having a brittle, hard texture and dark-wood-like appearance. The method of preparation of the masmin has been passed down through generations, and the process is followed even today with very few modifications. However, no scientific study has been conducted to evaluate the exact shelf life of the product due to the minor variation in processing steps across islands. The gross abuse of raw material during processing stages including unhygienic handling of fish, with low or no use of ice and delay in pre-processing activities, compromises the quality of masmin. In this background, the present study was conducted to assess the microbial quality of traditional masmin collected from the various islands of Lakshadweep. The samples (N=30) were screened for the presence of pathogens including, *E. coli, Salmonella, Vibrio*, and *Staphylococcus.* Total Plate Count (TPC), Total Halophilic Count (THC), and Total Fungal Count (TFC) were also examined. The result showed the microbial load in the range of 2.5×10^2 to 2.8×10^6 cfu/g. The possible reason for the high microbial load in some samples can be due to high moisture content and also due to the post-process contamination. A number of moderately halophilic bacteria (growth in 5% NaCl) and moulds/yeasts were isolated from the samples, which may be linked to the high salt content (3-7 %) and low moisture content of the masmin, respectively. The study concluded that it is necessary to have good hygienic handling of the fish throughout the process and improved packaging of the products.

Keywords: Masmin, Lakshadweep, Microbial Quality, Halophilic Bacteria, Moulds, Contamination

FIM-21 (Poster)

Statistical Optimization of Cellulase Production by *Aspergillus fumigatus* PSF1 under Submerged Fermentation (SmF)

Vinuthana V H*, Santhoshkumar Subramaniam and Sivakumar Uthandi
*vinuthana1998@gmail.com

Biocatalysts Laboratory, Department of Agricultural Microbiology, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu (641003), India

Abstract: Cellulose is the major component of most biological components, especially plant bodies. Cellulose also can be defined as an abundant biomolecule found in the biosphere. Cellulose-degrading microorganisms hold immense significance in utilizing cellulose resources efficiently. Microbial cellulases are highly versatile catalysts with significant potential in various industries, including pulp and paper, textile manufacturing, laundry, biofuel production, food and animal feed, brewing, and agriculture. However, the yield of cellulase under submerged fermentation condition is constrained by optimal growth parameters like inoculum load, pH, temperature, carbon and nitrogen source. The present study aimed to optimize the optimal growth parameters which influences on cellulase yield under submerged conditions using response methodology. The cellulase activity was assayed by filter paper activity. Initially, filter paper activity was 12.45 IU mL^{-1} on first day, which gradually increased and the highest yield was to 22.04 IU mL^{-1} on 9th day and thereafter it was gradually

reduced. The filter paper activity was enhanced to 59.45 IU mL^{-1} after optimization and the optimum conditions include 5 discs of inoculum load per 100 mL, pH 5, temperature 40 °C, beef extract 1 gL^{-1} as nitrogen source, and 1 % CMC as carbon source. The R^2 value was 0.92 signifying the effectiveness of model and the optimized conditions increased xylanase yield significantly.

Keywords: Carbon source, Inoculum loads, Nitrogen source, pH, Submerged fermentation, Temperature, Cellulase

FIM-22 (Poster)

Harnessing the Microbiome for Health and Environmental Resilience

Puneet*, Sunita Devi, Parul Sharma, Subhash Chand and Megha Sharma
*puneetsuru007@gmail.com,

Microbiology Laboratory, Department of Basic Sciences, College of Forestry, Dr. YS Parmar University of Horticulture and Forestry- Nauni, Solan, Himachal Pradesh (173230), India

Abstract: The microbiome, comprising diverse microorganisms in environments such as the human body, soil, and water, plays a pivotal role in health and disease, shaped by factors like diet, geography, and lifestyle. These factors influence microbial community composition, which impacts health outcomes. Microbial communities are also crucial for nutrient cycling, pollutant degradation, and ecosystem stability. Emerging research reveals a bidirectional interaction between the microbiome and environmental stressors, such as pollutants and climate change, where disturbances can increase disease susceptibility. Advances in high-throughput sequencing and multi-omics technologies have enhanced our understanding of microbial-environmental dynamics, enabling more comprehensive assessments of both ecosystem functionality and health. This complex relationship is central to sustainability, requiring interdisciplinary collaboration and innovative research to inform future strategies for health and environmental stewardship.

Keywords: Microbiome, Environmental sustainability, Metagenomics, Metatranscriptomics, Ecosystem

FIM-23 (Poster)

Prevalence and Characterization of Carbapenem-resistant ESBL- producing *Escherichia coli* from Seafood

Prerana, Manjusha Lekshmi, Girisha S.K., Binaya Bhusan Nayak and Sanath Kumar H*
*sanathkumar@cife.edu.in

Fish Processing Technology, ICAR-Central Institute of Fisheries Education, Versova, Mumbai, Maharashtra (400061), India

Abstract: Carbapenems are a strong class of antimicrobial agents used in treating life-threatening bacterial infections and disease caused by antibiotic resistant bacteria. They are the last resort antibiotics and rapid increase in carbapenem-resistant Enterobacterales (CRE) such as *Escherichia coli* is a serious concern mainly contributed by the "Big Five" group carbapenemases, KPC, IMP, VIM, NDM, and OXA-48-like enzymes. This study was conducted to understand the genetic mechanisms and characteristics of mobile genetic elements harbouring carbapenem resistance genes in extended spectrum-β-lactamase producing *E. coli.* Of 113 ESBL-producing *E. coli*, 37 (32.45%) were resistant to meropenem, 33 (28.94%) to imipenem, and 17 (14.91%) to ertapenem. For three carbapenems tested, 9 isolates (7.89%) were resistant to all, followed by 26 (22.80%) to 2 carbapenems, and 51 isolates (44.73%) were resistant to at least one carbapenem. Molecular screening showed the presence of bla_{VIM} in 8 (7.01%) isolates, bla_{KPC} and bla_{NDM} in 2 (1.75%) isolates each, bla_{OXA} in 14 (12.28%) and bla_{AmpC} in 13 (11.4%) isolates. Of 51 isolates, only 8 (15.68%) were positive by combined disc diffusion test. CarbaNP test detected carbapenemase production in only 7 (6.14%) isolates suggesting discrepancies in the phenotypic and genotypic detection methods of metallo-β-lactamases. This study suggests the prevalence of carbapenem-resistant *E. coli* in seafood with the mobile genetic elements carrying high-risk

resistance genes that can be transmitted to susceptible strains in the aquatic environment, thus highlighting the need for continuous surveillance of seafood and the coastal-marine environment.

Keywords: Seafood, ESBL, CRE, *bla*$_{NDM,}$ CarbaNP, *Escherichia coli*

FIM-24 (Poster)

Process Development for Improving Lignin Yield from Rice Stubble for Developing Bioactive Products

Indu wala* and Deepak Kumar Rahi
*isusankhyan@gmail.com

Department of Microbiology, Panjab University, Chandigarh (160014), India

Abstract: India produces 120–150 MT of rice stubble annually much of which is burned, contributing to severe environmental pollution. However, rice stubble is an abundant source of lignin, a valuable aromatic polymer that provides plants with rigidity, hydrophobicity, and antibacterial defence. Lignin has great potential for commercial applications, yet its extraction and utilization are still underdeveloped. Conventional extraction methods like Kraft, soda, and Organosolv are widely used but enzymatic pre-treatment of lignin is least explored which is as a greener and potentially more efficient method for lignin extraction. In the present study, lignin was extracted from rice straw using an enzymatic pre-treatment, followed by chemical extraction through the kraft and soda processes. Extraction parameters such as pH, reaction time, temperature, and alkali concentration etc. were optimized, resulting in lignin yields initially from 315.6mg/g to 500 mg/g. The enzymatic pre-treatment improved extraction efficiency, reduced chemical usage, and helped minimize environmental impact. Post-extraction, the lignin was modified using laccases from white rot fungi to enhance its reactivity by altering its functional groups. FTIR analysis confirmed these modifications, and the total phenolic content of lignin increased from 22.4 µg/ml to 26.6 µg/ml. The modified lignin exhibited enhanced antioxidant properties and significant antibacterial activity. This study highlights the potential of modified lignin in advanced applications. "Lignin's unique bioactivity turns it into a multifunctional ingredient, capable of improving the performance of resins, fertilizers, and hydrogels while offering protection against microbial threats."

Keywords: Stubble, White Rot fungi, Lignin modification, Antioxidant, Antibacterial FTIR

FIM-25 (Poster)

Identification of Mycotoxin Producing Fungi from the Spices and their Growth Inhibition by using Lactic Acid Bacteria

Amol Vishwas Pawale[1,] Devadharshini Chelladurai[1,] Ramalakshmi Alaguthevar[1,2*] and Balakrishnan Murugesan[2]
*ramalakshmi.a@tnau.ac.in

[1] *Department of Agricultural Microbiology, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu (641 003), India*
[2] *Department of Food Process Engineering, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu (641 003), India*

Abstract: The spices samples including black pepper, cardamom, fennel seeds and cumin in packed and loose form collected from the various stores analysed for the microorganism presence; mostly for the mycotoxin producing fungi. The microbial analysis identified the *Aspergillus niger*, *A. amoenus*, *A. nidulans*, *A. flavus* fungi. The methanol-based extraction of aflatoxin produced from the isolated fungi done and quantified using the HPLC. The black paper shown the highest concentration of the aflatoxin presence followed by fennel and cumin; and least in the cardamom among the four samples. The lactic acid bacterial (LAB) strains from pulses and millets isolated and characterised for the inhibition of growth of identified fungi *Aspegillus flavus* at temperature 17°C, 27°C and 40°C. Among the isolated LAB strains, ME25, ME26 identified promising inhibitor

against *Aspegillus flavus* at all temperature condition while, other LAB strains shown inhibition zone at 27°C. Among the all strains, ME26 shown highest inhibition ability among all the LAB strains and identified as *Weiseella sp.* So, from the study, can conclude that, the LAB control the growth of mycotoxin producing fungi which prevents the production of the health threatening mycotoxins.

Keywords: Aflatoxin, *Aspergillus sp.,* Growth inhibition, Lactic Acid bacteria, Spices

FIM-26 (Poster)

Genomic Characterization of a *bla*$_{NDM-5}$-carrying *Escherichia coli* Sequence Type 167 Isolated from Seafood in Mumbai, India

Dhanush C.K., Jerusha S, Manjusha L and Sanath H. Kumar*
*sanathkumar@cife.edu.in

Fish Processing Technology Department, ICAR-Central Institute of Fisheries Education, Seven Bungalows, Versova, Andheri (W), Mumbai, Maharashtra (400061), India

Abstract: Anthropogenic contamination of coastal-marine environments significantly impacts the microbial safety of fish and shellfish harvested from these environments. Pathogenic bacteria, often multidrug-resistant (MDR), are increasingly being reported in seafood in India, raising concerns about seafood acting as vehicles of MDR bacterial transmission in the community. *Escherichia coli* ST167, an emerging, high-risk clonal type, is a dominant extraintestinal pathogenic *E. coli* likely harbouring carbapenem resistance determinants. In this study, the whole genome of a *bla*$_{NDM}$-harbouring, MDR *E. coli* strain EC121 isolated from seafood was sequenced. The whole genome sequence (WGS) was gene annotated, and the functional categorization and phylogenetic analysis were performed. The assembled genome had an overall length of 4,885,003 bp with 4,863 protein-coding sequences (CDS) and an average G+C content of 50.69%. MLST analysis revealed that this strain belonged to sequence type 167 and was identified as an O101:H9 serotype. The isolate harbored different virulence genes, suggesting it was a potential human pathogen. Many acquired antibiotic resistance genes including *bla*$_{NDM-5}$, *bla*$_{CMY-42}$, *bla*$_{OXA-1}$, *bla*$_{TEM-116}$, *catA1, sul2,* and *tet(B)* were detected in the WGS. Point mutations in *gyrA* and *parC* responsible for quinolone resistance were also identified. The combination of virulence and antibiotic resistance genes highlights the significant risk associated with emerging *E. coli* clonal types contaminating the seafood supply chain. Proper implementation of hygienic practices in domestic markets and continuous surveillance is necessary to contain possible public health risks.

Keywords: Seafood, *E. Coli,* Human pathogen, Genome, Multidrug-resistance, Virulence

FIM-27 (Poster)

Enhancement of Vitamin Content in Sweet Potatoes through Fermentation with *Lactobacillus plantarum*

Purnima Bharati Mohapatra[1], Vishakha Raina[1*] and Sandeep Kumar Panda[2]
*vraina@kiitbiotech.ac.in

[1]*Environmental Biotechnology Lab, School of Biotechnology, KIIT University, Campius-11, Bhubaneswar, Odisha (751024), India*
[2]*Applied Research Lab, School of Biotechnology, KIIT University, Campus-11, Bhubaneswar, Odisha (751024), India*

Abstract: Odisha stands as the largest sweet potato producing state in India, with an estimated production of 335,450 tonnes by 2024. This production accounts for approximately 29.52% of the national sweet potato yield. Sweet potato (SP) (*Ipomoea batatas*), a sweet tasting tuber root is nutrient-dense and rich in dietary fibre which offers numerous health benefits. The fibre, that aids digestion, regulates blood sugar, and promotes gut health. SP varieties also contain antioxidants like beta-carotene and anthocyanins that helps in protection against oxidative stress and may reduce chronic disease risk. However, the bioavailability of B vitamins (B_2, B_9, B_{12},

B_6), particularly folic acid (B_9), may be restricted. Here, we aim to investigate and quantify the enhancement in nutritional content of B vitamins after fermentation using *Lactobacillus plantarum*. The design of experiments involved use of RSM (Response Surface Method) for optimization of fermentation conditions. SP flakes were subjected to fermentation under anaerobic conditions along with a control group of unfermented sweet potato. Post fermentation samples were analysed by HPLC to quantify the levels of the different B vitamins. All experiments were statistically performed to ensure reliability. The results of the above experiments will be discussed and presented. The findings suggested potential applications of SP in food processing, particularly in regions where they are a dietary staple and where folate deficiency is prevalent in pregnant women.

Keywords: Sweet potatoes, *Lactobacillus plantarum*, Fermentation, Folic acid, Vitamins, HPLC

FIM-28 (Poster)

Assessment of GABA Production in Bacterial Strains from Traditional Indian Fermented Foods using LC-MS and NMR

Souparno Paul and Gunjan Goel*
*ggoel@cuh.ac.in,

Department of Microbiology, Central University of Haryana, Jant-Pali, Mahendragarh, Haryana (123031), India

Abstract: Gamma-aminobutyric acid (GABA) is a non-protein amino acid that is a major inhibitory neurotransmitter in the mammalian central nervous system with several well-characterized physiological functions- relieving hypertension and anxiety disorders. Using the microbiota–gut-brain axis (GBA), some probiotics can control the host's neurobehavioral system. Indian fermented foods like batter of dosa, jalebi, sour rice, curd, pickled bamboo shoots, misthi doi etc from various states were screened for bacterial strains that can produce GABA. The production of GABA was evaluated using primary screening like plate assay, Thin-layer chromatography, GAD activity, and their confirmation by NMR and LC-MS analysis. A total of 48 colonies were obtained on MSG-supplemented MRS agar plates. The production of GABA was confirmed using Thin Layer Chromatography on silica 60F254 TLC plates. The best resolution and separation of GABA was obtained in n-butanol: acetic acid: water (5:2:2 (v/v/v)) solvent. Further, the amplification of genes encoding the glutamate decarboxylase system, including two gad genes (gadA and gadB) and the glutamate antiporter gene (gadC) was observed in 10 isolates. The optimum conditions for GABA production were seen when the bacterial strains were grown in MRS medium supplemented with 0.5mM MSG at 37^0C for 24-48 hours. The LC-MS/MS analysis and subsequent search on Compounded Discoverer software showed GABA production in all the selected ten isolates with simultaneous production of other important precursors of neurotransmitters like phenylalanine and L-Tyrosine. The study indicates that fermented foods can serve as a reservoir of GABA producing bacteria with additional health benefits. Further studies are in progress to evaluate these strains for probiotic activities.

Keywords: Gamma-aminobutyric acid (GABA), Thin Layer Chromatography, GAD activity, NMR and LC-MS analysis

FIM-29 (Poster)

A Multi-Substrate Specific Glycoside Hydrolase Family 53 Galactanase (*At*GH53) from *Acetivibrio thermocellum* with β (1→4) and β (1→6) Bond Cleavage Activities

Shreya Biswas* and Arun Goyal
*shreya.biswas@iitg.ac.in

Department of Biosciences & Bioengineering, Indian Institute of Technology Guwahati, Assam (781039), India

Abstract: A gram-positive, thermophilic, cellulolytic bacterium *Acetivibrio thermocellum* possesses a lignocellulolytic multienzyme complex, containing cellulases, hemicellulases and pectinases; termed as

cellulosome. Several cellulosomal enzymes have been reported from *Acetivibrio thermocellum* but an endo-*β*-1,4-galactanase has never been reported. Endo-*β*-1,4-galactanase activity is currently exclusive to the glycoside hydrolase family 53 (GH53) as per the CAZy database. Endo-*β*-1,4-galactanases, in particular hydrolyze the *β*-1,4-glycosidic bonds of galactan and arabinogalactan present in the pectin, which is a major component of the primary plant cell wall. In this study, the gene (927 bp) encoding an endo-*β*-1,4-galactanase (*At*GH53) from *A. thermocellum* (GenBank accession: WP_003518272) was cloned in an expression vector pET-21a(+). The protein was purified from the cell extract by Immobilized Metal-ion Affinity Chromatography (IMAC), followed by Size Exclusion Chromatography (SEC). The purified *At*GH53 displayed molecular mass around 36 kDa in SDS-PAGE analysis. *At*GH53 showed optimal temperature, 70□C and thermostability with half-life, 15 h at 70□C. *At*GH53 displayed stability at both acidic and alkaline pH ranges (pH 4.0-10.0) while the optimal pH of the enzyme is pH 7.5. The activity of the enzyme significantly increased over 30% in presence of transition metal ions such as Ni^{2+} or Co^{2+}. *At*GH53 showed broad substrate specificity as it displayed activity against a range of galactan substrates showing highest V_{max}, 1432 U/mg and K_M, 1.2 mg/mL with potato pectic-galactan. TLC and HPLC analysis of hydrolysis of potato galactan by *At*GH53 showed initial concomitant endo- and exo-lytic cleaving property of *At*GH53 and finally shifting to only exo-lytic mode as it released galactooligosaccharides (□-1,4-linked) of higher degrees of polymerization (DP>3) for the first 2 h and then producing the disaccharide and galactose monomer till 24 h. Hydrolysis of arabinogalactan by *At*GH53 with 148.6 U/mg specific activity released □-1,6-galactobiose from the side chain of the polymer. This signifies that *At*GH53 primarily works on β-1,4-galactan chain in an endolytic manner and also is capable of hydrolysing β-1,6-galactan with a lower efficiency. The thermostability, pH stability and broad substrate specificity of *At*GH53 makes it a versatile enzyme for biotechnological applications in the food sector, wine processing and galactooligosaccharide synthesis.

Keywords: *Acetivibrio thermocellum,* Endo-B-1,4-Galactanase, Kinetics, Galactooligosaccharides, B-1,6-Galactobiose

FIM-30 (Poster)

Enhanced Production and Purification of Prodigiosin from a Sequentially Mutated Strain of *Serratia marcescens* MCA-3

Anjali Anjali[1, 2], Vandana Sharma[2, 3], Deepika Singh[2, 3] and Saurabh Saran[1, 2]
*anjalibiotechnologist@gmail.com

[1]*Fermentation and Microbial Biotechnology, CSIR-Indian Institute of Integrative Medicine, Canal Road, Jammu, Jammu & Kashmir (180001), India*
[2]*Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, Uttar Pradesh (201002), India*
[3]*Quality Management & Instrumentation Division, CSIR-Indian Institute of Integrative Medicine, Canal Road, Jammu, Jammu & Kashmir (180001), India*

Abstract: The present study emphasizes on the development of a bio-process aimed at enhancing the production of prodigiosin pigment from a newly isolated *Serratia* sp MCA-3 strain. The study combines sequential random mutagenesis techniques and the exploration of low-cost substrates to enhance prodigiosin pigment production while ensuring cost-effectiveness and environmental sustainability. The hyper-prodigiosin-producing mutant strain of *Serratia marcescens* MCA-3 was generated through mutagenesis with a notable two-fold increase in prodigiosin yield compared to the wild strain. Among the various low-cost substrates evaluated, the utilization of chia seed (1%) resulted in remarkably high in prodigiosin yields of 1900.25 ± 6.71 mg/L in comparison of 604.08 ± 5.89 mg/L in basal media. Prodigiosin was purified using a two-step chromatographic process. Initially, column chromatography was employed to separate the prodigiosin pigment, achieving a significant purification. This was followed by preparative high-performance liquid chromatography (prep-HPLC) to further refine and achieve a purity of 97% for the prodigiosin. In addition; its antimicrobial activity was assayed against *Bacillus subtilis, E. coli, S. aureus*, and MRSA (Methicillin-resistant *Staphylococcus aureus*) which exhibited inhibition zones against them. These findings substantially underscores its potential as a valuable candidate in for various pharmaceutical drug developments. Moreover, the utilization of chia seeds serves as an innovative method for generating value-added prodigiosin.

Keywords: Prodigiosin, *Serratia marcescens* MCA-3, Mutagenesis, Chia seed, Antimicrobial activity

FIM-31 (Poster)

Optimizing Culture Conditions of the Newly Isolated Cyanobacterium Nostoc BGLR1 for Nutraceutical Development

Diksha Garg* and Urmila Gupta Phutela
*diksha.garg1232@gmail.com

Department of Microbiology, Punjab Agricultural University, Ludhiana, Punjab, India

Abstract: Euryhaline cyanobacteria are autotrophic microbes that hold potential for nutraceutical development due to their high metabolic activity, adaptability to euryhaline environments, rapid multiplication, and ability to accumulate valuable bioactive compounds. This study aimed to characterize *Nostoc* BGLR1 for the production of nutraceutical compounds, including carbohydrates, proteins, lipids, carotenoids, flavonoids, phenols, astaxanthin, and phycocyanin, while also optimizing physicochemical parameters such as pH (7.5–11.5), temperature (20–40 °C), light intensity (4000–8000 lux), growth period (20–40 days), and inoculum concentration (1–10%). Following optimization, the contents of *Nostoc* BGLR1—biomass, chlorophyll a, chlorophyll b, total chlorophyll, carbohydrate, protein, and lipid—increased by 28,708.03%, 651.9%, 410.34%, 283.98%, 656.25%, 164.6%, and 860%, respectively. Twelve therapeutic compounds, including acetoxyisobutyryl chloride, cyclohexasiloxane, dodecamethyl, caryophyllene, and cycloheptasiloxane tetradecamethyl, were identified using gas chromatography-mass spectrometry. BGLR1 also contained compounds such as ethyl 3-octyl butyl ester, 9,12-octadecadienoic acid, 9-octadecenoic acid (Z), methyl ester, 1-monolinoleoylglycerol trimethylsilyl ether, phytol, and methyl stearate. 16S rRNA gene sequencing confirmed that BGLR1 belongs to the genus *Nostoc* (GenBank accession number OQ600797.1). The cyanobacterium *Nostoc* BGLR1 represents a promising source for nutraceutical formulation.

Keywords: *Nostoc* BGLR1, Nutraceuticals, Cyanobacteria, Culture optimization, Bioactive compounds

FIM-32 (Poster)

Metagenome, Metabolome and Metagenome-Assembled Genomes of Some Naturally Fermented Soybean Foods of the Eastern Himalayas

Pynhunlang Kharnaior and Jyoti Prakash Tamang*
*jyoti_tamang@hotmail.com

Department of Microbiology, Sikkim University, Tadong, Gangtok, Sikkim (737102), India

Abstract: Fermentation of soybeans is one of the common practices in the Eastern Himalayas to produce an aromatic product through natural fermentation. The current study focused on investigating the microbial community in unexplored naturally fermented soybean (NFS) foods. The dominance of the bacterial population compared to other microbial domains was observed after examination using shotgun metagenome sequencing. We observed the abundance of *Bacillus* species, mainly *B. subtilis*, some lactic acid bacteria and coagulase-negative staphylococci (CNS). In addition to the microbial community structure, metagenome-assembled genomes (MAGs) analysis was performed to extract the potential single genome from metagenomic sequences, which led to the identification of seven MAGs such as *B. subtilis* and *B. thermoamylovorans* from *kinema*, *B. subtilis* and *E. faecalis* from *grep-chhurpi*, *P. acidilactici* from *peha*, *B. subtilis* from *peron namsing* and *B. velezensis* from *peruñyaan*. Annotation of the genome revealed the presence of several biomarkers corresponding to different biofunctional properties. Furthermore, metabolic studies revealed the presence of several compounds that may contribute to the flavor development and therapeutic properties of Eastern Himalayan NFS foods. In addition, a comparison of the microbiome and metabolites of *kinema, grep-chhurpi, peha, peron namsing* and *peruñyaan* with other fermented soybean foods from Asia revealed a discreteness that can be influenced by multiple factors such as pH, temperature, aeration, substrate and nutrient availability. The overall information of the present study clarified the detailed information on both the microbiome and metabolome of NFS foods in the Eastern Himalayas and their contribution to potential health beneficial properties of the products.

Keywords: Naturally fermented soybean foods, Spontaneous fermentation, Shotgun metagenomics, Microbial community, *Bacillus*, Metabolomics

FIM-33 (Poster)

In vitro Evaluation of the Probiotic and Functional Attributes of Yeast Isolated from Naturally Fermented Yak Milk Products of Sikkim

Sonam Lama* and Jyoti Prakash Tamang
*sonam.lama6233@gmail.com

Department of Microbiology, School of Life Sciences, Sikkim University, Gangtok, Sikkim (737102), India

Abstract: Naturally fermented milk (NFM) products from yaks (*Bos grunniens* L.) are predominantly produced by nomadic *Lachungpas*, *Lachenpas*, and *Dokpa* herders living at high altitudes in the Sikkim Himalaya. *Dahi*, *Chhurpi*, *Marr*, *Philu*, *Churkam*, *Shyow*, and *Khachu* are NFM products produced from yak milk. Culture-based studies have reported the coexistence of yeast in NFM products with lactic acid bacteria. However, the probiotic potential of yeast has not been evaluated. Therefore, the novelty of this study lies in the exploration of Saccharomyces and non-Saccharomyces yeast strains as potential probiotics from Yak NFM products. In this study, we isolated yeast strains from yak *dahi* and *chhurpi* collected from high altitudes in Sikkim. After isolation, yeast strains were preliminarily screened based on low pH tolerance (pH 2.0), bile tolerance (0.3% w/v), and hydrophobicity (≥ 80%), and the screened isolates were identified by phenotypic and genotypic methods. Furthermore, the strains were processed for other *in vitro* probiotic screening tests for adhesion, colonization, and antimicrobial activity, and probiotic gene detection was performed. Hemolytic activity, DNase test, gelatinase activity, and biogenic amine production test were performed for safety assessment, and cholesterol-lowering activity, antioxidant activity, antifungal activity, beta-galactosidase activity, and phytate hydrolyzing activity were assessed for functional characteristics. The strains were further processed for safety screening tests and functional property screening. Based on the statistical analysis for above-mentioned tests, *Saccharomyces cerevisiae* DCY-27 from yak *dahi* and *Kluyveromyces lactis* CUBY-19 from yak *chhurpi* were found to have probiotic potential.

Keywords: Yak, Fermented Milk products, Functional properties, Probiotic yeasts, *Saccharomyces cerevisiae, Kluyveromyces lactis*

FIM-34 (Poster)

Production and Purification of Indigenous *Lactobacillus* sp. Derived Biosurfactant

Kamini Pandey and Barkha Singhal*
*barkha@gbu.ac.in

School of Biotechnology, Gautam Buddha University, Greater Noida, Uttar Pradesh, India

Abstract: Microbial biosurfactants (BS) are structurally diverse group of surface-active agents produced by a wide variety of bacteria, yeast, and fungi from different environmental habitats. BS have diverse chemical structures, compositions, and an extensive variety of applications in dairy, food, cosmetics, detergent, and pharmaceutical industries. BS production from GRAS organisms such as *Lactobacillus* species is thrust area of research now-a-days, therefore we took indigenous *L. helveticus* for biosurfactant production. The selected Lactobacillus strain was subjected to growth curve analysis. It was carried out in 100 ml flask for 100 hours and readings have been taken at every 2 hours at 37℃ at to optimize the suitable conditions. The cell pellet was removed, and the acid precipitation was done by the adjustment of pH to 2.0, followed by the solvent extraction by adding an equal amount of mixture of chloroform and methanol (2:1, v/v) in a separating funnel. Biosurfactant was extracted and further stored at 4◦C. Various qualitative analysis was done to screen for BS production such as; BATH assay, Drop collapse method, Oil spreading assay and Emulsification assay. Extracted cell free BS and selected oil for every qualitative analysis (mustard oil, refined oil, petrol, and diesel) were kept in an equal ratio for incubation. The percentage adhesion (% adhesion) showed the presence of BS. Drop collapse was obtained by the oil-coated wells and the drop size after 1 min was observed for BS production. The oil displacement area is directly proportional to the surface-active compound in the solution, oil was displaced with oil-free clearing zone, and diameter of this clearing zone indicates the surfactant activity, and E24 test with selected oils showed the activity of biosurfactant by emulsifying the hydrocarbons present. Thus, the present manuscript is contributes to the novelty of biosurfactant production in *Lactobacillus* species.

Keywords: Probiotics, *Lactobacillus sp.*, BATH assay, Qualitative analysis, Emulsification

FIM-35 (Poster)

Biofortification of Probiotic Yoghurt using Microalgae *Spirulina*

S H Manoj [1], Sunil Pabbi[1*], Pranita Jaiswal[1], Shalini Gaur Rudra[2], Livleen Shukla[1] and D Vijyasri[1]
[*]sunil.pabbi@gmail.com

[1]*Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi (110012), India*
[2]*Division of Post Harvest technology, ICAR-Indian Agricultural Research Institute, New Delhi (110012), India*

Abstract: *Spirulina*, the superfood, is a rich source of proteins, antioxidants, pigments, vitamins and minerals. Utilizing this in our diet can immensely improve health and wellbeing. Currently, research is focussed on incorporating *Spirulina* into daily foods and its regular consumption can be a good option to address malnutrition and health issues caused due to busy lifestyle and bad food habits. In the present investigation, a potential *Spirulina* culture is used for biofortification of yoghurt. Of different *Spirulina* strains, *Spirulina platensis* (CCC477) was chosen based on higher biomass production and nutraceutical content. It was cultivated in raceways and the dried biomass thus obtained was used to prepare *Spirulina* enriched yoghurt (SEY) with 1%, 2.5% and 4% concentration. The physico-chemical properties of different SEYs *viz.* pH, %acidity, Syneresis% increased with increase in *Spirulina* concentration and during storage, while texture, rheology, sensory evaluation, colour and LAB population decreased with increase in *Spirulina* concentration and time of storage. Nutritional characteristics such as protein, carbohydrate, antioxidants, phenol and flavonoids increased with increasing *Spirulina* concentration from 4.7% to 6.54%, 10.48% to 12.46%, 41.47% to 61.65%, 146.6mg/100g to 213.34mg/100g, 0.95 mg/g to 1.4 mg/g respectively. The minerals *viz.* calcium, iron and zinc also increased from 389mg/100g to 395.3mg/100g, 10.48µg/g to 21.45 µg/g and 1.09 µg/g to 1.44 µg/g respectively. It was found that 1% SEY had comparable physicochemical properties but better nutritional composition than control. 1% SEY was also comparable to control for sensory evaluation suggesting it to be a better biofortified yoghurt than other SEYs and control.

Keywords: *Spirulina*, SEY (*Spirulina* enriched yoghurt), Physico-chemical, Nutraceuticals, Nutritional

FIM-36 (Poster)

Isolation and Virulence Gene Profiling of *A.butzleri*- an Emerging Foodborne Pathogen

Aimen Firdous, Vasanthi Kalli, Fathima Salam, Manjusha Lekshmi, Sanath Kumar and B.B Nayak[*]
*nayakbb@cife.edu.in

Fish processing Technology - FRHPHM Division, ICAR- Central Institute of Fisheries Education, Mumbai, Maharashtra (400061), India

Abstract: *Arcobacter*, a gram-negative bacterium has gained significant attention from the scientific community in recent years, primarily due to its emergence as a potential threat to human health and its role as zoonotic agent. Despite being relatively overlooked, *Arcobacter* species, particularly *Arcobacter butzleri*, is increasingly recognized for causing gastroenteritis. *A.butzleri* is concerning due to its array of virulence factors, like the ability to adhere to and invade epithelial cells, produce toxins, and resistance against multiple antibiotics. The study aimed to assess prevalence and distribution of Arcobacter in fish and shellfish samples and detect putative virulence genes in *A.butzleri*. A total of 30 seafood samples-14 finfish and 16 shellfish were procured from different fish markets of Maharashtra. *Arcobacter* was successfully isolated from 97% of samples, and most of the isolates (60) were identified as *A.butzleri* by molecular confirmation using PCR *A.butzleri* isolates were subjected to a set of 10 uniplex PCR assays targeting putative virulence genes (*ciaB, pldA, tlyA, mviN, cadF, hecA, hecB, iroE, irgA and cj1349*). The findings of the study were alarming since, almost all samples examined were positive for *Arcobacter* (97%- finfish and 100%- shellfish) and *A.butzleri* was detected in 99% of positive samples, indicating its notable predominance in seafood. Further, 100% *butzleri* isolates harboured 4 *putative virulence genes (cadF*, *ciaB*, *pldA* and *tlyA)* while 17% of *butzleri* isolates harboured all 10 putative virulence genes signifying potential of *A.butzleri* as a foodborne pathogen. This high presence of *A.butzleri* in seafood could act as a source of contamination, potentially spreading to the environment and humans. Thus, these

findings highlight the critical need for increased surveillance to address possible health concerns associated with this pathogen.

Keywords: *Arcobacter butzleri*, Zoonotic agent, Seafood, Contamination

FIM-37 (Poster)

A Surviellance of Foodborne Pathogens and Detection in Milk

Pooja Devi and Subburamu Karthikeyan*
*skarthy@tnau.ac.in

Department of Agricultural Microbiology, Tamil Nadu Agricultural University (TNAU)
Coimbatore, Tamil Nadu (641003), India

Abstract: Dairy products are incredibly nutritious and hence are also susceptible to contamination by a variety of microorganisms, including pathogenic bacteria. The microbiological safety of milk and non-fermented dairy products is critical because they might include a variety of foodborne pathogens that represent major threats to public health. This study systematically investigates the presence of critical pathogens in milk and non-fermented dairy products, focusing on *Salmonella* spp., *Escherichia coli*, *Pseudomonas* spp., and *Staphylococcus aureus*, as well as the assessment of total plate count (TPC) and total coliforms as indicators of overall microbial load and hygiene. The study uses a combination of traditional culture-based methods, which are known for their accuracy in quantifying live bacteria, and advanced molecular techniques, which provide great sensitivity and specificity in pathogen detection. This dual technique ensures a thorough examination of the microbiological quality of dairy samples, capturing both the presence of specific diseases and the whole microbial ecosystem within these products. The study finds that contamination levels vary across dairy products, with some bacteria being more frequent in various product kinds. The identification of *Salmonella* spp., and *Escherichia coli* (3*10^5cfu/ml), both major sources of foodborne disease, emphasizes the serious health concerns associated with consuming contaminated dairy products. Furthermore, the presence of *Pseudomonas* spp., which is frequently associated with spoiling and *Staphylococcus aureus* (4.2*10^4cfu/ml), which is associated with poor hygienic practices, highlights the crucial importance of monitoring both pathogenic and spoilage organisms in dairy production. These findings highlight the importance of strict cleanliness measures throughout the dairy production chain, from farm to processing and distribution. Proper sanitation, temperature control, and handling methods are essential for reducing contamination risks and ensuring customer safety. This study gives useful insights into the current condition of microbiological safety in the dairy business, as well as a call to action for further surveillance and the improvement of food safety regulations.

Keywords: Milk, Pathogen, Quality, Microorganisms, Hygiene

FIM-38 (Poster)

Technological Evaluation of Two Wild Yeast Strains Isolated from Rice Wine from Cold Dessert Region of Western Himalayas

Deepanshu Punyani*, Nayan Rishi, Souparno Paul and Gunjan Goel
*deepunyani1111@gmail.com

Department of Microbiology, Central University of Haryana, Mahendergarh (132031), Haryana, India

Abstract: Yeast is widely recognized for its ability for production of alcoholic beverages with established health benefits. In Indian context, Yeast mediated alcoholic fermentation is an unlatched research area with high throughout applications in food industry. Therefore, there is a need to explore more wild type yeast strains with better fermentation kinetics and added advantages for production of characteristic aroma, flavour and texture of rice-based wines. The present study reports the isolation of two wild type strains from starter mix known as Phab and Dhalli available in the regions of Himachal Pradesh. The technological performance of yeast strains was determined by their ability to tolerate different pH (2.0-4.0), temperature (25° C-55° C), sugar concentrations (0-50%), ethanol tolerance (0-25%) through viable cell culture assays. A higher survival of yeast

strain isolated from Phab was observed at different osmotic concentrations whereas the strain isolated from Dhalli was able to tolerate pH of 2.0 with higher survival rate. Both the strains were observed as thermotolerant strains as these were able to grow at a temperature of 37˚ C to 55˚ C although the with strain from Phab exhibited higher survival. The strains were able to tolerate an ethanol concentration of 20%. A lab scale fermentation of rice was conducted using both strains. The fermentation was conducted using rice as base along with jaggery and sugar as major ingredients. The fermentation was conducted at 30˚ C upto 7 days. A continuous drop in Brix value was observed during the period of 7 days indicating the completion of fermentation. The LC MS analysis of fermentation broth indicated the presence of various antimicrobial substances, Organic acids, Phenolics such as Ferulic acid, Caffeic acid and other derivatives, Fatty acids, Alkaloids and Terpenes, Amines and Sulfones.

Keywords: Yeast, Thermotolerant strain, LC MS analysis, Rice-based wines

FIM-39 (Poster)

Optimization of Growth Medium for β-galactosidase Production by *Streptomyces thermocarboxydus* (strain NBRC 16323) by Response Surface Methodology using Whey, Scale up and Enzyme Characteristics Study

Kalyani Neti,* Swati A Peshwe and Suchita Bharambe
*kalyanirmurthy@gmail.com

Department of Microbiology, Government Institute of Science, Aurangabad, Maharashtra, India

Abstract: In this study CCD (Central Composite Design) is employed the enhance production of β-galactosidase by the newly isolated *Streptomyces thermocarboxydus* (strain NBRC 16323) with Whey and $MgSO_4.7H_2O$. From the design, maximum enzyme production is observed at 7.3% whey and 0.05% $MgSO_4.7H_2O$. Statistical analysis of the model showed to be good with $p< 0.05$ and $R^2 = 0.78$. Enzyme activity of optimized medium is validated with that of basal medium and it showed an increase from 12.6 to 87.83 µmoles/min/ml by a 6.9-fold raise. Scale up of production medium is evaluated in various volumes ranging from 50ml -1500ml with a 3-day old inoculum and 1% seed volume and assayed. In all the volumes, enzyme activity is found to be nearly stable ranging from 90-98% of the optimized level, indicating that the isolate has high potential for industrial scale up. Enzyme purification and characteristics will be presented and discussed further.

Keywords: β-galactosidase, Whey, Central Composite Design, Validation, Scale up, Purification

FIM-40 (Poster)

Protein Estimation from *Spirulina platensis* Fermented with *Lactobacillus plantarum*

Taruna Sheoran* and Namita Singh
*tanusheoran@gmail.com

Lab no. 202, Microbial Biotechnology lab, Department of Biotechnology,
Guru Jambheshwar University of Science and Technology, Hisar, Haryana, India

Abstract: *Spirulina,* commonly known as Single Cell Protein, is used for consumption by humans due to its high nutritional content specially protein content and nutraceutical properties, anti-oxidant, and anti-diabetic properties. In order to meet the growing demand of protein, there is a need to find nutrient rich and cost-effective products suplimented with *spirulina* protein. In this study Zarrouk's medium is used for production of *Spirulina*, growth is evaluated in terms of growth kinetics. *Spirulina* was cultivated at 120 rpm and a light intensity of 156 µmol m^{-2} s^{-1} in a 250 ml flask with a working volume of 100 ml in triplicate. pH of all the sources is maintained at 9 and obtained spirulina was lyophilised for further studies. *Spirulina* is fermented with *L. Plantarum* (NCDC-25) and samples were obtained at 0, 24, 48 and 72 hr of incubation at room temperature. Shift of pH toward acidic side was observed as with increase in time. Protein was isolated from fermented and

non-fermented spirulina by Trizol method and estimated by BCA method. the protein content in the Sample- I (Spirulina at 0hr fermentation), Sample- II (After 24hr fermentation), Sample-III (After 48hr fermentation) and Sample-IV (after 72hr fermentation) were estimated as 2.3 mg/g, 2.5 mg/g, 3.2 mg/g and 3.63 mg/gm respectively in pellet and 1.9 mg/ml, 3.09 mg/ml, 2.58 mg/ml and 2.1 mg/ml respectively in supernatant. Further analysis was done with SDS Page and bands od protein are observed.it is observed that content of protein increases upon fermentation.

Keywords: *Spirulina,* Single cell protein, Zerrouk's medium, Protein

FIM-41 (Poster)

Enhancement of therapeutic properties of prebiotic Amaranthus fortified novel synbiotic yogurt fermented with probiotic *Lactobacillus spicheri* G2

Karuna Thakur* and Nivedita Sharma
*karunathakur2108@gmail.com

Microbiology Laboratory, Department of Basic Sciences, College of Forestry, Dr. Yashwant Singh Parmar University of Horticulture and Forestry, Nauni-Solan, Himachal Pradesh (173230) India

Abstract: Synbiotic milk products containing prebiotics (millets, cereals and pseudo cereals) and probiotics fermenting Lactic acid bacteria (LAB), play a significant role in the fanjunctional food industry by producing enzymes required for the synthesis of bioactive compounds, such as fatty acids, inulin-type fructans, polyphenols and bioactive peptides. These substances offer numerous therapeutic products that have not been commercially produced and promoted in India at large scale for many years due to their traditional household use and lack of standardized technology. So, the present study introduces an innovative approach to functional foods by leveraging *Lactobacillus spicheri* G2, a potent probiotic strain, to ferment amaranth plant milk extract + cow milk into a superior synbiotic yogurt. Over a five-day assessment, our novel yogurt showcased exceptional physiological and biological properties, including optimal pH, titratable acidity, and antioxidant activity. Notably, G2 fermentation resulted in a yogurt with significantly higher levels of total protein, total phenolic content, and total flavonoid content as compared to traditional native strain. This enhancement was observed in both formulations: amaranth extract combined with cow milk and cow milk alone as the control. Sensory evaluations further confirmed the enhanced appeal and quality of the G2-fermented product. This ground-breaking development highlights the therapeutic potential of *L. spicheri* G2 but also sets a new benchmark for high-value vegan yogurt in the market.

Keywords: Amaranthus, Fermentation, *Lactobacillus spicheri*, Prebiotic, Synbiotic, Therapeutic

FIM-42 (Poster)

Pigmented Microbes: A Potential Source of Natural Colors and Nutraceuticals

Sangeeta Yadav* and Prof. Alka Sharma
*sangeetafoodtech12@gmail.com

Department of Food Technology, Guru Jambheshwar University of Science & Technology, Hisar, Haryana (125001), India

Abstract: Pigments are used in the food industry to improve the acceptability & overall sensory attributes of food. Recently it is observed that consumers are shifted towards the natural pigments from synthetic food colors, however there are some limitations of these pigments including low yield, temperature & pH sensitivity, short shelf life, light stress and susceptible to high food processing conditions. In this context, microbial pigments are potential solution. They offer sustainable, eco-friendly and cost - effective substitute with high yield and improved food safety & quality. These pigments are highly resistant towards light stress, nutrient stress, and salinity stress. Currently these pigments are extracted through different non-conventional techniques such UAE (Ultrasound-assisted extraction), MAE (Microwave-assisted extraction), SFE (Supercritical fluid extraction) &

PLE (Pressurised liquid extraction) as they offer several benefits such as high extraction yield, rapid extraction and extraction at room temperature. Biopigments, including carotenoids, anthocyanins, prodigiosin, anthraquinones, chlorophyll and phycobiliproteins are derived from bacteria, fungi, and microalgae which provides a wide range of colours, including red, orange, yellow, blue, and purple. Therefore, pigmented microbes are utilized in the food industry as a source of natural colorants. Additionally they can be used as dietary supplements and functional ingredient due to various properties including antioxidative, antilipidemic, anti-tumor, anti-inflammatory, antimicrobial, antiproliferative, anti-obesity, anti-diabetic and anti-cancerous. Furthermore, the versatile use of biopigments highlights their potential as sustainable bioresources for future advancements in food technology and human health.

Keywords: Biopigments, Phycobiliproteins, Prodigiosin, Microbial pigments, Natural colorants, Non-conventional techniques

FIM-43 (Poster)

Whole Genome *de novo* Sequence Analysis of a Novel Environmental Isolate *Bacillus drentensis*: Untargeted Metabolomics and Validation of Hyaluronic Acid Production

Simran Gagneja[1], Neena Capalash[2] and Prince Sharma[1*]
*princess@pu.ac.in

[1]*Department of Microbiology, Panjab University, Chandigarh, India*
[2]*Department of Biotechnology, Panjab University, Chandigarh, India*

Abstract: Hyaluronic acid, a non-sulfated glycosaminoglycan, is an integral component of extracellular matrix of vertebrate tissues. It regulates vital biochemical pathways and assists is tissue hydration and homeostasis. Due to extensive physiological properties, it has become a holy grail ingredient in cosmetic formulations and is considered a gold standard in the field of aesthetic surgeries. Its biocompatible and biodegradable nature has helped in the development of effective drug delivery platforms for cancer therapy as its lowers the toxicity of chemotherapeutic drugs and enhances drug retention. Initially isolated from vitreous humor of bovine eyes, its multitude applications in cosmetology and pharmacology have led the scientific research to focus on devising bacterial fermentation-based technology for higher yield and reduced production cost. *Bacillus drentensis*, a novel environmental isolate belonging to family firmicutes, was investigated for hyaluronic acid production through initial screening process developed in our lab using recombinant hyaluronidase treatment of cells and visualization of cell surface morphology using FE-SEM. Whole genome consisted of 5,683,500 bp with a GC content of 43.4%, including 4662 coding sequences (CDS), 108 tRNAs, 1 tmRNAs and 7 rRNAs genes. This work reveals complete genomic analysis of *B. drentensis* and predicts the metabolic pathway for hyaluronic acid production. To understand metabolic diversity of the strain, we performed *in-silico* predictions of metabolic pathways and untargeted metabolomics study was carried out through LC-MS analysis of the fermentation broth. Hyaluronic acid production was validated through NMR and FTIR of the purified product. Statistical optimization through RSM increased its production to ~8 gL^{-1}.

Keywords: Hyaluronic acid; Complete genome; *Bacillus drentensis*; Environment isolate, Metabolic diversity, Untargeted metabolomics

FIM-44 (Poster)

Development of Probiotic Health Drink from Vegetable Juice (Bottle Gourd)

Mandeep Kumar*, Supriya Sheokand and Namita Singh
*nainmandeep70@gmail.com

Lab 202, Microbial biotechnology Lab, Department of Bio & Nano Technology,
Guru Jambheshwar University of Science & Technology, Hisar, Haryana (125001), India

Abstract: The purpose of this study was to develop a non-diary probiotic drink for individuals who have dietary restrictions (such as vegan) or lactose intolerances that prevent them from consuming dairy products. This study

sought to determine how the physiochemical characteristics of bottle gourd juice were affected by lactobacillus probiotics. Fermentation of bottle gourd juice was done for 48 hours by lactic acid bacteria (LAB); *Lactobacillus plantarum (*NCDC-20), *Lactobacillus acidophilus* (NCDC-17), *Lactobacillus fermentum* (NCDC-141), and *Lactobacillus rhamnosus* (NCDC-347). Total soluble solids and pH of fermented juice were analysed at every eight-hour interval for 48 hours, and total sugar, total phenolic content, total flavonoid content, and antioxidant activity were recorded before and after fermentation. It was observed that total sugar content was decreased, whereas, total phenolic content, total flavonoid content, and antioxidant activity were increased after the fermentation.

Keywords: Probiotics, Lactobacillus, Bottle gourd

FIM-45 (Poster)

Recombinant Laccase Mediated Bio-Melanin Synthesis for Cosmeceutical Applications

Annu George[1*], Neena Capalash[2] and Prince Sharma[1]
*annugeorge951@gmail.com

[1]*Department of Microbiology, Panjab University, Chandigarh, India*
[2]*Department of Biotechnology, Panjab University, Chandigarh, India*

Abstract: Melanin, a complex polymer responsible for pigmentation in many organisms, is synthesized through a series of enzymatic reactions. The global melanin market is projected to grow to USD 18 million by 2028, with melanin currently valued at $544 per gram, which is significantly higher than gold. Due to its extensive applications, there is a rising demand for natural melanin production, as opposed to synthetic alternatives, to avoid harmful effects and boost efficiency. Our research focuses on producing natural, toxin-free eumelanin from L-DOPA, a natural precursor, via enzymatic oxidation using recombinant bacterial laccase. We expressed laccase from *Rheinheimera* sp. which was fused with signal peptide of *Staphylococcus aureus* hyaluronidase: (Hylsig: RhLacc Fusion) in *E. coli* using the pET28a vector and purified it through a Ni-NTA column. The purified laccase optimally polymerized L-DOPA into eumelanin at pH 7 and 50℃ in 20 mins. Eumelanin was easily purified by centrifugation at 4000 x g for 15 minutes and characterized by SEM, FTIR analysis, and UV-visible spectra, confirming its similarity to human eumelanin produced by melanocytes. Additionally, the purified melanin exhibited 87.65% free radical scavenging (antioxidant) activity when tested with ABTS radical cations. This purified melanin can be produced on a large scale and utilized in various cosmetic applications.

Keywords: Eumelanin, Recombinant laccase, L-DOPA, Enzymatic oxidation, Antioxidant, Cosmetic application

FIM-46 (Poster)

Safety Assessment of *Pediococcus acidilactici NCDC 252* Strain as a Probiotic in Mice Model

Pooja Gahlyan[a], Suman Dhanda[a], Sandeep Kumar[b] and Shobhna Singh[c]
*pooja152gahlyan@gmail.com

Kurukshetra University, Kurukshetra, Haryana, India

Abstract: Pediococcus acidilactici NCDC 252 is lactic acid bacteria with essential probiotic attributes. Its's various probioceuticals and enzymes have been purified and characterized. NCDC 252 exhibited aggregation, coaggregation and adherence to intestinal epithelium. In-silico genome analysis and in-vitro studies confirmed its safety as probiotic but thorough in-vivo examination of safety is essentially required for using it for humans and animals. Present study was conducted to assess its safety at two doses (1×109 CFU/kg, 1×1010 CFU/kg) by in-vivo acute and sub-acute oral toxicity tests in mice.

Haematological and serum biochemical parameters were analysed to investigate any pathophysiological damage as histopathological studies were conducted to assess any organ damage. Its effect on β-glucosidase and

β-glucuronidase was also studied. No toxicity was observed in acute and sub-acute tests in NCDC 252 fed mice. No adverse effect was reported with respect to growth and feed consumption in NCDC 252 fed group. No significant difference was observed in haematological, serum biochemical parameters and organs in any of NCDC 252 treated groups. β-glucosidase and β-glucuronidase activities decreased
Significance: The current study of NCDC 252 suggests that both its studied doses are safe for animal consumption. NCDC 252 can be recommended to be used as probiotic

Keywords: *Pediococcus acidilactici*, β-glucosidase, β-glucuronidase, NCDC 252, In-silico genome analysis

FIM-47 (Poster)

Purification and Characterization of *A.tamarii* β-mannanase for the Generation of Prebiotic Mannooligosacharides (MOS)

Dharini Pandey* and Naveen Kango
*dharini2112@gmail.com

Dept of Microbiology, Dr. Harisingh Gour Vishwavidyalaya (A Central University), Sagar, Madhya Pradesh

Abstract: The agricultural waste is disposed improperly by burning and dumping, resulting in polluted habitats and posing safety and ecological concerns. In the present study agro waste copra meal was utilized for the production of β-mannanase from *A. tamarii* NKRC1229. Process parameters used to produce enzyme were optimized through the Response Surface Methodology (RSM) and an artificial neural network coupled with a genetic algorithm (ANN-GA). Resulting in 62-fold increased β-mannanase yield (4399.67 U/gds) as compared to the unoptimized process (70.9 U/gds). The purified β-mannanase (75kDa) showed specific activity of 225.91 U/mg and 8.98-fold purification. The enzyme was stable at 50℃ up to 60 min retaining 97.09% residual activity. Zinc, chloroform, β-mercaptoethanol, and acetonitrile significantly enhanced the β-mannanase activity,whereas Hg^{2+}, EDTA, sodium azide, and SDS strongly inhibited it. β-mannanase generated MOS by hydrolyzing various mannnas, LBG, KG, and GG yielding 46.32 mg/mL, 34.80 mg/mL, and 1.37 mg/mL, respectively. Mannotriose (M3), Mannotetraose (M4), and higher DP oligos (DP 6-5) were the major products. Further, in silico molecular modelling and docking studies were performed to evaluate the physico-chemical nature and catalytic behariour of the A.tamarii β-mannanase.

Keywords: β-mannanase, *A.tamarii*, ANN-GA, Mannooligosaccharide (MOS), Molecular modeling, Molecular docking

FIM-48 (Poster)

Screening, Production, Optimization, Characterization, and Biotechnological Applications of L-asparaginase from Indigenous Fungal strain *Fusarium solani*

Shivangi Mudaliar* and Pradeep Verma**
*shivimudaliar094@gmail.com, **pradeepverma@curaj.ac.in

Department of Microbiology, School of Life Sciences
Bioprocess and Bioenergy (BPBEL) Laboratory, Central University of Rajasthan
Bandarsindri, Kishangarh, Ajmer, Rajasthan (305817), India

Abstract: Microbial L-asparaginase has attracted considerable attention due to its extensive applications in the pharmaceutical and food industries. L-asparaginase (L-asparagine hydrolase, E.C.3.5.1.1) hydrolyzes L-asparagine, resulting in the formation of aspartic acid and ammonia. In this study, screening of native fungal isolates was carried out for L-asparaginase production. The qualitative plate assay was performed using a modified Czapek dox medium supplemented with dye phenol red. Among the seven (7) fungal isolates screened, four (4) of them, i.e., *Fusarium solani*, *Podaxis* sp., *Anulate* sp., and *Entoloma* sp., produced a pink zone suggesting the production of L-asparaginase. The zone diameter of the isolates was measured, and the strains with maximum diameter indicated higher L-asparaginase production. The quantitative assay was performed for

L-asparaginase production in a modified Czapek Dox media via submerged fermentation. Amongst the four (4) strains, one culture, i.e., *Fusarium solani* was selected based on its higher L-asparaginase activity. Further, optimization was performed using the One-Factor-At-A-Time (OFAT) approach, and various organic and inorganic carbon and nitrogen sources were optimized. The strain *Fusarium solani* showed the highest activity of 50.80 U/mL at pH 6.2 and 37°C after 3 days of incubation when glycerol was used instead of glucose as the carbon source. After optimization, L-asparaginase was further purified using 70% chilled acetone, resulting in a 0.28-fold purification yield. Depending on the organism it originates from, the partially purified protein exhibits a band ranging from approximately 85 kDa to 160 kDa, and its characteristic features will be studied to determine its biotechnological applications.

Keywords: L-asparaginase, Fungi, OFAT, Enzyme activity, Fermentation, Czapek dox

FIM-49 (Poster)

Radiation Sensitivity Studies of a Bacterium, *Methylorubrum thiocyanatum* Isolated from Irradiated Chilli Powder

Milind Kumbhare[1*], Shrutika Kadam[2], Ramakant Sahu[1] and Pradip Mukherjee[1]
*kumbhare@britatom.gov.in

[1]*Board of Radiation & Isotope Technology, Sector-20, Vashi, Navi Mumbai, Maharashtra (400703), India*
[2]*SIES College of Arts, Science & Commerce, Sion (W), Mumbai, Maharashtra (400022), India*

Abstract: Preservation of spices by gamma radiation is a well-known technology. Radiation processing plant, Vashi is the first irradiation facility for spices in India. The microbiological data on variety of spices processed at the facility showed frequent occurrence of radiation resistant, pink coloured, Gm -ve, rod shaped bacterium in most of the irradiated chilli powder. 16S rRNA sequencing data (~1200 bp) of the bacterium showed 99.93% similarity with the bacterium *Methylorubrum thiocyanatum.* The said bacterium when studied for its radiation sensitivity showed a D_{10} value (decimal reduction value) of 1.94 kGy in phosphate buffered normal saline. The same studies when repeated in chilli powder showed D_{10} value of 2.47 kGy with 27% increase in its resistance to radiation which might be due to radio-protective effect of the carotenoids present in chilli powder. Similar studies when carried out with *S. aureus* there observed 50% increase in its D_{10} value. US FDA regulations allow the irradiation of herbs & spices up to 30 kGy of radiation dose, however Government of India has approved radiation dose of 6-14 kGy for irradiation of spices. Thus, the dose limits for irradiation of chilli powder needs to be increased for better inactivation of microorganisms considering the radiation protective effect of chilli powder.

Keywords: Irradiation, Spices, Chilli powder, D_{10} value, Radiation

FIM-50 (Poster)

Purification, Characterization, and Pharmacological Evaluation of the Biosurfactant from *Lactobacillus plantarum* JBC5: *In Vitro* and *In Vivo* Toxicity Assessment

Anushree Roy[a,b] and Ashis K. Mukherjee[a,b*]
*akm@tezu.ernet.in

[a]*Division of Life Science, Institute of Advanced Study in Science and Technology, Paschim Boragaon, Guwahati, Assam (781035), India*
[b]*Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, India*

Abstract: Bacteria-produced biosurfactants are increasingly being recognized as novel substitutes for chemical surfactants in diverse industries. Due to their robust surface activity and exceptional emulsification capabilities, they are highly suitable for use in the food and pharmaceutical industries. The biosurfactant obtained from the probiotic strain *Lactobacillus plantarum* JBC5 obtained from a local curd is secure for human consumption because it is classified as Generally Recognized as Safe (GRAS) organism. The biosurfactant production

capacity of LPJBC5 was assessed, indicating that lactose and yeast are the most suitable carbon and nitrogen sources, respectively, at pH 6 and 30°C for achieving the highest biosurfactant yield. The strain yielded a biosurfactant concentration of 2.37 ± 0.2 g/L, predominantly cyclic lipopeptides, determined through mass spectrometry analysis. This biosurfactant demonstrated excellent emulsifying activity (E_{24}) with mustard, olive, and refined oils and showed antimicrobial activity against *E. coli* 1687, highlighting its potential applications in the food and pharmaceutical industries. Toxicity studies using MTT assays on CC1 liver, L9-29 mouse fibroblast, and NRK-52e rat kidney cell lines showed no significant toxicity at concentrations of 250 µg/mL and 500 µg/mL post 48 hours of incubation. *In vivo* testing in Swiss albino female mice revealed the high safety of this biosurfactant for human use. The partially purified biosurfactant can be applied for various human purposes such as antimicrobials, food industries, etc.

Keywords: Biosurfactant, *Lactobacillus plantarum,* Cyclic lipopeptides, Antimicrobials

FIM-51 (Poster)

Comparative Virulence Profiling of Microaerophilic *Arcobacter Spp.* in Seafood and its Environment

Fathima Salam, Vasanthi Kalli., Aimen Firdous., Manjusha Lekshmi., Sanath Kumar H., and Nayak B. B.*
*nayakbb@cife.edu.in

Fish Processing Technology, FRHPHM Division, ICAR-Central Institute of Fisheries Education, Off Yari Road, Panch Marg, Andheri West, Mumbai, Maharashtra (400061), India

Abstract: *Arcobacters* have emerged as important zoonotic pathogens associated with foodborne outbreaks worldwide. These are gram-negative microaerophilic bacteria with stringent growth requirements, often isolated from domestic animals, meat (poultry, seafood, pork, goat, beef), vegetables and humans. *Arcobacters* are implicated as causative agents of bacteraemia, endocarditis, and gastroenteritis in humans. This investigation deals with the isolation of major pathogenic species such as *A. butzleri*, *A. cryaerophilus*, and *A. skirrowii* from 63 seafood samples comprising 26 finfish, 24 shellfish and three water samples collected from fish landing centres and retail markets of Mumbai, India. The virulence gene characterisation of these isolates revealed the presence of major putative virulence genes *cadF, ciaB, cj1349*, *mviN*, *hecA* and *hecB* associated with adhesion, invasion, and toxin secretion. Fourteen samples were positive for at least one *Arcobacter* spp. with an overall incidence of 28.5 %. A total of 64 isolates were recovered, which were predominantly identified as *A. butzleri* (n=26, 41.8%), followed by *A. skirrowii* (n=12, 19.76%) and *A. cryaerophilus* (n=10, 16.27%). Fifteen isolates of each of the three pathogenic species including isolates from laboratory repository were screened for the presence of seven major virulence genes as mentioned above. Thirteen isolates of all the species carried at least one virulence gene, *cadF* which codes for fibronectin-binding protein. No less than five virulence genes were present in 80% of *A. butzleri* isolates, whereas 53% and 46% of *A. skirrowii* and *A. cryaerophilus* respectively harboured at least 4 virulence genes. The study reveals the pathogenic potential of seafood-borne *Arcobacter* spp., which could be similar to that of the clinical isolates as well. Among the isolates recovered in the study, *A. butzleri* is considered to be the most prevalent and virulent species, a fact which points at the need for mitigation measures to contain the incidence of this bacterium in seafood.

Keywords: Zoonotic pathogen, Microaerophiles, *Arcobacter,* Virulence genes, Pathogens

FIM-52 (Poster)

Production of high-value sandalwood fragrance in yeast through synthetic biology

Ananth Krishna Narayanan[1,2], Rakesh Rao K. R[1], Megha K[1] and Dinesh A. Nagegowda[1,2*]
*nananthkrishna1996@gmail.com

[1]*Molecular Plant Biology and Biotechnology Lab, CSIR- Central Institute of Medicinal Aromatic Plants, Research Centre, Bengaluru, Karnataka (560065), India*
[2]*Academy of Scientific and Innovative Research, Ghaziabad, Uttar Pradesh (201002), India*

Abstract: Sandalwood oil, obtained from the steam distillation of the heartwood of the Sandalwood tree, *Santalum album* L., is one of the most expensive essential oils. The exploitation of wild sandalwood for its oil has decimated natural populations and has put the species in the "vulnerable category" of the IUCN RED list. Commercial plantations of sandalwood are limited by its slow growth, long rotation times of 15-20 years, poaching and significant variation in oil yield and quality depending upon geographic locations, age of the plant, etc. The main constituents of sandalwood oil are sesquiterpene alcohols Z-α-santalol, Z-β-santalol, Z-*epi*-β-santalol and Z-α-*exo*-bergamotol and are responsible for the characteristic fragrance of sandalwood oil. Chemical synthesis of these compounds has been attempted before but the process is multi-step, consumes environmentally harmful chemicals and solvents, and is low yielding, hence none of them have reached economically viable scales of production. Biological production of these compounds in an engineered microbial platform is a more enticing alternative to chemical synthesis of these compounds. Of these, *Saccharomyces cerevisiae,* hereafter 'yeast', is an excellent and proven platform for the production of sesquiterpenes. The precursors of sesquiterpenes are produced in this organism by the mevalonate pathway (MVA pathway), which is usually required for the production of ergosterols. This study presents the journey thus far in engineering yeast for enhanced production of sandalwood fragrance using sandalwood essential oil pathway genes, along with different engineering strategies to achieve higher production.

Keywords: *Saccharomyces cerevesaie*, Synthetic biology, Terpenoids, Sandalwood oil, Metabolic engineering

FIM-53 (Poster)

Enzymatic Production of Xylo-Oligosaccharides from Banana Pseudo-Stem Fiber

Oviya Govindaraj*, Nellaiappan Olaganathan Gopal and Sivakumar Uthandi
*goviya96@gmail.com

Biocatalysts Laboratory, Department of Agricultural Microbiology, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu (641003), India

Abstract: In recent years, lignocellulosic biomass has gained a lot of attention, enacting as one of the promising feedstocks for the production of value-added biochemicals and biofuels. Being the top producer of banana, India generates around 60-80 million metric tonnes (MMT) of banana pseudostem wastes which remains unutilized. Banana pseudostem fibers are rich in lignocellulosic resources and thus the present study aimed to utilize the banana fiber biomass for production of xylo-oligosaccharides. Initially, the banana fiber was subjected to EnZolv pretreatment and the influential parameters in the EnZolv process were optimized for efficient delignification. The pre-treated banana fiber was used for extraction of xylan using alkali assisted hydrothermal extraction process which resulted in the highest xylan (81%) recovery when incubated with 12 % alkali for 8 h followed by steam treatment. The extracted xylan was used as a feedstock for xylooligosaccharides production by using the enzymatic hydrolysis. The optimized process parameters from RSM revealed a significant XOS yield of 2.929 mg mL^{-1} was obtained when the process was run at 2% w/v biomass load with 100 U g^{-1} solid state xylanase (WBX) load by maintaining the initial pH (4.5) followed by incubation at 45 °C for 36h. The optimized process parameters from the design produced XOS yield of 4.051 mg mL^{-1} when the process was run at 3% w/v biomass load with 80 U g^{-1} xylanase (BWX) by maintaining the initial pH 5.0 followed by incubation at 45 °C for 24 h. The produced xylo-oligosaccharides was estimated for their prebiotic efficacy and the results indicated that the probiotic *Lactobacillus plantarum* LP1401 was able to grow at 1% XOS with a prebiotic index of 1.47. From the observations, it could be evident that the banana pseudostem waste can be utilized for the generation of value-added products thus eliminating environmental pollution through waste management and paves the way for circular economy.

Keywords: Banana fiber, Xylo-oligosaccharides, Xylanase, Optimization, Response Surface Methodology, Prebiotics

FIM-54 (Poster)

Production of Bioethanol from Waste Newspapers

Rashmi Meena* and Zahabiya Badshah
*rashmimeena799@gmail.com

Maharaja Ranjit Singh College of Professional Sciences, Indore, Madhya Pradesh, India

Abstract: Bioethanol is currently being considered as a potential replacement for conventional gasoline, especially as it possesses similar and some superior qualities enabling a reduction in greenhouse gases and increasing fuel reserve. Ethanol is increasingly becoming popular as a fuel alternative to petrol, or in a blend with gasoline to cope up with the rising petroleum crisis. Bioethanol is produced through the fermentative process of biological matter, either waste products or crops grown specifically to create ethanol. In this study, we aim to provide a biodegradative solution to cellulosic waste in the form of newspapers into fermentable sugar which can further be fermented to ethanol. Cellulose in the newspaper was saccharified to sugar using cellulase produced by *Streptomyces sp. SA19*. For carrying out fermentation of derived sugar, screening was done and yeast was isolated from different fruit juices on two different media. High-yielding yeast isolate was used for the production of bioethanol by submerged fermentation. The isolate BJ1 was identified by 16S r RNA sequencing method at CSIR-National Chemical Laboratory, Pune as *Candida sp.* Our isolate was found to be closely similar to *Candida neerlandica* NRRL Y-27057. Furthermore, optimization was carried out to determine the ideal fermentation period. The highest bioethanol production was observed on the sixth day of the fermentation. Further optimization of the process shall be done to increase the efficiency of bioconversion. The encouraging results of our study shall help us to materialize the mindful use of waste materials that can help to develop cleaner environment and shall meet the demand of decreasing fossil fuels.

Keywords: *Saccharomyces cerevisiae*, Yeast, Newspaper, Fruit juices

FIM-55 (Poster)

Exploring Amylase Activity in Bacteria Isolated from Cereal- Infesting Insects: A Microbiological Approach and Usefulness in Industries

Dattabhushan Karvir Thakare
bkthakare41287@gmail.com

Yogeshwari Mahavidyalaya Ambajogai. Department of Microbiology

Abstract: Microbial amylases have emerged as a cornerstone in biotechnology due to their diverse applications and cost-effective production. These enzymes, primarily produced by bacteria, fungi, and yeast, catalyze the hydrolysis of starch into sugars, offering immense industrial significance. This poster presentation delves into the production, properties, and applications of microbial amylase, highlighting its role in various sectors such as food, textile, paper, and biofuel industries. We will explore the genetic and environmental factors influencing microbial amylase production, with a focus on optimizing fermentation processes to enhance yield and enzyme activity. Recent advancements in genetic engineering and microbial fermentation techniques have revolutionized the production and functionality of amylases, making them more efficient and adaptable to industrial needs. Furthermore, the presentation will discuss the biochemical characteristics of microbial amylases, including their stability, substrate specificity and activity under different environmental conditions. Case studies showcasing successful industrial applications and innovations in microbial amylase utilization will be presented, illustrating the enzyme's pivotal role in enhancing process efficiency and product quality. The granary weevil, *Sitophilus granarius*, is a notable pest in stored grain products, but recent research has uncovered its potential as a source of valuable enzymes. This presentation focuses on the characterization of microbial amylase derived from *Sitophilus granarius*. Amylases are crucial enzymes in the conversion of starches into sugars, and they have extensive applications in industries such as food, biofuel, and textiles.

Our study involves isolating and purifying amylase enzymes from *Sitophilus granarius*, followed by a comprehensive analysis of their biochemical properties, including optimal pH, temperature stability and substrate specificity. We also explore the genetic basis of these enzymes and compare their efficiency and stability with commercially available amylases.

The findings reveal that the microbial amylase from *Sitophilus granarius* exhibits unique characteristics that make it a promising candidate for industrial applications. Its high thermal stability and broad pH range offer

advantages in processes where traditional amylases may be less effective. Moreover, the enzyme's performance in hydrolyzing various starch substrates highlights its versatility. This research not only provides insights into the potential biotechnological applications of *Sitophilus granarius* amylase but also paves the way for developing innovative solutions to enhance industrial processes. By turning a pest into a resource, we demonstrate how biological research can contribute to sustainability and economic efficiency.
Amylases are significant industrial enzymes with diverse applications across various industries. This study aimed to isolate and screening of amylase-producing microorganisms from the gut and salivary gland microflora of cereal-spoiling insects. Samples were collected from cereals infested by pests such as the Lesser grain borer, Granary weevil, Rice weevil, and Angoumois grain moth in the Beed district. The whole gut of *Sitophilus granarius* were dissected, homogenized and serially diluted. The dilutions were spread on nutrient and starch agar plates and incubated to isolate gut flora. Bacterial isolates were tested for amylolytic activity using the starch hydrolysis test. Among the isolates, one coded as SG6 demonstrated the highest amylolytic activity with 2mm and 3mm zone of clearance on starch agar plates. Morphological and Gram staining analysis identified the isolate as gram-positive and rod- shaped. The clear zones observed around the colony indicate starch hydrolysis by amylase production. The colony characteristics of isolate SG6 were circular, medium-sized, off-white, with smooth edges, raised elevation, no pigmentation, and motile in nature. The optimum temperature for growth and amylase production were found to be 45-50°C for *Sitophilus granarius.* Most of the *Bacillus* species commercially used for the production of bacterial amylases have optimum pH of 6.0-7.0 for growth and enzyme production. The optimum pH for the enzyme production *by Bacillus* isolated from the gut and salivary gland microflora was found 7.5. This study confirms the presence of amylase-producing bacteria in the gut microflora of cereal-spoiling insects and highlights the potential of isolating SG6 for industrial application.

Keywords: Amylase enzyme, Cereal spoiling insects, Gut microflora, Starch hydrolysis, Gram staining, Optimal pH, Optimum temperature, Food, Biofuel, Textiles, *Sitophilus granarius, Bacillus* species

FIM-56 (Poster)

Comparative Study of Bacterial Cellulose Produced in Coconut Water and HS Media: Characterization of Properties and Bioactive Compounds

Vasanth Kumar U and Sivakumar Uthandi*
*usiva@tnau.ac.in

Biocatalysts Laboratory, Department of Agricultural Microbiology, Tamil Nadu Agricultural University (TNAU), Coimbatore, Tamil Nadu (641003), India

Abstract: Bacterial cellulose (BC) is recognized for its high purity, mechanical strength, crystallinity, and biocompatibility, making it suitable for diverse industrial applications. This study compared the structural, thermal, and mechanical properties of BC synthesized by *Acetobacter senegalensis* MA1 using coconut water medium (CWM) and HS medium (HSM) under static conditions. Structural characterization was performed using scanning electron microscopy (SEM) and Fourier-transform infrared spectroscopy (FTIR), while thermal properties were analyzed through thermogravimetric analysis (TGA) and differential scanning calorimetry (DSC). Mechanical properties were assessed via tensile strength testing, and crystallinity was determined using X-ray diffraction (XRD). Both BC samples showed similar thermal stability, with major decomposition between 200-400°C and approximately 30% residual weight at 700°C.However, DSC analysis highlighted distinct thermal transitions: BC from CWM showed a peak at 295.01°C, while BC from HSM had peaks at 163.95°C and 242.74°C, indicating differences in structural characteristics. BC produced in CWM demonstrated superior mechanical properties, with a tensile strength of 327.5 MPa compared to 67.5 MPa for BC from HSM. Although BC from HSM had higher crystallinity (96.35%) than BC from CWM (89.67%), the BC from CWM had a slower water release rate, requiring 80 hours to fully dehydrate versus 60 hours for BC from HSM. Additionally, BC from CWM exhibited a higher water absorption rate, reaching 90% saturation in 50 hours compared to 60 hours for HSM. Metabolite profiling via gas chromatography-mass spectrometry (GC–MS) of the spent medium identified bioactive metabolites such as 9,17-octadecadienal, known for its antimicrobial properties, and 1-methyl-cycloundecanol, which may enhance transdermal drug delivery. These findings underscore the potential of using coconut water as a sustainable medium for producing high-quality BC with distinct properties.

Keywords: Bacterial cellulose, Metabolite profiling, Structural characterization, Thermal stability, Tensile strength

FIM-57 (Poster)

Enhancement of Histamine Production through Fish Broth Passages

Vasanthi Kalli, Layana P, Manjusha L and Nayak B, B.
nayakbb@cife.edu.in

Fish Processing Technology, ICAR- Central Institute of Fisheries Education, Versova, Andheri (W), Mumbai, Maharashtra (400061), India

Abstract: Histamine is a biogenic amine formed in fish tissue due to the decarboxylation of free histidine by decarboxylase enzymes released by microbes. Histamine poisoning is a food-borne illness with varied symptoms similar to allergic reactions. Histamine-producing bacteria are generally introduced in fish muscle as a result of contamination, i.e., before, during, or after the processing of fish. Histamine-forming bacteria are mostly mesophilic, and have the ability to grow more rapidly at high temperatures than at moderate temperatures. This study was performed using *Proteus vulgaris* (PV-M20), *Klebsiella variicola* (KV-M12), *Providencia rustigianii* (PR-G20), *Morganella morganii* (MM-I5) from laboratory repository which were earlier recorded to be prolific hisamine formers. Though all the selected bacteria were able to grow rapidly none of them were able to produce histamine at detectable level. Hence passages of the bacteria were done in different fish broths to check if they regain their histamine production ability. Eight repeated passages of the bacteria were performed in Tuna Fish Infusion Broth (TFIB) and Shrimp Meat Infusion Broth (SMIB). Histamine production was observed after 5th passage in Tuna Fish Infusion Broth (TFIB) and after 6th passage in Shrimp Meat Infusion Broth (SMIB) whereas no histamine was observed in Bombay duck Meat fish infusion broth, Carp Meat Infusion Broth and organic media. All the selected bacterial strains produced significant amounts of histamine in 8th passage. Among the screened bacterial strains, *Proteus vulgaris* showed highest histamine production of 662.9 ppm, whereas *Klebsiella variicola* showed the least in TFIB. On the contrary in SFIB, though there was increase in histamine production it was not seemed to be very significant. This study suggests that Tuna Fish broth passages will help in enhancing histamine production capability of histamine formers.

Keywords: Histamine, Fish broth, *Proteus vulgaris* (PV-M20), *Klebsiella variicola* (KV-M12), *Providencia rustigianii* (PR-G20), *Morganella morganii* (MM-I5)

FIM-58 (Poster)

Saccharification and Isomerization Studies using Actinobacteria

Tannu Kushwah[1**] and Sheetal Bhasin[2*]
*sheetalrbhasin@gmail.com, **tanukushwah1234@gmail.com

[1]*Banasthali Vidyapith, Tonk, Rajasthan, India*
[2]*Maharaja Ranjit Singh College of Professional Sciences, Indore, Madhya Pradesh, India*

Abstract: The natural reserve consisting of immense potential for biocatalysis was tapped to solve environmental issues. An extremely adaptive group of heterogenous microorganisms, the Actinobacteria were employed for the production of cellulase and glucose isomerase. Saccharification of cellulosic material was done by cellulase produced by submerged and solid-state fermentation technology using *Streptomyces sp. SA19*. The production ability was checked by assaying FPase and CMCase. Solid state fermentation process yielded better cellulase production with FPase activity of 5.53 U/g and CMCase activity of 5.95U/g. This was aimed to facilitate the disposal by saccharification of ever accumulating agro-residue in the agricultural field in current Indian scenario. Biotransformation of the argo-residue shall not only solve the disposal issue but also give rise to useful products which can be employed in the production of further value-based products. In this investigation we used the glucose released from saccharification for the production of fructose. Isomerization of glucose into fructose was carried out by glucose isomerase produced using *Streptomyces sp. T.S.A.KP.* Solid state fermentative process proved better for the production of glucose isomerase also with the yield of 13.44 U/g as compared to 11.93 U/ml by submerged fermentation method. Saccharification of CMC yielded 12.86µg/ml. of glucose which was isomerized to 9.22 µg/ml of fructose yielding 71.69 % isomerization. Significantly high

isomerization efficiency of the enzyme makes it a very suitable candidate to be picked up for industrial and biotransformation processes.

Keywords: Actinobacteria, Cellulase, Fermentation, Saccharification, Isomerization, *Streptomyces*

FIM-59 (Poster)

Genetic Engineering of Yeast for Increased Nitrogen Metabolism

Ashish Kumar
ashishk62k@gmail.com

Department of Biological Sciences and Biotechnology, Institute of Chemical Technology, Mumbai, Maharashtra, India

Abstract: Single-cell proteins (SCP) are nutrient supplements for human, animal and poultry. SCP are usually composed of dried cell mass of microorganisms that are cultivated in bioreactors to high cell densities. Yeasts, such as those belonging to the genus Candida, are potential sources of SCP as they can grow to high cell densities on cheap fermentation media. However, nitrogen content of yeasts need to be increased to make them attractive SCP candidates. In the present study, we sought to increase nitrogen content in the model yeast Saccharomyces cerevisiae by overexpressing enzymes involved in nitrogen metabolism. Genes coding for Gdh1p and Gln1p were cloned in an expression vector and transformed in S. cerevisiae CEN PK.1D. Nitrogen content in cells grown in minimal medium was determined by Kjeldahl and elemental analysis of the dry cell mass. Preliminary results indicate that while overexpression of GDH did not lead to a change in nitrogen content of the cells, overexpression of GLN lead to a 3.4% increase in nitrogen content. Work is in progress to further increase N content by modulating expression of other genes involved in nitrogen metabolism.

Keywords: Fermentation, Bioreactor, Single cell protein, *Saccharomyces cerevisiae*

FIM-60 (Poster)

Production and Characterization Strategies of Microalgae-derived α-Tocopherol for Therapeutic Applications

Udaypal, Rahul Kumar Goswami and Pradeep Verma*
*2022phdmb005@curaj.ac.in, *pradeepverma@curaj.ac.in*

Bioprocess and Bioenergy Laboratory, Department of Microbiology, Central University of Rajasthan, Bandarsindri, Kishangarh, Ajmer, Rajasthan (305817), India

Abstract: α-Tocopherol is a highly active form of antioxidant molecules involved in scavenging free radicals and protecting cell membranes from reactive oxygen species. Natural tocopherols are only synthesized by photoautotrophs, and microalgae can accumulate a considerable amount of tocopherol, up to 4 mg/g DW, in which α-tocopherol content is up to 97%, which is remarkably higher than other phototrophs. In this study, we explored various cultivation modes (heterotrophic, phototrophic, and mixotrophic) to achieve higher biomass and α-tocopherol production from three potential microalgae: *Tetraselmis indica* BDUG001, *Picochlorum* sp. BDUG100241, and *Chlorella vulgaris* BDGUG003. Maximum biomass production from *Tetraselmis indica* BDUG001, *Picochlorum* sp. BDUG100241, and *Chlorella vulgaris* BDGUG003 of 1.89 ± 0.08, 1.99 ± 0.02, and 1.97 ± 0.13 g/L, were achieved sequentially in mixotrophic cultivation mode over supplementation of 7.5 g/L methanol, 7.5 g/L sodium acetate, and 1 g/L glucose, respectively. α-Tocopherol production obtained from *Tetraselmis indica* BDUG001, *Picochlorum* sp. BDUG100241 and *Chlorella vulgaris* BDGUG003 were 1.47 ± 0.13, 0.79 ± 0.15, and 0.26 ± 0.00 mg/g DCW respectively. Furthermore, microalgal α-tocopherol was purified by column chromatography, and explored for its therapeutic applications e.g. antioxidant activity, and its characterization was done using FTIR and ^{1}H and ^{13}C NMR spectroscopy. The findings of the present study suggest that *Tetraselmis indica* BDUG001, *Picochlorum* sp. BDUG100241 and *Chlorella vulgaris* BDGUG003 are potential sources of natural α-tocopherol with antioxidant activity and mixotrophic mode is an ideal cultivation mode to achieve higher biomass and α-tocopherol production from all three microalgae. Finally, the

study emphasizes strategies for increasing tocopherol production from microalgae and exploring its potential applications.

Keywords: Microalgae, α-Tocopherol, *Tetraselmis indica* BDUG001, *Picochlorum* sp. BDUG100241, *Chlorella vulgaris* BDGUG003, Mixotrophic cultivation

FIM-61 (Poster)

Exploration of Microbial Resources for Lignocellulosic Biomass-Degrading and Other Industrially Important Enzymes

Ridhi Taneja[1,2*], DVemuluri Venkata Ramana[1] and Vinod Chhokar[2]
*ridhi.taneja99@gmail.comr

[1]*Microbial Type Culture Collection, CSIR-Institute of Microbial Technology (IMTECH), Chandigarh (160036), India*
[2]*Department of Bio & Nano Technology, Guru Jambheshwar University of Science and Technology, Hisar, Haryana (125001), India*

Abstract: The enzymatic degradation of lignocellulosic biomass holds significant promise for sustainable biofuel production and environmental remediation. In this study, we aimed to explore microbial resources for the production of enzymes (pectinase, cellulose, inulinase, amylase, xylanase) involved in lignocellulosic biomass degradation, focusing particularly on xylanase activity. Xylanases hold a special place as a catalyst in carbon recycling through degradation of plant residues such as leaf litter as well as biotechnological applications such as in bio-bleaching, food and feed industry. Xylanase enzymes play a vital role in the bioconversion, cellulose pulp preparation and fiber liberation technology. The cost-effective production of xylanase is essential for the widespread use of xylanase for various applications. Microorganisms represent a valuable source for enzyme production on a large scale, and our research objectives encompassed screening, characterization, fermentation, purification, and biochemical analysis of xylanase-producing bacterial strains. The study involved the isolation of bacterial strain from agricultural waste, which demonstrated robust xylanase activity under optimized conditions. Xylan from bran served as an xylan inducer, facilitating the production of xylanase in a screening medium containing nutrient agar media. Subsequently, the study focused on the optimization of xylanase enzyme activity by varying parameters such as incubation time, pH, and temperature. Furthermore, efforts were made to partially purify the xylanase enzyme and determine its biochemical characteristics, optimization of production parameters and purification techniques to obtain a highly pure form of the enzyme. The findings of this study are anticipated to contribute significantly to future research on the applications of xylanase enzymes derived from microbial resources, particularly in lignocellulosic biomass degradation and related biotechnological processes.

Keywords: Lignocellulosic biomass, Xylanase, Enzymes, Pulp-bleaching, Fermentation, Biomass degradation

FIM-62 (Poster)

Screening of Microbial Diversity of Lactococcus Cultures and its Effects on the Formation of Ghee Flavor Compounds

Nishu Devi and Pradip V. Behare*
*pradip_behare@yahoo.com

Dairy Microbiology Division, ICAR-National Dairy Research Institute, Karnal, Haryana (132001), India

Abstract: The selection of mesophilic *Lactococcus* starter cultures plays a crucial role in achieving rapid acidification and desired flavor profile. Industrial-scale production of high-flavored ghee economically relies on ripening cream with lactic acid cultures. In this study, out of an initial pool of 30 *Lactococcus* species, four strains (NCDC912, NCDC284, NCDC 621, NCDC636) exhibiting rapid acidification and high diacetyl

production were quantified by HPLC for further investigation. Compatibility among these selected cultures was confirmed through plate assay and disk diffusion method. Various combinations of these four *Lactococcus* species were optimized, leading to the selection of a specific combination based on acidity, curd setting flavor profiles and viable cell count. Among tested combinations, 912:621(1.5:0.5v/v) combinations were selected for further investigation. Molecular identification validated the distinct strains within this chosen blend combination. Additionally, the shelf life and stability of this selected culture combination was evaluated using the optimized growth media and different additive concentration, with one combination (0.05, 1% w/v) demonstrating extended shelf life under refrigerated conditions. The selected combination under gone the development of different forms of starter culture viz liquid concentrated, liquid unconcentrated, direct vat set (DVS) culture for ghee production. Ghee samples underwent fatty acid and volatile flavor compounds analysis by GC-FID, GC-MS/MS, solid phase microextraction (SPME) techniques. Results shows palmitic and oleic acids were the dominant fatty acids in all samples. Volatiles flavor compounds such as dodecane, acetone, butyric acid, hexanoic acid, 2-pentanone, 2-heptanone, and 2- undecanone were present, might be accumulated as the results of oxidative, hydrolytic, or microbial activities, contribute to the flavor of ghee. The study's quantitative and qualitative metrics may be helpful in evaluating the ghee's quality and assisting the sector in increasing its commercial output.

Keywords: *Lactococcus,* Ghee samples, HPLC, GC-FID, GC-MS/MS, SPME

FIM-63 (Participate only)

Isolation and Biochemical characterization of the Lactic acid bacteria isolated from the *fermented Eleusine* coracana flour: An In-vitro study

Heena Choudhary[1], Raj Singh[3] and Dipjyoti Chakraborty[3*]
*cdipjyoti@banasthali.in

Banasthali Vidyapeeth, Rajasthan,304022, India
Maharishi Markandeshwar deemed to be University, Mullana, Ambala, Haryana,133207

Abstract: Most of the probiotic food are of dairy origin, considering several known health risks associated with the consumption of dairy-based probiotic foods, i.e., milk sugar lactose resistance, milk protein allergy, high fat, and cholesterol content in the milk have led scientist to pursuit alternative substrates to produce non-dairy probiotic food of non-dairy origin. This study aims to isolate and identify lactic acid bacteria from the fermented flour of selected *Eleusine coracana* variety "ML 365" procured from the ICAR-Indian Institute of Millets Research. The millets samples were washed with sterile water and then oven dried followed by their grinding in the rotor mill and was packed in sterile pouch followed by storage at 4^0C after sieve. For isolation of the LAB the 25g of sample was mixed with 100ml of sterilized tap water and left for fermentation in a biological safety cabinet for 18hrs.Stock was prepared from the sample by adding 1ml of sample in 9ml of distilled water. All samples were serially diluted from 10^{-1} to 10^{-9}. The 0.1ml of the from each dilution was mounted by spread plate method on the sterilized petri plates. Purified strains were identified by the gram staining and by the biochemical characterization like catalase test, indole test, citrate test, Gas production from glucose, H_2S production, sugar fermentation, Antibiotic susceptibility and isolated LABs were then stored for further molecular testing. To conclude the isolated LAB from the ML365 *Eleusine coracana* demonstrated the probiotic attributes so far and can be used as the non-diary probiotics.

Keywords: *Eleusine coracana,* Lactose resistance, Non-dairy probiotic food, LAB

MN-1 (Oral)

Biofortification and Growth Enhancement of Wheat via Bacteria Assisted Iron and Zinc Nanoparticles

Anuj Rana [1]*, Pradeep Kumar [1] and Rahul Kumar Dhaka [2]
*anujrana@hau.ac.in

[1] *Department of Microbiology, College of Basic Sciences and Humanities, CCS Haryana Agricultural University, Hisar, Haryana, India*
[2] *Department of Chemistry, College of Basic Sciences and Humanities, CCS Haryana Agricultural University, Hisar, Haryana, India*

Abstract: Microbial synthesis of biocompatible nanoparticles (NPs) using bacteria and fungi is a sustainable approach for the development of nanobiofertilizers. In this study, four bacteria tolerance to ferric chloride and zinc sulfate up to 9 mM were selected from metal-enriched sites and rhizosphere soil. Bacterium AW5 performed best for the synthesis of iron and zinc nanoparticles. It produces siderophores, indole-3-acetic acid, and solubilized zinc and phosphorus. The size (nm) of the iron and zinc nanoparticles was 135 and 197 , respectively. The NPs had an amorphous nature with inverse spinel and wurtzite structures, respectively after annealing. The biologically synthesized iron and zinc NPs enhanced the bacterium growth and PGP traits at 20 ppm. Transcriptome analysis revealed differentially expressed genes and proteins during the NPs-bacterium interaction and provided insights into their regulatory pathways. Biosynthesized NPs in isolation and combination with PGPR significantly enhanced wheat dry biomass (upto 96 %), 100 grain weight (upto 34 %), iron (35 %), and zinc (27 %) under pot house experiment. This study provides valuable insights into the efficient synthesis of bacteria assisted nanoparticles. The transcriptomic analysis of iron and zinc NPs induced bacterial plant growth promoting traits and provides insight into the mechanism of interaction of such nanomaterials. This technology material minimizes the ecological impact associated with the application of conventional agrochemicals to achieve agricultural sustainability and productivity.

Keywords: Biofortification, Iron and Zinc Nanoparticles, Wheat, Micronutrients, Bacteria

MN-2 (Oral)

Biogenic Copper Oxide @ rGO Nanocoatings for Decontamination of a Food Threat *B. cereus* in Packaged Cooked Rice Bowls

Shruti Shukla[1]*, Yuvraj Haldorai[2], Mercyland Pamshnong[1], Ibansaralang Kharthangmaw[1]
*shrutishukla1983@gmail.com

[1]*Department of Nanotechnology, North-Eastern Hill University (NEHU), East Khasi Hills, Shillong, Meghalaya (793022), India*
[2] *Department of Nanoscience and Technology, Bharathiar University, Coimbatore, Tamil Nadu (641046), India*

Abstract: Infectious diseases resulting from pathogenic microorganisms are one of the most important menaces to health all over the world. This issue of increased microbial resistance to antibiotics and other antimicrobial agents seems to be critical day-by-day. Among all the nanoparticles (NPs), copper oxide (CuO/Cu_2O) NPs are one of the most popular ones because they are inexpensive and abundant compared to other antibacterial NPs, such as silver or gold NPs. Furthermore, CuO/Cu_2O NPs are chemically stable, and have a long shelf life. In this study, we have synthesized graphene oxide (GO) *via* Hummers' method followed by the synthesis of copper NPs using copper benzoate dihydrazinate precursor for developing a CuO/rGO composite. The developed composite was characterized for its structure, morphology and compositions *via* TEM, Raman, XRD etc. We report a facile one-step synthesis of biocompatible, copper oxide @ rGO nanocomposite coating as a multifunctional agent for the food matrix decontamination. The developed copper oxide @ rGO coating exhibited high toxicity towards *B. cereus*, as confirmed by the means of fluorescent live-dead cell counting, disruption of membrane permeability/potential, changes in the levels of cellular ions, genetic materials, and proteins, as well as intracellular production of reactive oxygen species. Moreover, the copper oxide @ rGO coating was used as a rinse solution (5, 10, and 20%) for rice bowl packages. Interestingly, a 20% rinsing solution applied for 40-60 min inhibited the *B. cereus* counts significantly on cooked rice packaged bowl. This research highlights the

effectiveness of copper oxide @ rGO coating against food menace *B. cereus*, suggesting that the developed copper Oxide @ rGO coating can be used as an effective antimicrobial rinse for packaged cooked rice preservation.

Keywords: Copper oxide @ rGO nanocomposite, *B. cereus*, Packaged cooked rice, Food test model

MN-3 (Participate only)

Mictrobial Nanotechnology in Cancer Treatment

Priyanka Singh
priyankabbk12@gmail.com

Dev Bhoomi Uttarakhand University, Dehradun, Uttarakhand, India

Abstract: Microbial nanotechnology is an emerging interdisciplinary field that integrates microbiology with nanotechnology to harness the unique capabilities of microorganisms for the development of nanoscale materials and devices. This field explores the ability of microbes to produce nanomaterials naturally or through genetic and environmental manipulation. Applications range from biosynthesis of nanoparticles, bioremediation, and biosensors to the development of novel drug delivery systems and environmental monitoring tools. The convergence of microbial processes with nanotechnology offers innovative solutions for challenges in medicine, environmental science, and industry.

Keywords: Nanoparticles, Bioremediation, Biosensors

MN-4 (Poster)

Optimizing the 'Green' Synthesis of Copper Nanoparticles using *Bacillus licheniformis* CPJN13S

Simran Rani[1], Shikha Dhankher[1], Pradeep Kumar[1], Priyanka Dahiya[1], Kiran Arora[2], Amita Suneja Dang[3] and **Pooja Suneja[1]**
*poojapavit@gmail.com

[1]*Department of Microbiology, M. D. University, Rohtak, Haryana, India*
[2]*Kirori Mal College, University of Delhi, Delhi (10007), India*
[3]*Centre for Medical Biotechnology, M. D. University, Rohtak, Haryana, India*

Abstract: Nanoparticles (NPs) possess unique properties due to their higher surface-to-volume ratio and reactivity. Negative environmental impact along with high cost of traditional modes of synthesis has driven a shift towards the utilization of microbes and plants for the synthesis of NPs. This study reported extracellular synthesis of copper (Cu) NPs using cell free supernatant of *Bacillus licheniformis* CPJN13S. The parameters affecting this process were optimized by one factor at a time (OFAT) approach and optimum biotransformation achieved at 5mM concentration of copper sulfate ($CuSO_4$), 32h incubation time, 18h reaction time, 20:20 filtrate/substrate ratio, 7 pH, and 37ºC temperature. CuNPs produced a characteristic absorption peak between 550-650 nm on UV-Visible spectrophotometer, Z-average, 305.3 nm and Zeta potential, -24.7 mV. Scanning electron microscopy (SEM) and high Resolution-transmission electron microscopy (HR-TEM) revealed hexagonal NPs having average size of 12.4 nm. Antimicrobial assay conducted using 100µg/ml CuNPs led to highest inhibition of 20.4 % (*Bacillus subtilis*) and 43 % (*Staphylococcus aureus*), at 21h and 27h, respectively. The results suggest that biogenic synthesis can serve as the eco-friendly alternative of physical and chemical modes of synthesizing CuNPs that can be used to develop highly effective antibacterial agents.

Keywords: Antimicrobial; Microorganisms; Nanoparticles; OFAT; TE

MN-5 (Poster)

Expression, Characterisation, and Enhancement of Immunogenicity of SARS-CoV-2 RBD Recovered from Inclusion Bodies in *E. coli* by Mild Solubilisation Technique

Rahul Ahuja[1,3*], Sudeepa Srichandan[1], Jairam Meena[2], Amulya K Panda[1]
*ahujar.nii@gmail.com

[1]*Product Development Cell, National Institute of Immunology, Aruna Asaf Ali Marg, New Delhi (110067), India*
[2] *Department of Pharmaceutical Engineering and Technology, Indian Institute of Technology (Banaras Hindu University), Uttar Pradesh (221005), India*
[3]*Translational Health Science and Technology Institute, Faridabad, Haryana (121001), India*

Abstract: Next-generation SARS-CoV-2 as well as Pan-beta coronavirus vaccines are based on proteins. In order to quickly fulfil the demand for vaccines and diagnostics worldwide in case of an emergent pandemic, it is critical that untagged protein expression be accelerated, inexpensive, and simple to scale up. Complicated procedures involving cell lines are expensive and restrict the availability of many vaccines in developing countries as witnessed during the COVID-19 pandemic. In this work, the *E. coli* expression system was used to express the SARS-CoV-2 receptor binding domain (RBD) which still remains the prime vaccine target. The RBD without any purification tag was homogenised without the need for several chromatographic processes through thorough washing and the application of a gentle solubilisation technique. The predominant beta sheet structure of purified RBD included some alpha helices. For a month, RBD remained steady at 37 degrees Celsius and resisted any significant structural alterations. Additionally, the RBD was improved in immunogenicity when it was formed into polymer nanoparticles. Rapid production, lower costs, and more accessibility in resource-constrained environments are some of the ways that thermally stable protein-based vaccine manufacturing from E. coli systems can aid in addressing the severe vaccine crisis. In addition, the 5 L bioreactor is being used to optimise the manufacture of this vaccine candidate in order to maximise the yield per unit biomass.

Abbreviations: RBD: Receptor-Binding Domain, SARS-CoV-2: Severe Acute Respiratory Syndrome Coronavirus 2, COVID19: *Coronavirus* disease of 2019

Keywords: Vaccine equity, RBD vaccine, SARS-CoV-2, Protein expression, Inclusion body, Thermal stability

MN-6 (Poster)

Mycosynthesis of Selenium Nanoparticles by *Hericium erinaceus*: Promising Antimicrobial and Antioxidant Agents

Nadarge Prathmesh[1], Shivani Sharma[1] and Anu Kalia[2*]
*kaliaanu@pau.edu

[1]*Department of Microbiology, Punjab Agricultural University, Ludhiana, Punjab (141004), India*
[2]*Electron Microscopy and Nanoscience Laboratory, Punjab Agricultural University, Ludhiana, Punjab (141004), India*

Abstract: Fungi hold promising potential in nanotechnology for synthesis, application, and development of novel products. The application of fungi in nanotechnology has gained increased attention recently due to their eco-friendly, metabolite-mediated nanoparticle (NP) production, safety, and versatility. Metallic NPs, in particular, exhibit broader application potentials. In this study, the culinary medicinal mushroom *Hericium erinaceus* was employed to synthesize selenium nanoparticles (SeNPs). The cell-free extract of *H. erinaceus* was treated with varying concentrations of sodium selenite (50, 100, 150, and 200 mM), which led to a visible color change from light cream to orange-red after 24 hours, indicating the formation of biogenic SeNPs. UV-Vis spectroscopy indicated the highest absorption peak after 24 hours of incubation for the optimal precursor salt concentration (200 mM). Transmission electron microscopy revealed the irregular spherical morphology of the NPs with an average diameter of 75nm. Fourier transform infrared spectroscopy analysis identified fungal biomolecules to functionalize the NPs surface. Dynamic light scattering (DLS) analysis revealed a hydrodynamic diameter with an average particle size of 170 nm and a polydispersity index (PDI) of 0.337. The antimicrobial efficacy of the synthesized SeNPs was assessed in a dose-dependent manner against

Staphylococcus aureus, *Listeria monocytogenes*, *Escherichia coli*, and *Salmonella* and compared it with the antibiotic gentamicin. The SeNPs demonstrated notable antimicrobial activity against both gram-positive and gram-negative bacteria and was comparable to gentamicin. Additionally, SeNPs exhibited dose-dependent scavenging of DPPH and ABTS radicals, showcasing their antioxidant potential. These findings suggest that *H. erinaceus*-derived SeNPs possess significant antimicrobial and antioxidant properties and their role as a promising, safe, and reliable candidate for biomedical applications, as well as for pharmaceutical and industrial uses.

Keywords: Antimicrobial activity; Antioxidant activity; Eco-friendly nanomaterials; Fungal nanotechnology; *Hericium erinaceus* Mycosynthesis; Selenium nanoparticles

MN-7 (Poster)

Effect of Phytonutrients on Gut Beneficial Bacteria under Simulated Gastric Fluid

Maulesh Gadani[1*], Kedar Ahire[2] and Viral Shukla[1]
*drmauleshgadani@gmail.com

[1] *LJ Institute of Applied Sciences, Lok Jagruti Kendra University, Ahmedabad, Gujarat, India*
[2] *Dept of Zoology, Savitribai Phule Pune University, Pune, Maharashtra, India*

Abstract: This study investigates the impact of phytonutrients on gut-beneficial bacteria under simulated microgravity conditions, focusing on the bacterium *Bacillus clausii*. The research explores the morphological and biochemical characterization of *B. clausii*, assessing its growth dynamics in different media (LB and MRS broths) under both aerobic and microaerophilic conditions. The study also evaluates the bacterium's antibiotic susceptibility and its response to phytochemicals such as nano-curcumin and nano-ashwagandha. Results indicate that while *B. clausii* exhibits resistance to certain antibiotics, it is sensitive to others, and its growth can be significantly suppressed by nano-phytochemicals. Additionally, tolerance to simulated gastric fluid was tested to understand the bacterium's survivability in gastrointestinal conditions. These findings contribute to our understanding of the potential applications of probiotics in space missions and their interaction with novel phytonutrient formulations.

Keywords: LB and MRS broths, *B. clausii*, Phytonutrient formulations, Nano-phytochemicals

MN-8 (Poster)

Evaluation of effectiveness of Zinc Nanoparticles for Control of Whitefly, *Bemisia tabaci*

Ankit Kumari, Soniya Tanwar and Darshna Chaudhary
darshnarajan.cbt@mdurohtak.ac.in

Centre for Biotechnology, M. D. University, Rohtak, Haryana (124001), India

Abstract: *Bemisia tabaci* are a major threat to plants due to their direct feeding damage and role as vectors for plant viruses. Their nymphs produce honeydew on leaf undersides, which decreases photosynthesis, deteriorates leaf quality, and encourages sooty mold growth. Conventional control methods have been largely ineffective in managing whitefly populations and preventing virus spread. Nanotechnology, however, offers a novel and promising solution, providing new strategies for tackling these pest issues. In this study, we synthesized zinc nanoparticles using an extract from *Rubia cordifolia* roots and characterized them using FTIR, zeta potential, and transmission electron microscopy. We prepared zinc nanoparticles at three different concentrations (1000 ppm, 10000 ppm, 100000 ppm) and conducted insecticidal bioassay (root dip bioassay). Over a 7-day period, we observed the mean percentage mortality of *Bemisia tabaci* (whiteflies) at these concentrations compared to a control group. Mean percentage mortality of *Bemisia tabaci* at 7th day was 55% and 85%, 100% and 100% for control, 1000 ppm, 10000 ppm, 100000 ppm respectively. Increase in concentration leads to higher mortality. these findings highlight the potential of *R. cordifolia* ZnONPs as a biopesticide or pest management strategy for controlling whiteflies in agricultural settings.

Keywords: Whitefly, Control, Insecticidal, Zinc nanoparticles

MN-9 (Poster)

Synthesis and Characterization of Carbon Dots using Waste

Neha Rawat, Pratishtha Raturi, Nirjara Singhvi and Nabeel Ahmad*
*nabeel.biotech@gmail.com

School of Allied Sciences
Dev Bhoomi Uttarakhand University, Dehradun, Uttarakhand , India -248007

Abstract: In this work we have synthesized carbon dots using household waste, here we have used 4 different household wastes i.e. peels of galgal [NG], peels of Malta [NM], leaves of pineapple [NP] and leaves of strawberry [NS]. The scientific name of Galgal, Malta, Pineapple & Strawberry are *Citrus pseudolimon Tanaka*, *Citrus sinensis*, *Ananas comosus*, *Fragaria* × *ananassa*, respectively. The synthesis of carbon dots using household waste is done via microwave method. Change in color from yellowish to brownish and Florescence under UV light indicated the presence and biosynthesis of carbon dots using the waste extract. These synthesized carbon dots was further characterized using techniques i.e. UV – Vis, SEM, TEM, FTIR. FTIR spectrum suggests the presence of hydroxyl groups (alcohols or carboxylic acids), alkanes, carbonyl groups (ketones, aldehydes, esters, or carboxylic acids), aromatic or alkene groups, and C-O bonds (alcohols, ethers, or esters). UV-VIS spectrum shows strong absorption peaks from the UV to the visible range, indicating various electronic transitions, including π-π*, n-π*, and d-d transitions. These transitions suggest the presence of conjugated systems, aromatic rings, carbonyl groups, metal complexes, and highly conjugated organic dyes. The peaks in the visible range are particularly indicative of colored compounds, potentially involving transition metals or extensive conjugation. The anti-bacterial and anti-fungal activity of biosynthesized carbon dots with the activity of reference antibiotics against human pathogens was investigated.

Keywords: Synthesis, Characterization, Carbon dots, FTIR, UV-Vis spectroscopy, Florescence.

MN-10 (Poster)

Synthesis of Silver Nanoparticles by *Bacillus subtilis* and Evaluation of their Antimicrobial Activity

Madhumita Bisht[1]* Neeraj Dilbagi[2], Rajesh Gera[1], Jagdish Parshad[1] and Monika Kayasth[1]
*madhumitabisht0@gmail.com

[1]*Department of Microbiology, CCS Haryana Agricultural University, Hisar, Haryana (125004), India*
[2]*Department of Bio-Technology, Guru Jambheshwar University of Science and Technology, Hisar, Haryana (125001), India*

Abstract: Nanotechnology, a rapidly advancing field, focuses on creating smaller, lighter, stronger, and environmentally safe materials with diverse applications across various sectors such as material science, medicine, electronics, and catalysis. The present study explored the extracellular synthesis of stable silver nanoparticles (AgNPs) using the cell-free extract of *Bacillus subtilis* (NCDC 441). The synthesized nanoparticles were characterized using UV-vis spectroscopy, particle size analysis (PSA), Fourier-transform infrared spectroscopy (FTIR), and transmission electron microscopy (TEM). The UV-vis spectrum showed a maximum absorption peak at 407 nm, confirming the formation of AgNPs. TEM analysis revealed spherical nanoparticles with a size range of 15-25 nm. Additionally, the antimicrobial activity of these nanoparticles was evaluated against *Escherichia coli* (MTCC), *Pseudomonas aeruginosa* (NCDC 0105), and *Staphylococcus aureus* (MTCC 290). The results demonstrated significant antibacterial effects against both Gram-positive and Gram-negative bacteria, highlighting the potential of *Bacillus subtilis* in biosynthesizing effective antimicrobial agents.

Keywords: Silver nanoparticles, *Bacillus subtilis*, Antimicrobial activity, Nanotechnology biosynthesis

MN-11 (Poster)

Synthesis, Characterization of Fungal Nanocomposites & its Functionality Evaluation for Waste Water Treatment

Annu Yadav[1*], Nitai Debnath [2] and Namita Singh[1]
*annuyadav51298@gmail.com

[1]*Lab no. 202, Microbial Biotechnology Laboratory, Department of Biotechnology, Guru Jambheshwar University of Science and Technology, Hisar-Haryana (125001), India*
[2]*Amity Institute of Biotechnology, Amity University Haryana, Gurugram, Haryana (122413), India*

Abstract: The extraction of heavy metal ions from water containing waste, particularly copper ions, is crucial for environmental sustainability. This study compares the efficacy of two distinct nanomaterials (magnetite and silica) and their fungal nanocomposites in removing copper ions from aqueous solutions. Magnetite nanoparticles and silica nanoparticles were evaluated individually and in combination with fungal materials to form nanocomposites. The characterization techniques used for characterization were UV-Vis spectroscopy, FTIR analyses and SEM analysis. The SEM results of fungal nanocomposites showed a fiber like appearance with rough surface which was mainly due to the loading of silica nanoparticles on its surface. The SEM results of nanoparticles showed clustered structures with rough surface which showed great potential in applications like catalysis and applications. The EDX results of Magnetite nanoparticles depicted higher iron content which confirmed the formation of Magnetite nanoparticles. The higher silica content in Silica nanoparticles' EDX results confirmed the formation of Silica nanoparticles. The UV-Vis peaks were between 200-300 nm for both nanoparticles. The FTIR results were also used to detect the specific groups of functions that are present their surfaces. The PSA detected diameter of silica nanoparticle to be 491.5 nm and 429.5 nm for magnetite nanoparticles. AAS was used to detect the presence of Cu II ions after removal process. The AAS result showed that silica loaded fungal nanocomposites showed maximum removal efficiency of 99.17% over other nanoparticles and nanocomposites. This might be due to the combination of silica and fungal biomass which created a synergistic effect where the properties of both components are enhanced. Silica provided a large surface area and stability, while fungal biomass offered multiple binding sites and functional groups, leading to improved copper ion removal. This comparative study contributes to the advancement of nanotechnology-based solutions for sustainable environmental management and water purification strategies.

Keywords: Heavy metals, Magnetite, Silica, Nanoparticles, Fungal nanocomposites, Nanotechnology

MN-12 (Poster)

Unveiling the Potential of Mycogenic Copper Oxide Nanoparticles for Yamuna Wastewater Remediation

Somani Chandrika Rath[1] and Arti Goel [*1]
*agoel2@amity.edu

Amity Institute of Microbial Technology, Amity University, Noida, Uttar Pradesh (201313), India

Abstract: Wastewater generation poses a significant global challenge in developing nations like India. Conventional treatment methods including physical, chemical and biological have proven inefficient in removing complex pollutants. To combat the limitations of traditional approaches nanotechnology emerged as a revolutionary solution. This study investigated the potential of mycogenic copper oxide (CuO) nanoparticles for wastewater remediation. *Serendipita indica*- mediated CuO nanoparticles were characterized by an average hydrodynamic diameter of 179.1 nm. UV-Vis spectroscopy confirmed nanoparticle formation, while XRD analysis revealed a crystalline monoclinic structure. SEM and TEM imaging demonstrated a cubic morphology, and FTIR analysis indicated the presence of aliphatic amine functional groups on the nanoparticle surface. EDX analysis confirmed high purity with a copper composition of 95.66%.
The wastewater sample was collected from Okhla Barrage (28°32'44" N, 77°18'57" E), exit point of River Yamuna from Delhi. Treating wastewater using 100 ppm of mycogenic copper oxide nanoparticles demonstrated significant improvements across various physicochemical parameters. Substantial reductions were observed concerning control in total hardness (67.58%), nitrate (60.47%), BOD (52.38%) and COD (51.85%), indicating

effective removal of organic pollutants and dissolved minerals. Turbidity decreased by 50%, suggesting enhanced clarity of the treated water. Reductions were also seen in TDS (40%), phosphate (32.32%) and sulphate (24.29%), exhibiting improved water quality. The treatment moderately lowered TSS (21.05%) and alkalinity (18.21%), while also reducing the pH from 8.9 to 7.1, bringing it closer to neutral. Qualitative improvements were noted in odor and appearance changing from strong foul to foul and from pale yellow to lighter respectively. These results indicate that the mycogenic copper oxide nanoparticle treatment is effective in improving multiple aspects of wastewater quality, particularly in reducing organic content, dissolved solids, and specific ionic contaminants.
Hence, this study will be able to highlight the potential of nanotechnology in addressing critical wastewater treatment challenges, offering a paradigm shift in environmental remediation strategies.

Keywords: Wastewater, Mycogenic Copper Oxide Nanoparticles, Physicochemical parameters, Contaminants, Environmental remediation

MN-13 (Poster)

Mysterious Nucleic Acid Binding Domain in a Micro-Compartment Shell Protein - towards Developing Nucleic Acid Protein Container

Aishwarya Davkhar[1,2] and Chiranjit Chowdhury[1,2*]
*c.chowdhury@ncl.res.in

[1]*Biochemical Sciences Division, CSIR-National Chemical Laboratory, Pune, Maharashtra (411008), India*
[2]*Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, Uttar Pradesh (201002), India*

Abstract: Proteinaceous subcellular bacterial micro-compartments (MCPs) are structures that self-assemble into a selectively permeable protein shell containing an enzymatic core. It is possible to engineer BMCs to improve the efficiency of biochemical reactions. They can improve metabolic flux towards desired products, such as bioplastics or pharmaceuticals, by compartmentalizing reactions and reducing competition from other pathways by encasing pollution-breaking enzymes, it can be used in bioremediation procedures. By displaying antigens in a way that both protects them from degradation and improves immune response, BMCs can be utilised as platforms for the delivery of vaccines. They function as illustrations of non-viral proteins suitable for carrying nucleic acids.
Recently, scientists repurposed the *Citrobacter freundii* propanediol utilization (Pdu) MCP to be used as a nucleic acid container. In this study, we used the *Salmonella enterica* Ethanolamine utilization (Eut) MCP. EutK, a shell protein in Eut MCP, has an additional 60 amino acids in its C-tail, forming a helix-turn-helix pattern. We explore the control of Eut operon expression by the enigmatic shell protein EutK. It is well known that the helix-turn-helix motif binds nucleic acids and is essential for controlling various metabolic activities. We used chromatin immunoprecipitation to determine the nucleic acid sequence and found that a eutK mutant expressed the eut operon 40% less than the wild type. Our system allows for the packaging of DNA segments into the Eut shell through specific protein-DNA interactions. Creating an artificial organelle that houses a specific DNA segment could lead to various applications, such as developing gene delivery vehicles and enhancing Nano reactors where selected enzymes attached to DNA-binding domains are strategically placed on a DNA scaffold. Therefore, our primary goal in this study was to design a bacterial system capable of packaging a specific DNA fragment within the lumen of the Eut shell.

Keywords: *Salmonella*, Micro-compartment, EutK shell protein, Helix-turn-helix motif, Nucleic acid container

MN-14 (Poster)

Hydrogel Based Encapsulation and Antimicrobial Properties of *Bacillus cereus* NSD MTCC 10072 Derived Bioactive Compound

Renuka Sharma, Bharti Sharma and Namita Singh*
*namitasingh71@gmail.com

Lab -202, Microbial Biotechnology Laboratory, Department of Bio and Nanotechnology, Guru Jambheshwar University of Science and Technology, Hisar, Haryana (125001), India

Abstract: Skin is susceptible to damage due to various factors, necessitating the development of effective wound healing materials. Wounds require timely and efficient healing to prevent complications such as infections and delayed recovery. Chitosan, a natural polymer, offers numerous benefits for wound healing including biocompatibility and antimicrobial properties, but it also has several drawbacks such as poor mechanical strength and stability. Polyvinyl alcohol overcomes these drawbacks by providing enhanced mechanical properties and stability. This study has aimed at the formulation of a Bioactive compound encapsulated CS-PVA hydrogel cross-linked with glutaraldehyde for the sustained release of Bioactive compound. The hydrogel swelling ratio was determined to measure its capability to absorb wound exudate. Drug encapsulation efficiency was calculated to find the percentage of Bioactive compound encapsulated in the disc. An in vitro drug release study was conducted to determine the rate of release of Bioactive compound from the hydrogel. Antibacterial activity against E. coli (MTCC 723), S. aureus (NDRI 110), and S.typhi (MTCC 3224) were tested to ensure their potential to prevent wound infections. Structural and morphological analysis was conducted using FTIR, XRD, and SEM. Elemental analysis of encapsulated Bioactive compound was done by EDX along with elemental mapping. Encapsulation of the Bioactive compound in hydrogel facilitates controlled release, improved solubility, protection from degradation, and ease of application at the wound site. These features conclude that Bioactive compound encapsulated CS-PVA hydrogel is a good choice for effective wound healing applications.

Keywords: Hydrogel, Skin, Wound healing, Bioactive compound, PVA, CS, Drug release

MN-15 (Poster)

Advancing Organic Farming: The Scope and Application of Nano-Biofertilizers

Ravi Kumar and Tanvi Bhatia*
*bhatiatanvi54@hau.ac.in

CCSHAU College of Agriculture, Bawal, Rewari, Haryana (123501), India

Abstract: Modern cropping systems profoundly rely on synthetic fertilizers to deliver necessary nutrients, yet their prolonged and persistent administration is hazardous to the environment, soil fertility, and nutritional dynamics of the rhizospheric microbiome. With time, nanotechnology has emerged as one of the promising technologies for the wide range of applications in agriculture and related fields. Nano-biofertilizers (NBF) represent a promising innovation in sustainable agriculture, particularly within the realm of organic farming. These advanced fertilizers integrate nanotechnology with biological materials to enhance nutrient availability, improve soil health, and increase crop productivity without compromising environmental integrity. By providing a slow and controlled release of essential nutrients, nano-biofertilizers promote efficient plant growth while reducing nutrient losses to the environment. As organic farming continues to expand globally, the use of nano-biofertilizers offers a sustainable solution to meet the growing demand for eco-friendly agricultural practices as well as examines their role in minimizing the ecological footprint of farming practices, boosting soil microbial activity, and enhancing nutrient uptake in plants. Nano-biofertilizers have emerged as a more economically and environmentally sustainable, highly versatile, and long-lasting agricultural tool. Microbe-based green synthesis using the encapsulation of inorganic nanoparticles of Si, Zn, Cu, Fe, Ni, Ti, and Ag as well as organic materials, including chitosan, cellulose, and starch, to formulate NBFs can eliminate the constraints of conventional fertilizer contamination.

Keywords: Chemical fertilizers, Organic fertilizers, Nano-biofertilizers, Nanotechnology, Environment, Fertilizer contamination

MN-16 (Poster)

The Utilization of Bacterial Exopolysaccharides (EPS) for Nanoparticle Synthesis and Their Role in Human Health

Shikha Rana*, Swati Panchal, Roshan Mohiddin, Rashi Rastogi, Suman Kapila and Rajeev Kapila
*ranashikha367@gmail.com

Animal Biochemistry Division, National Dairy Research Institute, Karnal, Haryana (132001), India

Abstract: The biosynthesis of nanoparticles using exopolysaccharides (EPS) derived from lactic acid bacteria offers sustainable and biocompatible methods with promising applications in human health. This study investigated the potential of EPS from *Lacticaseibacillus rhamnosus* (MTCC-5897) and five other strains for synthesizing silver nanoparticles (SNPs). Among the strains, *L. rhamnosus* 5897 produced the highest EPS yield. Structural characterization of the EPS confirmed its suitability for nanoparticle synthesis, resulting in silver nanoparticles (sEPS-SNPs) with an average size of 15-20 nm. The sEPS-SNPs exhibited potent antimicrobial activity against *Bacillus cereus*, *Escherichia coli*, and *Staphylococcus aureus*, surpassing the performance of conventional silver nanoparticles. In addition to their antimicrobial effects, sEPS-SNPs demonstrated significant antioxidant properties, as indicated by their ability to scavenge free radicals, including ABTS and DPPH. *In vitro* studies using human keratinocyte (HaCaT) cells showed that sEPS enhanced cell viability under oxidative stress conditions (induced by H_2O_2) and promoted cell migration, suggesting its potential in wound healing and skin protection. Additionally, sEPS-SNPs demonstrated reduced intracellular reactive oxygen species (ROS) levels, further indicating their protective role against oxidative damage. These findings highlight the potential of EPS, particularly sEPS-SNPs, as biocompatible agents with antimicrobial, antioxidant, and wound-healing properties, providing a promising approach for developing functional materials in human health applications

Keywords: Exopolysaccharides, *Lacticaseibacillus rhamnosus*, Silver nanoparticles, Antimicrobial activity, Human health, Oxidative stress

MN-17 (Poster)

Unraveling the Mechanisms of Nanoparticles in Antimicrobial Therapeutics: Pathways to Enhanced Efficacy against Resistant Pathogens

Priyanka and Tanvi Bhatia*
*bhatiatanvi54@hau.ac.in

CCSHAU College of Agriculture, Bawal, Rewari, Haryana (123501), India

Abstract: The misuse of antibiotics in human and animal health as well as in agriculture, contributes to the spread of resistance genes creating a "Silent Pandemic" that could surpass other causes of mortality by 2050. Collaborative efforts have been undertaken between researchers and the industry to develop technologies for a more effective treatment for diseases. Development of nanotechnology, especially nanostructured particles and formulations, is providing new opportunities to combat these infectious diseases more effectively. Metal and metal oxide Nanoparticles (NPs) have become the research hotspot of new antibacterial materials due to their small particles, large specific surface area, physical, mechanical chemical as well as antibacterial properties. These properties are applied to facilitate the applications of antimicrobial drugs, thereby overcoming some of the limitations of traditional antimicrobial therapeutics. NPs have been established to possess potent antimicrobial activities against various types of pathogens due to their unique characteristics and cell-damaging ability through several known and unknown mechanisms. The detailed antibacterial mechanisms of NPs are currently under investigation, but the presently accepted mechanisms include oxidative stress induction, metal ion release, and non-oxidative mechanisms. The multiple simultaneous mechanisms of action against microbes would require multiple simultaneous gene mutations in the same bacterial cell for antibacterial resistance to develop; therefore, it is difficult for bacterial cells to become resistant to NPs. The future of nanoparticle-based antimicrobial research holds tremendous potential for improving human health and addressing the global challenge of antibacterial resistance.

Keywords: Nanoparticles, Antimicrobials, Antibiotic resistance, Oxidative stress induction, Antimicrobial mechanisms, Global challenge

MN-18 (Poster)

Antagonistic Activity of Silver Nanopaticles against Microbial Phytopathogens in Tomato Crop

Preeti Kaleramana[1], Seema Sangwan[1]*, Pooja Swami[1], Mukesh Kumar[1] and Kuldeep Kumar[2]
*seema_sangwan80@yahoo.co.in

[1]*Department of Microbiology, CCS Haryana Agricultural University Hisar, Haryana (125004), India*
[2]*Department of Vegetable Science, CCS Haryana Agricultural University Hisar, Haryana (125004), India*

Abstract: The growing incidences and severity of plant diseases pose a significant and increasing risk to the primary productivity, food security and biodiversity. Microorganisms such as bacteria, fungi, viruses along with nematodes act as causative agents of various severe diseases of crops. In plant disease management, nanoparticles have been established as a potent alternative to conventional products and methods as a result, there is an increasing interest in eco-friendly and economically feasible methods for synthesizing silver nanoparticles. In the present study we used biosurfactants for the synthesis of silver nanoparticles as it improve the synthesis and stability of nanoparticles and chemically synthesized nanoparticles for comparison and tested their antimicrobial activity against the microbial phytopathogns of tomato crop. The size of the nanoparticles synthesized by chemical (CsAgNPs) and green (BsAgNPs) method was 87.88 and 100.9nm having 95.43 and 94.28% particle size distribution, which indicates the excellent stability of silver nanoparticles. The maximum zone of inhibition of 4.03 and 4.3 cm was shown by CsAgNPs and BsAgNPs against *Xanthomonas campestris.* The minimum growth diameter of *Fusarium oxysporum* was 2.20 and 2.33cm by CsAgNPs and BsAgNPs at 400ppm. The BsAgNPs reduced 20% disease incidences in fungal and bacterial infested plants and enhanced the tomato yield. This innovative approach offers a sustainable solution for agriculture, reducing the reliance on chemical inputs and promoting eco-friendly practices. The use of biosurfactants as stabilizing agents also highlights the potential for sustainable nanotechnology solutions in agriculture.

Keywords: Biosurfactant; nanosilver; *Xanthomonas campestris; Fusarium oxysporum;* Tomato; Disease incidences

MN-19 (Poster)

Multifunctional smart micronutrient nanomaterial for controlling phytopathogenic fungus

Monika*, Sumistha Das and Nitai Debnath
*monikasohlot86@gmail.com

Amity Institute of Biotechnology, Amity University Haryana, Gurugram, Haryana (122413), India

Abstract: This study introduces a novel smart nanocarrier for the controlled delivery of fungicides to combat phytopathogenic fungi. Tricyclazole, a potent fungicide, was encapsulated within pectin-capped copper nanoparticles (Tri@CuO-Pec). Copper, a micronutrient essential for plant health, serves as a carrier while also exhibiting inherent antimicrobial properties. This antimicrobial micronutrient nanomaterial is capped with pectin, a stimuli-responsive gatekeeper that releases the fungicide only in the presence of fungal pectinase enzymes. Tricyclazole, a common fungicide, inhibits ergosterol biosynthesis in fungus and disrupt fungal cell wall integrity. When combined with nano sized copper oxide, the synergistic effects can enhance fungal control. Copper oxide nanoparticles (CuONP) can generate reactive oxygen species (ROS) within fungal cells, causing further damage. These ROS generated by CuONP coupled with the inhibitory effects on ergosterol

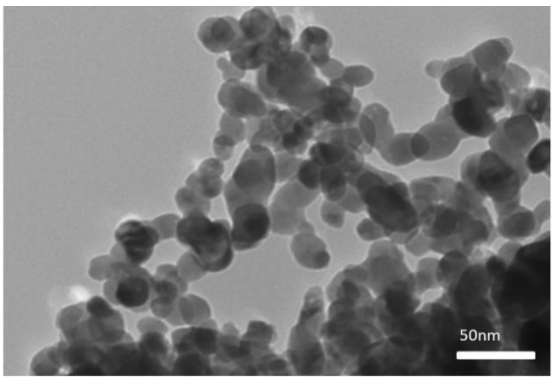
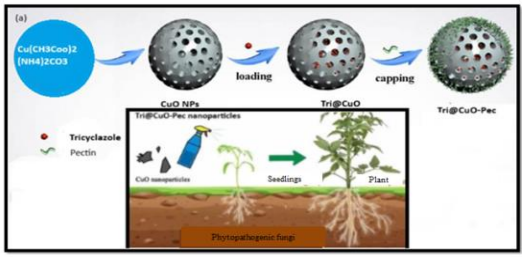


Fig.1 TEM image of Pectin capped Copper oxide nanoparticle (CuONP)



biosynthesis caused by tricyclazole can potentially amplify its inhibitory effects on ergosterol biosynthesis eventually lead to a better fungal control regime. Physico-chemical characterization confirmed successful nanoparticle synthesis and pectin capping thereafter. Additionally, LC-MS/MS analysis confirmed controlled sustained release of tricyclazole from Tri@CuO-Pec in the presence of pectinase. Stimuli-responsive nanocarriers offer a significant advantage over traditional slow-release nanocarriers for fungicide delivery and the control of plant fungal infections. By releasing the fungicide only in the presence of specific fungal enzymes, stimuli-responsive nanocarriers can target the pathogen directly, minimizing off-target effects and reducing the risk of environmental contamination. This targeted approach can also help to prevent the development of fungal resistance, ensuring the long-term efficacy of the fungicide. Tri@CuO-Pec represents a promising approach towards sustainable agriculture and has significant implications for microbiology by providing targeted fungicide delivery, particularly in the development of novel strategies for controlling plant diseases.

Keywords: Smart nanocarrier, Copperoxide nanoparticle, Fungicide, Tricylazole, pectin, Stimuli-responsive

MN-20 (Poster)

Fabrication, Characterization and Anti-Rhizobial Activity of Green Synthesized Zinc Oxide Nanoparticles using *Trifolium alexandrinum* Leaves Extract

Oshin Verma[1], Tejveer Singh[2], Radhakrishna Auji[2] and **Ramesh Kumar[1]**

[1]*Department of Biochemistry, Bundelkhand University, 284128, Jhansi, UP, India ; Department of Biochemistry, Bundelkhand University, 284128, Jhansi, Uttar Pradesh, India*
[2]*ICAR-Indian Grassland and Fodder Research Institute, 284003, Jhansi, Uttar Pradesh, India*

Abstract: Nanotechnology plays an interesting role in the areas of computing, power generation, optics, drug delivery, and environmental sciences. In this respect, green synthesis of NPs, especially using extracts from different plants, is a growing trend that is considered simple, cheap, and nontoxic in green chemistry. Yet, green nanoparticle synthesis is a tool of choice that can be easily prepared and engineered. In the present work, green synthesized zinc oxide nanoparticles (ZnO-NPs) were prepared from aqueous leaf extracts of *Trifolium alexandrinum* (Egyptian clover). The ZnO-NPs were characterized by different techniques such as ultraviolet (UV) spectroscopy, Fourier transform infrared (FTIR) spectroscopy, field emission scanning electron microscopy (FESEM), dynamic light scattering (DLS), and zeta potential. ZnO-NPs formation was prior confirmed by colour change then followed by UV–Vis spectra at 318 nm. The particle size and zeta potential of synthesized ZnO-NPs were reported as 1307 nm and −15.1 mV, respectively, via the DLS technique can be considered a moderately stable colloidal solution. It is considered that NPs with zeta potential values greater than +25 mV or less than −25 mV typically have high degrees of stability. FESEM analyses of synthesized NPs confirmed their spherical or elliptical shape. Furthermore, the biological activity of the biosynthesized ZnO-NPs was examined. The anti-rhizobial test approved the higher bactericidal activity of the resulting ZnO-NPs on the rhizobium bacteria with the visible zone of inhibition compared to the standard. However, the effects of ZnO-NPs on agriculture could also be explored that also depend on several factors, including the dose, plant species and age, exposure route and duration, and environmental conditions.

Keywords: *T. alexandrinum*, Zinc oxide nanoparticles, Green synthesis, Anti-rhizobial Activity

MN-21 (Participate Only)

Production of Nanobiochar using Agro-Industrial Waste by Alliance of Nanotechnology

Ajay Kamboj, Pardeep Kumar Sadh, Babli Yadav, Inderjeet Singh,
Prabhat Kumar and Joginder Singh Duhan*
*duhanjs68@gmail.com

[1]*Department of Biotechnology, Chaudhary Devi Lal University, Sirsa, Haryana (125055), India*

Abstract: Modern science innovation based on the unifying features of nature at the nano scale contributes a new foundation for the integration of knowledge and technology. There is a longitudinal process of convergence and divergence in the broad fields of engineering and science. In the field of nanotechnology, advanced nanostructured materials are the solution to many problems of the modern era. In recent years, carbon nanomaterials have been developed as powerful tools due to their unique characteristics and number of applications in various fields such as energy, materials, agriculture, and environment, especially in phytoremediation of various technologies. Nanobiotechnology may result in the production of carbon-based nanomaterials, including biochar nanocomposites, to revolutionize research in its field. Nano-biochar is small particle of biochar material with good physical, chemical and surface properties. Biochar research originated from a soil called terra preta in the Amazon basin, which has high fertility and carbon content. It has many benefits for plant growth, soil properties, plant disease management, bioremediation of contaminants and pesticides, wastewater treatment and enzyme immobilization. This is very traditional approach due to its cost friendly, sustainability, and environment friendly as well. Nano-biochar has excellent ability to absorb pollutants, nutrients, pollutants as compared to biochar. Therefore, this review paper represents the comprehensive properties, production, and biochar-based nanocomposites.

Keywords: Nano-biochar; Biochar; Nanotechnology; Phytoremediation; Bio-remediations

MTAMR-1 (Oral)

Antibiofilm Potential of Farnesol against *S.aureus* MRSA

Nitika Bhasin[1,2], Mohd Murtaza[1,2], Poonam Choudhary[1,2], Priya Kumari[1,2]
and Sundeep Jaglan[1,2*]
*sundeepjaglan@iiim.res.in

[1]*Fermentation & Microbial Biotechnology Division, CSIR-Indian Institute of Integrative Medicine, Jammu, Jammu & Kashmir (180001), India*
[2]*Academy of Scientific & Innovative Research (AcSIR), Ghaziabad, Uttar Pradesh (201002), India*

Abstract: Staphylococcus aureus and MRSA are among the leading opportunistic pathogens capable of causing various superficial and systemic infections in humans. The pathogenesis and resistance of these bacteria are caused by virulence factors and biofilm development. Due to biofilm formation the pathogens are developing resistance against the antibiotics, which is a global health concern, requires discovery of new targets to tackle the infections. Therefore, this study aimed to investigate the antibiofilm properties of natural compounds (Farnesol and Berberine derivatives) and their combination with antibiotics against Staphylococcus aureus and MRSA. Farnesol and Berberine sulfate hydrate at 128 µM/mL and 256 µM/mL inhibited S. aureus and MRSA biofilm. Additionally, it was also noted that the combination of these natural drugs with antibiotics showed synergistic antibiofilm potential. Further, the microscopic examinations showed a decrease in biofilm structure after the treatment, and also the synthesis of extracellular polysaccharide and S. aureus and MRSA biofilm-associated slime was inhibited by these drugs. According to our research these natural compounds in combination with antibiotics can be employed as therapeutic agents to prevent infections caused by biofilms and may promote the reversal of drug resistance.

Keywords: Biofilm, Natural products, Anti-Biofilm, Methicillin resistant *S.aureus*

MTAMR-2 (Oral)

Detection of Carbapenem Resistant Genes among Carbapenem resistant *Pseudomonas aeruginosa* Clinical Isolates

Gaurav Verma[1]*, Nipa Singh[1], Subhra Snigdha Panda[1], A Raj Kumar Patro[1], Dipti Pattnaik[1], Ashok K. Praharaj[1] and Sukanta Tripathy[2]
*gaurav.verma95578@gmail.com

[1]Department of Microbiology, Kalinga Institute of Medical Sciences, KIIT Deemed to be University, Odisha, India
[2]Department of Transfusion Medicine, Kalinga Institute of Medical Sciences, KIIT Deemed to be University, Bhubaneswar, Odisha, India

Abstract: Introduction*: Pseudomonas aeruginosa*, a Gram-negative opportunistic pathogen, is known for causing a broad spectrum of nosocomial infections, which encompass surgical-site infections, septicaemia, urinary tract infections, and lower respiratory tract infections. The treatment of *P. aeruginosa* infections has involved the use of different antimicrobial agents, including anti-Pseudomonas penicillin, cephalosporins, and carbapenems.
Objective: The aim of this study was to detect the presence of various carbapenem resistance genes in *Pseudomonas aeruginosa* clinical isolates.
Methods: 75 clinical isolates of *Pseudomonas aeruginosa* resistant to carbapenem, were examined. *Pseudomonas aeruginosa* was identified using the Vitek AST automated system (AST N 405 panel). Carbapenemase production were identified by using mCIM and eCIM test. Carbapenem resistance genes were detected by real time polymerase chain reaction.
Results: *bla*NDM gene was present in 37.5% (12/32) isolates followed by *bla*OXA-48 gene was seen in 15.6% (5/32), *bla*NDM with *bla*OXA-48 gene was seen in 18.7% (6/32) and *bla*VIM with *bla*OXA-48 gene was observed in 3.1% (1/32). The co-occurrence of multiple genes was present in 25% (8/32)) isolates of *Pseudomonas aeruginosa*.
Conclusion: Both *bla*NDM and *bla*OXA-48 were detected in our clinical isolates of *Pseudomonas aeruginosa* and occurrence of two resistance genes seen in our clinical isolates. This highlights the need for further screening and continuous monitoring of drug resistance genes in *Pseudomonas aeruginosa*.

Keywords: mCIM; *P. aeruginosa*; Carbapenem resistance; CRPA; Resistant genes; blaNDM; blaOXA-48

MTAMR-3 (Oral)

Investigation of G-Quadruplex DNA Motifs in the *Helicobacter Pylori* Genome and their Potential as a Target for Pharmacological Intervention

Monika Kumari[1], Priyanka Payal[2], Neha R Sahu[3], Uma Shankar[2], Amit Kumar[2], Debasis Nayak[3], Sharad Gupta[2], Vikas Yadav[4] and **Puja Yadav[1]**
*pujayadav@cuh.ac.in

[1]Department of Microbiology, Central University of Haryana, Mahendergarh, Haryana, India,
[2]Department of Biosciences and Biomedical Engineering Indore, Simrol, Indore, Madhya Pradesh, India,
[3]Department of Biological Sciences, Indian Institute of Science Education and Research Bhopal, Bhopal, Madhya Pradesh, India
[4]School of Life Sciences, Jawaharlal Nehru University, New Delhi, India

Abstract: *Helicobacter pylori*, a significant human pathogen associated with duodenal ulcers and gastric cancer, poses an escalating health threat marked by rising resistance and resulting clinical complications. The diminishing efficacy of *H. pylori* treatment is attributed to the growing antibiotic resistance. Recent studies emphasize the role of DNA secondary structures, specifically G-quadruplexes, in various organisms, influencing biological processes and pathogenesis.
This study aimed to investigate the presence of putative G quadruplex (PGQs) motifs in the *H. pylori* genome and explore their significance in *H. pylori* pathogenesis and biological functions.

Utilizing the QGRS mapper algorithm, we identified a non-random distribution of G-quadruplexes, predominantly within ORF regions, enriching gene categories associated with cell wall/membrane/envelope biogenesis, and amino acid transport and metabolism. Evaluation of cytotoxicity revealed that G-quadruplex ligands (Braco-19, TMPyP4, and 360A) inhibited *H. pylori* growth, demonstrating IC_{50} values of approximately 26, 45, and 15.48 µM, respectively, indicating a potential therapeutic strategy against *H. pylori* infections. qPCR-stop assay, exhibited retardation in replication of G4- motifs containing genes with increasing concentrations of K^+ ions and G4 ligand- TMPyP4, suggesting the stabilization of PGQ motifs. Additionally, the mTFP-based reporter assay showed a decrease in mTFP gene expression on Braco-19 treated cells as compared to the untreated and further affirmed the formation of stable G-quadruplex structures in the HPGQ motifs *in vitro*. Subsequently, we found the downregulation of G4- harboring gene- *imaA* and *hopG* when treated with G4- ligands and observed morphological changes in shape of G4 ligands treated *H. pylori* cells compared to untreated control bacteria.
In conclusion, this study underscores the significant impact of G-quadruplexes on *H. pylori* pathogenesis and biological processes, proposing a promising therapeutic approach for combating *H. pylori* infections by targeting G4 structures.

Keywords: G-quadruplex, *H. pylori,* QGRS mapper algorithm

MTAMR-4 (Oral)

In Silico and In-vitro Analysis for Determining the Antibacterial Potential of Aztreonam against *Pasteurella multocida* Sialic Acid Protein

Subodh Soni, Manjeet Chahar, Pooja Chugh, **Hari Mohan***
*harimohan.cmbt@mdurohtak.ac.in

Centre for Medical Biotechnology, Maharshi Dayanand University, Rohtak, Haryana (124001), India

Abstract: *Pasteurella multocida,* a Gram-negative zoonotic bacterial pathogen, interacts with the host environment, immune response, and infection through outer membrane proteins, adhesins, and sialic acid binding proteins. Sialic acids provide nutrition and mask bacterial identity, hindering the complement system. In this study, in silico molecular docking assessed 11 antibiotics targeting sialic acid binding protein, comparing their docking scores to Amoxicillin. Aztreonam and Gentamicin displayed the highest docking scores (-6.025 and -5.718), followed by a 100 ns molecular dynamics simulation. Aztreonam exhibited stable simulation with protein RMSD fluctuations of 1.8-2.2 Å. The ligand initially had an RMSD of 1.6 Å, stabilizing at 4.8 Å. Antibiotic sensitivity testing confirmed Aztreonam's efficacy with the largest inhibition zone of 42 mm, while Amoxicillin and Gentamicin had inhibition zones of 32 mm and 25 mm, respectively. According to CLSI guidelines, all three antibiotics were effective against *Pasteurella multocida*. Aztreonam's superior efficacy positions it as a promising candidate for further investigation in targeting *Pasteurella multocida.*

Keywords: *Pasteurella multocida*, Sialic acid, Antibiotics, Docking, Simulations, Antibiotic sensitivity testing

MTAMR-5 (Oral)

Impact of Food Based Antimicrobial Peptides against the Biofilm of ESKAPE Pathogens and Oral Bacteria through Invitro and In Silico Approaches

Indranil Chattopadhyay
indranil@cutn.ac.in

Department of Biotechnology, School of Life Sciences,
Central University of Tamil Nadu, Thiruvarur, Tamil Nadu (610 005), India

Abstract: Antimicrobial resistance is a big concern worldwide, particularly in nosocomial illness caused by ESKAPE bacteria. Probiotics are gaining popularity as prospective antibacterial medicines that are both safe and very effective. The goal of this study is to find a potential therapeutic employing antimicrobial peptides (AMPs) produced by probiotics. Following a thorough screening and pruning strategy, 52 AMPs were collected from

multiple databases, and their powerful antibacterial and anticancer properties were determined using an in silico study. Twelve AMPs were investigated for 3D structural alignment prediction and validation, using the GH12 synthetic AMP as a control. These candidate peptides were comprehensively tested against six major virulence proteins of *P. gingivalis* and four of *F. nucleatum*. The lowest energy score of the docked complexes indicating binding affinity and interactions with active residues being chosen. Plpl_18 was identified as the most effective novel antimicrobial peptide, interacting with the virulence proteins RagB of P. gingivalis and Fap2 of F. nucleatum with docking scores of -238.24 Kcal/mol and -254.27 Kcal/mol, respectively. This AMP plpl_18 was designed to specifically target oral squamous cell carcinoma proteins that regulate such as cytokines, metallomatrix proteinase, MAPK, E-cadherin, and JAK-1. Among these proteins, it docked against MMP-9 with the highest negative docking score of -7.5Kcal/mol, -260.956 Kcal/mol, and -1361.9 Kcal/mol using AutoDock Vina, HPEPDOCK, and ClusPro2.0 respectively.The in vitro assay showed that AMP plsa_07 has antibacterial and antibiofilm activities, with a minimum inhibitory concentration of 1 to 4µg/ml. The AMP plsa_07 displayed biofilm inhibition and eradication action against a variety of bacteria, including *E.faecium, S.aureus, K. pneumoniae, A. baumannii,* and *P. aeruginosa*, with efficacy ranging from 17% to 70%. This study lays the groundwork for clinical investigations on the potential use of therapeutic peptides produced from probiotics to address the growing problem of drug-resistant illnesses.

Key words: Antimicrobial peptides, ESKAPE bacteria, Biofilm, Insilico study

MTAMR-6 (Oral)

The Rational Approach to Multikinase Inhibitor Discovery for the Development of Resistance Immune Antimalarial Drugs

Dhaneswar Prusty
dhaneswarprusty@curaj.ac.in

Department of Biochemistry, Central University of Rajasthan, Bandersindri, Kishangarh, Ajmer, Rajasthan (305801), India

Abstract: The persistent resistance in parasites to many primary antimalarial drugs has led to a significant rise in cases and deaths in nations afflicted by malaria. The root cause of this phenomenon is attributed to mutations in the targets of these drugs. In light of this, developing multitargeting drugs has emerged as a promising solution. It has been observed that the probability of multiple target mutations is highly unlikely as it would significantly impact the parasite's fitness. Notably, kinases, a class of enzymes that play a critical role in various stages of the parasite's life cycle, are among the most viable targets for malaria drug development. By using a High Throughput Virtual Screening approach against six chemically validated Plasmodium falciparum (Pf) kinases (PfPKG, PfMAP2, PfCDPK4, PfTMK, PfPK5, PfPI4K), we identified 21 multitargeting hits. The antimalarial properties of the top three hits were validated through parasite growth inhibition assays. Moreover, hierarchical clustering reveals the structural divergence of the compounds from the existing antimalarials, indicating less chance of cross-resistance. Our ongoing study on developing multikinase inhibitors has adopted an integrative approach, including computational methods, biochemical methods, and in vitro and in vivo studies to obtain potent antimalarial drugs immune to resistance.

Keywords: Multikinase, Multitargeting hits, Cross-Resistance

MTAMR-7 (Oral)

Biosynthesis, Characterization and Anti-Biofilm Activity of Silver nanoparticles on *Staphylococcus aures* (MRSA)

Prayrna Kulkarni, Rujula Deoghare and **Kedar Ahire***
*kedar_ahire@unipune.ac.in

Department of Zoology, Savitribai Phule Pune University, Ganeshkhind, Pune, Maharashtra (411007). India

Abstract: In the present study, silver nanoparticles (AgNPs) were synthesized and optimized using *Bryophyllum pinnatum* (*B. pinnatum*) extract. The characterization of AgNPs revealed that the nanoparticles were spherical in

shape and 30±5 nm in size. The zeta potential of -13.6 mV confirms the stable colloidal solution of nanoparticles. The FTIR analysis of AgNPs confirmed the coating of flavonoids on nanoparticles which have resulted into the synthesis and stabilization of silver nanoparticles. The *B. pinnatum* mediated silver nanoparticles showed potent inhibitory action with a minimum inhibitory concentration (MIC) of 20 µg/mL against Methicillin resistant *Staphylococcus aures* (MRSA). Microtiter plate assay, light microscopy, live and dead staining and scanning electron microscopy of biofilms of *Staphylococcus aures* (MRSA) revealed that the AgNPs efficiently inhibited biofilm formation or eradicated the biofilms. The medicinal property of the plant *B. pinnatum* also imparted antidiabetic (IC_{50} 21.43 µg/mL) and anti-inflammatory (IC_{50} 23.43 µg/mL) property to AgNPs.

Keywords: Silver nanoparticles, Biofilms, *Bryophyllum pinnatum, Staphylococcus aures,* Anti-inflammatory,

MTAMR-8 (Oral)

Echinomycin, a Peptide Antibiotic from New Bacterial Source and its Potential to Tackle Drug Resistance in Methicillin-Resistant *Staphylococcus aureus*

Mohd Murtaza[1,2], Nitika Bhasin[1,2], Priya Kumari[1,2], Avleen Kour[3], Poonam Choudhary[1,2], Manoj Kushwaha[1], Sandeep Sharma[3] and Sundeep Jaglan[1,2]*
*sundeepjaglan@iiim.res.in

[1]*Fermentation & Microbial Biotechnology Division, CSIR-Indian Institute of Integrative Medicine, Jammu, Jammu & Kashmir (180016), India*
[2]*Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, Uttar Pradesh (201002), India*
[3]*Department of Medical Laboratory Science, Lovely Professional University, Punjab (144411), India*

Abstract: The emergence of antimicrobial resistance (AMR) necessitates the development of new antimicrobials to tackle the growing threat of methicillin resistant *Staphylococcus aureus* (MRSA). In this study, we have isolated the echinomycin from new bacterial source, *Streptomyces pratensis* S26-11 and studied its anti-MRSA potential. To explore MRSA resistance mechanisms, we focused on gene responsible for the resistance (mecA and PrsA) and biofilm formation (agrA and sea), as well as the significance of NorA efflux pump using Staphylococcus aureus NorA mutant strains. Echinomycin effectively inhibited MRSA at 0.07 µM, reducing biofilm formation by 81 ± 2.44% and downregulating virulence genes at sub-inhibitory concentration of 0.01 µM. Additionally, in combination with piperine, a NorA efflux pump inhibitor, increased antibiofilm activity by reducing its minimum inhibitory concentration (MIC) to 0.03 µM. This synergistic action may also help the risk of echinomycin resistant development. Our findings highlight the echinomycin's potential as an effective drug candidate against MRSA by targeting the expression of virulence gene.

Keywords: Biofilm; Echinomycin; Efflux pump; MRSA; NorA; PBP2a

MTAMR-9 (Oral)

Metagenomic-Guided Bioprospecting of Antimicrobial Compounds from Bacterial Communities in the Biological Soil Crusts of the Thar Desert

Sudarshna*, Shubham Kumar, Aastha Kapoor and Manoharan Shankar
*sudarshna@iitj.ac.in

Department of Bioscience and Bioengineering, Indian Institute of Technology Jodhpur, Rajasthan, India

Abstract: The emergence of last-resort antimicrobial- resistant bacteria poses serious threats to global public health. Thus, there is a growing need for the discovery of new classes of antimicrobials. In this context, hitherto unexplored environments are potential sources of these much-needed antimicrobials. Biological soil crusts form in arid zones due to the concerted activity of various microbial species, which are individually and collectively adapted for desert survival. These unique microbial communities, prevalent in the Thar desert have been poorly studied despite being ecological engineers in the desert. Our earlier study using long-read, shotgun

metagenomics to investigate the microbial composition within a biological soil crust from Thar Desert revealed that members of the phylum Actinomycetota, dominated the Thar biocrust. Using this information, we isolated members of this phylum, which are known to produce bioactive compounds of potential interest, from the biocrusts and assessed their capacity for antimicrobial metabolite production. Among the isolate, a strain designated as HAC-1, secreted a distinctive blue pigment and exhibited potent antimicrobial activity against methicillin-resistant *Staphylococcus aureus* PT1648. However, no antimicrobial activity was detected against Gram-negative pathogens such as *Acinetobacter baumannii* B8342 and *Klebsiella pneumoniae* ATCC BAA-2146. The isolate was identified as a member of the genus *Streptomyces* spp. by morphological examination and confirmed by 16S rRNA sequencing. The metabolites produced by this strain were extracted, and the crude extract exhibited robust inhibitory activity against Gram-positive pathogens. We present our findings on the purification, chemical and functional characterization of the active component produced by HAC-1.

Keywords: Biological soil crust, Thar desert, Antimicrobial compounds, Actinobacteria, *Streptomyces*, Antimicrobial activity

MTAMR-10 (Oral)

Sexually Transmitted Infections among Tribal Women in the Shahdol Division of Madhya Pradesh: Prevalent Pathogens, Antibiotic Sensitivity Profile and Efficacy of Selected Essential Oils against Multidrug-Resistant Microbes

Poonam Sharma
pnm245@yahoo.com

Department of Zoology, Indira Gandhi Tribal University, Amarkantak, Madhya Pradesh, India

Abstract: Background: Sexually Transmitted Infections (STIs) are a significant global concern, with over 1 million new cases each day. In the tribal societies, the women are the main suffers. Due to lack of awareness of the diseases and non-availability of quality health support systems, the women are forced to practise witchcrafts and superstitions, ultimately worsening their conditions. No data is available on prevalence of STIs among tribal women in district Anuppur and Shahdol. Many STIs are asymptomatic, leading to under diagnosis and delayed treatment. Antimicrobial resistance in STI pathogens seriously compromises the management and control of these infections. Therefore, the aim of the study is to detect the occurrence of STI pathogen, their AST profile and alternate therapy to get rid of the infection.

Materials and Methods: Endocervical/vaginal swab samples (n=110) were collected from women (age group 20 to 55) visiting the OPDs of district hospital Anuppur and Medical College, Shahdol, Madhya Pradesh, India. Multiplex Real-Time PCR was performed for the simultaneous detection of 08 STI pathogens in the target population. Antibiotic susceptibility test was performed against prevalent STI pathogens. Efficacy of selected essential oils (6) were also studied to overcome the problem of multidrug-resistant micro-organisms.

Results: Out of 110, 85.45% of samples tested positive for at least one of the targeted eight STI pathogens. The most common pathogen detected in 74 (67.27%) samples was identified as *Mycoplasma hominis* followed by *Ureaplasma urealyticum* 65 (59.09%), *Ureaplasma parvum* 37 (33.64%), Herpes simplex virus 1 & 2 15 (13.64%), *Neisseria gonorrhoeae* 9 (8.18%), *Mycoplasma genitalium* 8 (7.27%), and *Chlamydia trachomatis* 6 (5.45%). The STIs were more prevalent in age groups 36–41. AST results showed multidrug resistance against prevalent pathogens. Spearmint essential oil exhibited the strongest antibacterial activity against *Neisseria gonorrhoea* (NG) followed by Palmarosa>Eucalyptus=Tulsi> Nagarmotha. Peppermint oil did not showed any inhibitory effect. MIC results of essential oils against NG revealed that Nagarmotha is more effective followed by Eucalyptus>Palmarosa>Spearmint>
Tulsi.

Conclusion: The study revealed the presence of 08 common pathogens in the tribal women in the study area. AST results serve as an alarming reminder of the critical need for responsible antibiotic usage and the development of alternative treatment strategies to combat this emerging public health challenge. In this context, essential oils derived from medicinal plants such as Nagarmotha, Eucalyptus, Palmarosa, Spearmint and Tulsi, and may offer a promising alternative remedy for *Neisseria gonorrhoea* infections.

Keywords: Sexually transmitted infections, Antibiotic resistance, Essential oils, MIC

MTAMR-11 (Oral)

Performance Comparison of Etest and MICRONAUT-AM Assay for Antifungal Susceptibility Testing of *Candida auris*: Underestimation of Fluconazole Resistance by MICRONAUT-AM and Overestimation of Amphotericin B Resistance by Etest

Suhail Ahmad*, Mohammad Asadzadeh and Wadha Alfouzan
*suhail.ahmad@ku.edu.kw, *suhail_ah2000@yahoo.com

Department of Microbiology, College of Medicine, Kuwait University, P. O. Box 24923, Safat 13110, Kuwait.

Abstract: Introduction: *Candida auris* is a recently emerged, multidrug-resistant pathogenic yeast that has caused major outbreaks in healthcare facilities. It is now regarded as a global public health threat. Accurate antifungal susceptibility testing (AST) of *C. auris* isolates is crucial for proper management of invasive infections. Recent reports have shown that commercial AST methods including SensiTitre Yeast One and Vitek2 either underestimate or overestimate resistance of *C. auris* to antifungal drugs fluconazole (FLU) and amphotericin B (AMB). This study evaluated AST results of *C. auris* isolates against FLU and AMB by Etest and broth microdilution-based colorimetric MICRONAUT-AM EUCAST assay (MCN-AM).
Materials & Methods: Clinical *C. auris* isolates (n=121) identified by phenotypic and molecular methods were tested. Essential agreement (EA, ± 1 two-fold dilution) between the two methods and categorical agreement (CA) based on tentative resistance breakpoints of Centers for Disease Control and Prevention's (CDC's) were determined. Molecular basis of resistance to FLU was studied by PCR-sequencing of hot-spot region of *ERG11* gene.
Results: All isolates were identified as *C. auris* by both phenotypic and molecular methods, belonged to the South Asian Clade I and contained FLU resistance-associated Y132F or K143R mutation in *ERG11*. The Etest-MCN-AM EA was poor (33%) for FLU and moderate (76%) for AMB. The CA for FLU was higher (94.2%, 7 discrepancies) than for AMB (90.9%, 11 discrepancies). Discrepancies were reduced when MCN-AM upper-limit-value of 4 µg/mL for FLU-susceptible *C. auris* and Etest upper-limit-value of 8 µg/mL for wild-type for AMB were used.
Conclusion: Our data show that resistance to FLU was underestimated by MCN-AM while resistance to AMB was overestimated by Etest by using the CDC's tentative resistance breakpoints of ≥32 µg/mL for FLU and ≥2 µg/mL for AMB. Method-specific resistance breakpoints should be devised for accurate AST of clinical *C. auris* isolates for proper patient management.
Keywords: *Candida auris*; Antifungal susceptibility testing; Etest, MICRONAUT-AM EUCAST assay; Comparative performan

MTAMR-12 (Oral)

Prevalence and Diversity of ESBL Producing ARB and Associated ARGs from Aquatic Environment Receiving Pharmaceutical Industrial Waste

Qazi Mohd Rizwanul Haq
qhaque@jmi.ac.in

Department of Biosciences, Faculty of Natural Sciences, Jamia Millia Islamia, New Delhi, India

Abstract: The presence of antimicrobial compounds in the environment exerts a selective pressure and favours the emergence and dissemination of antimicrobial resistance (AMR) in the environment and ultimately into clinical settings. India is the leading country in manufacturing and consuming antibiotics with a significant-fold surge in the environmental concentration of antimicrobials and/ or their by-products. AMR is a global threat to the human health as it is estimated in a recent report to cause around 300 million premature deaths and a loss of up to $100 trillion (£64 trillion) to the global economy by 2050 [1]. Water/ sediment/ soil samples were collected from the industrial hubs- Bhiwadi, Rajasthan and Derabassi, Punjab, India to study the contribution of pharmaceutical industrial waste in emergence and dissemination of AMR. All samples collected from different locations and seasons of the year were chemically analysed to find out antimicrobials and other compounds present in it. Furthermore, microbiological analysis of all samples were also carried out. Viable heterotrophic bacterial count was obtained on non-amended and antibiotics amended R2A plates for AMR analysis. Morphologically distinct bacterial colonies were selected and screened for the phenotypic resistance against selected antibiotics. The resistant bacterial isolates were further phenotypically screened for ESBL production.

Molecular screening of antibiotic resistance genes (ARGs) including ESBL genes (bla-CTX-M, bla-TEM, and bla- SHV) were carried out by designing genes-specific primers and PCR based amplification. A large number of antimicrobial compounds were present in the collected samples. A heavy load of members of Enterobacteriaceae, faecal coliform, and antibiotic-resistant bacteria (ARB) were observed in both studied locations. Upto 25% of ARB were positive for ESBL production. The phenotypically positive bacterial isolates were found to be having more than one ESBL gene. Further studies are in progress.

Keywords: Antimicrobial Resistance (AMR), Enterobacteriaceae, Expended spectrum beta-lactamases (ESBLs), Pharmaceutical industrial waste

MTAMR-13 (Oral)

Antibiotic Resistance and Biofilm formation in clinical isolate *Pseudomonas aeruginosa*

Bhagvat Lad, Sanjay Chavan and **T.A Kadam***
takadam67@gmail.com

Department of Biotechnology School of Life Sciences, Swami Ramanand Teerth Marathwada University Nanded, Maharashtra (431606), India

Abstract: The Pathogenic strains of *Pseudomonas aeruginosa* have threat of infection in people with cystic fibrosis, immunocompromised and hospitalized patients. The pathogenic strains have already reported which are resistant to antibiotics from class viz. aminoglycosides, beta lactam, quinolones, macrolides and peptides. The resistant mechanisms are mainly due to enzymatic breakdown, active efflux from the cell, obstruction of entrance and target structural modification. In addition to these biofilm formation ability in *Ps. aeruginosa* is also arguments antibiotic resistance. In present study *Ps. aeruginosa* isolates obtained from hospital environment to investigate drug resistance by disc diffusion and biofilm formation ability by using Congo-red agar (CRA) plate assay and microtiter plate assay. The clinical isolate PA6 and PA7 confirmed as multi drug resistance to beta lactam, aminoglycosides and quinolone class of antibiotic and also black colonies with a dry crystalline consistency was considered positive for biofilm formation on Congo red agar and in microtiter assay based on O.D. values of isolate PA6 (**0.121**) and PA7 (**0.125**), the isolate PA6 and PA7 are strong biofilmformers. The resistance of *Ps. aeruginosa* to these antibiotics and biofilm formation indicates isolate have more threat to hospitalized patients. The study reveals infection by these type of *Ps. aeruginosa strains* should be treated by using new class of antibiotics along with biofilm targeting molecules.

Keywords: *Pseudomonas aeruginosa*, Drug-resistance, Biofilm producer

MTAMR-14 (Oral)

In Vitro Antimicrobial Activity of Indian Propolis against Multidrug Resistant Extended Spectrum β-lactamase-Producing Clinical Isolates of *Escherichia coli* from Buffalo Mastitis

Sarita Yadav* and Ashok Boora
*drsaritanrce@gmail.com

ICAR-Central Institute for Research on Buffaloes, Hisar, HJaryana (125001), India

Abstract: Propolis, a natural resinous substance produced by honeybees, has a long history of therapeutic use dating back to ancient times, particularly with its antimicrobial properties. The current research investigated the antimicrobial activities of different crude propolis extracts, including methanol propolis extract (MPE), ethyl acetate propolis extract (EAPE) and water propolis extract (WPE) against five extended spectrum β-lactamase-producing *Escherichia coli* strains by three methods. Clinical strains of *E. coli* were isolated as prevalent environmental pathogens from cases of mastitis in Murrah Buffaloes. The study utilized minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) assays at different propolis concentrations, employing broth microdilution and diffusion methods (agar well and agar disc diffusion) against these strains. Results demonstrated the antimicrobial activities of crude MPE against *E. coli,* with MIC and MBC ranging from 0.390 to 0.781 mg/ml and 0.781 to 1.562 mg/ml respectively. The growth of *E. coli* was inhibited by EAPE

at concentrations of 0.781 to 1.562 mg/ml and 0.781 to 3.125 mg/ml respectively at both MIC and MBC. However, WEP exhibited no antimicrobial activity against the tested pathogens. By the agar-well diffusion method, all strains were inhibited by propolis at concentration of 6.25 mg/ml MPE and EAPE. The mean zone of inhibition by concentration of 6.25, 12.5, 25, 50 mg/ml of MPE and EAPE were 13.6, 16.6, 19.8, 21.4 mm and 10.4, 12.8, 14.6, 15.4 mm respectively. The propolis extracts were more active than their corresponding solvents ($p< 0.001$). The lesser inhibition zones of 12.8 ± 1.5 to 19.6 ± 0.8 mm and 10.4 ± 1.1 to 14.6 ± 1.5 mm were observed from MPE and EAPE respectively at concentrations of 6.25 to 50 mg/ml in the agar disc diffusion method. Methanol extract proved to be more effective compared to ethyl acetate extract, as shown by its lower MICs for *Escherichia coli*. In addition, Indian propolis had a dose-dependent activity against *E. coli* strains tested. The results obtained from diffusion methods against 5 *E. coli* strains suggested that propolis at concentrations of 6.25 mg/ ml was effective to inhibit multidrug resistant extended spectrum β-lactamase-producing clinical isolates of *Escherichia coli* from buffalo mastitis. Data from the study suggest that methanol extract of propolis has antibacterial potential and could serve as an alternative antimicrobial source against *E. coli.* Additionally, further purification and characterization of bioactive compounds from active propolis fractions is recommended for potential application as antibacterial agents.

Keywords: Antimicrobial, *E. coli,* Environmental mastitis, Propolis, Minimum inhibitory concentration

MTAMR-15 (Oral)

Optimizing Media Formulation for Enhanced Hyphal Growth: Future Applications for Anticandidal Research

Rachana Arvind* and Ritu Raval
*rachana1.mitmpl2023@learner.manipal.edu

[1]*Department of Biotechnology, Manipal Institute of Technology, Manipal Academy of Higher Education, Manipal, Karnataka (576104), India*

Abstract: *Candida albicans* is an opportunistic commensal organism commonly found in healthy individuals. The transition from a commensal to a pathogenic state is influenced by a delicate balance of factors from both the fungus and the host. The pathogenesis of *C. albicans* is complex, driven by various virulence factors that enable its survival in diverse host environments. Among these factors, the yeast-to-hyphal transition is particularly significant, as the hyphal form is critical for breaching epithelial barriers and evading macrophage defences, often through the release of proteinases that degrade macrophages. The rise of antimicrobial resistance underscores the need for alternative therapeutic strategies, with the hyphal form representing a promising target. While several synthetic media have been documented to induce the hyphal form, many are complex, expensive, or slow to produce mature hyphae. Therefore, optimizing a media formulation that is simple, cost-effective, and efficient in inducing hyphal growth is of great interest. Such a medium could be valuable for future anticandidal studies, as well as for investigating hyphal-specific gene expression and metabolite production.

Keywords: *Candida albicans,* Yeast to hyphal transition, Media optimization, Anticandidal

MTAMR-16 (Oral)

Detection of OXA Gene in Carbapenem Resistance Uropathogens Isolated from Urine Samples at Angul, Odisha

Lopamudra Rath
lopamudrarath1995@gmail.com

PhD Clinical Microbiology continuing, Lovely Professional University, Phagwara, Punjab, India

Abstract

1. Multidrug Resistance is a public health concern in Urinary tract infection patients due to presence of OXA gene in carbapenem resistance uropathogens in urine samples. We can use PCR &gene sequencing for further confirmation.

2. Resistance to carbapenem in gram negative bacteria is attribute to their ability to produce carbapenem enzymes but here we have focus on gram positive bacteria.
3. OXA gene under category-D showing the resistance gene due to fast mutation and narrow therapeutic option.

Keywords: OXA gene, Carbapenem resistance, Uropathogens, Angul

MTAMR-17 (Oral)

Antimicrobial and Antibiofilm Potential of Resveratrol against *Streptococcus pneumoniae*

Ruth Zomuansangi and Mukesh Kumar Yadav*
mukiyadav@gmail.com

Department of Microbiology, Central University of Punjab, Bathinda, Punjab (151401), India

Abstract: *Streptococcus pneumoniae* infections remain a significant global health concern, with increasing antibiotic resistance posing treatment challenges. This study investigated the antimicrobial and antibiofilm potential of resveratrol against *S. pneumoniae*. The minimum inhibitory concentration (MIC) of resveratrol was determined to be 128 µg/mL utilising broth microdilution. Resveratrol significantly inhibited biofilm formation at sub-MIC concentrations and eradicated pre-established biofilms. Confocal microscopy revealed reduced biofilm density and increased non-viable cells following resveratrol exposure. Resveratrol treatment increased membrane permeability, resulting in nucleic acid leakage, as evidenced by the release of DNA and RNA. The crystal violet absorption assay further corroborated the alteration of bacterial membrane permeability upon resveratrol treatment. Cytotoxicity testing utilising an MTT assay demonstrated that resveratrol exhibited no cytotoxicity to human nasal epithelial cells at concentrations up to 64 µg/mL. These findings elucidate the promising antimicrobial and antibiofilm activity of resveratrol against *S. pneumoniae* through membrane disruption, with low cytotoxicity to human cells. Resveratrol's potential as an alternative therapeutic approach for pneumococcal infections warrants further investigation, particularly in the context of increasing antibiotic resistance.

Keywords: Resveratrol, *Streptococcus pneumoniae*, Antimicrobial, Antibiofilm, Membrane permeability, Cytotoxicity, Antibiotic resistance

MTAMR-18 (Poster)

Computational Approach to Identify Antifungal Potential of Endophytic Metabolites of *Staphylococcus*

Mehak Dangi*, Sudesh Kumari and Anil Kumar Chhillar
mehak.bioinfo@mdurohtak.ac.in

Center for Bioinformatics, Maharshi Dayanand University, Rohtak, Haryana, India

Abstract: Exploration of solutions available naturally to fungal resistance is the aim of explores and researchers worldwide. The current study aims to assess the antifungal potential of endophytic bacterial metabolites of medicinal importance through both *in-vitro* and *in-silico* studies. Bioactive metabolites from the bacteria were extracted to assess their antifungal potential through DDA, and MIC determination. Gas Chromatography-Mass Spectroscopy characterized the diverse composition of the endophytic extracts. Molecular Docking and Dynamics studies revealed the interactions between metabolites and target proteins of interest. The findings of the study emphasized the potential of few metabolites as a promising antifungal agent to combat fungal infections.

Keywords: *in-silico* studies, Gas Chromatography-Mass Spectroscopy, DDA, MIC determination

MTAMR-19 (Poster)

Metabolites from *Anabaena fertilissima* CCC597 Affected Membrane Integrity of *E.coli* Leading to its Bactericidal Activity

Trashi Agrah Singh
trashisingh24@gmail.com

Bhagyoday Tirth College of Paramedical Science, Sagar, Madhya Pradesh, India)

Abstract: Cyanobacterial strains are not much explored genera of microorganisms which posess a number of metabolites which can be used for a number of purposes. Major problem that is being faced today is of drug resistance in pathogens. Most of the pathogens have become resistant against a number of commercially available drugs. So this study was designed to exploit cyanobacteria *Anabaena fertilissima* CCC597 for the production of metabolites and screening them against known pathogenic bacteria. Post screening major focus was shifted towards analysis of antagonistic activities for which a series of tests were conducted. Major reason for this was to confirm weather the metabolite isolated was bactericidal or bacterioststic. The studies revealed MIC and MBC to be 8 µg/ml and further investigation suggested rate of oxygen consumption was affected in presence of metabolite extract and upon studying membrane integrity, it was revealed that inner membrane permeabilization was affected leading to cell death proving the extracted metabolite to be of bactericidal nature. GC and HPLC studies were performed further for the identification of the metabolite.

Keywords: Metaboloites, Membrane integrity, Bactericidal, Drug resistance, antagonistic, Membrane permeabilization

MTAMR-20 (Poster)

Mitochondria with endoplasmic reticulum membrane connections control drug sensitivity and virulence in *Cryptococcus neoformans*

Deepika Kumari[1], Mohit Kumar[2], Naseem A. Gaur[2], Nadezhda Sachivkina[3], **Ritu Pasrija[1*]**
ritupasrija@yahoo.com; ritupasrija.biochem@mdurohtak.ac.in

[1]*Department of Biochemistry, Maharshi Dayanand University, Rohtak, Haryana 124001, India*
[2]*International Centre for Genetic Engineering and Biotechnology, New Delhi, 110067, India*
[3]*Department of Microbiology, Peoples' Friendship University of Russia, Moscow, Russia-117198*

Abstract: Fungal infections caused by various species have seen a dramatic increase in recent decades, leading to more than 1.5 million deaths (CDC).. In October 2022, the WHO classified *Cryptococcus neoformans* as serious invasive fungi and placed it alongside *Candida auris*, *Aspergillus fumigatus* and *Candida albicans* in the 'critical priority group' of fungal priority pathogens list (FPPL). *C. neoformans* is universally prevalent and opportunistic pathogen is capable of causing life-threatening cryptococcosis (Zhao et al. 2023). The limited availability of antifungal drugs and the increasing resistance in fungal pathogens underscore the urgent need to identify novel, fungal-specific drug taOrganelle communication is essential for cellular metabolism in eukaryotic cells. The ER-mitochondria encounter structure (ERMES) complex, a fungal-specific multiprotein complex, has emerged as a promising target due to its critical role in maintaining mitochondrial morphology and function. ERMES complex has four subunits, Mmm1 (Maintenance of mitochondrial morphology), Mdm12 (Mitochondrial distribution and morphology), Mdm10, and Mdm34, are crucial for mitochondrial stability and affect fungal virulence and drug resistance. In this study, we investigated the role of ERMES in *C. neoformans* by deleting these four core subunits. The results revealed that disrupting ERMES impacted mitochondrial morphology and altered ROS production. The mutants exhibited increased sensitivity to drugs including echinocandins, suggesting compromised cell wall integrity. ERMES disruption also led to reduced production of virulence factors *in vitro*, which was consistent with decreased virulence observed in an *in vivo* model *Caenorhabditis elegans*. Taken together, these results suggest that targeting the ERMES complex could be a promising strategy for developing novel antifungal therapies against *C. neoformans* infections.

Keywords: Drug resistance, *Cryptococcus neoformans*, ERMES, membrane contacts, virulence, mitochondria.

MTAMR-21 (Poster)

Mitigating Neurodegenerative Disorder with Novel *Lactiplantibacillus pentosus* C87 Exopolysaccharides to Reduce Oxidative Stress

Abinash. R and Dr Ieshita Pan*
*ieshitapan.sse@saveetha.com

Institute of Biotechnology, Department of Medical Biotechnology and Integrative Physiology, SIMATS School of Engineering, Saveetha Institute of Medical and Technical Sciences, Thandalam, Chennai, Tamil Nadu (602 105), India

Abstract: Neurodegenerative disorders, characterized by progressive neuronal damage and loss, are increasingly linked to oxidative stress, which exacerbates neuronal injury. Recent studies have highlighted the potential of probiotics in combating oxidative stress and promoting neuroprotection. Exopolysaccharides (EPS) are high-molecular-weight polysaccharides that possess various biological activities, including antimicrobial and antioxidant potential. This research focuses on the exploration of nonconventional probiotic strain *Lactiplantibacillus pentosus* C87 and its EPS production strategies, to mitigate oxidative stress, and neurodegenerative disorders. Through cabbage fermentation for 45 days *L. pentosus* C87 was isolated out of 90 probiotic strains and identified based on its gram +ve , catalase – ve, endospore negative, hemolactate fermentation with acid +ve and gas -ve behaviour. The selected organism was further analysed for growth and EPS production optimization. Qualitative analysis revealed the produced EPS is heteroplysaccharide in nature with antimicrobial and antioxidant potential. *L. pentosus* C87 produces a bacteriocin that is equally effective against *Serratia* and *Vibrio* species when compared to streptomycin. At a concentration of 14.46 µg/mL, the bacteriocin achieves a significant inhibition of over 65% against these pathogens. *L. pentosus* C87 EPS amount under different condition, 47.4mg/ml. The *invitro* antioxidative assays results demonstrated that EPS from *L. pentosus* C87 when treated with fructose, produces exopolysaccharides (EPS) that have the significantly reduced the levels of reactive oxygen species (ROS). Thus the *L. pentosus* C87 EPS isolated from the non-conventional food source may offer a novel therapeutic approach for managing neurodegenerative diseases by controlling ROS and managing gut health with its probiotics potential.

Keywords: Neurodegenerative disorders, Oxidative stress, Probiotics, Exopolysaccharides (EPS), Nonconventional probiotic strain

MTAMR-22 (Poster)

Assessing the Antimicrobial Potential of *Kappaphycus Alvarezii*: An Investigation into the Efficacy of Pure Algal Powder against Gram-Positive Bacteria

Pardha Saradhi Ayyanngar Eyyunni
epardhasaradhiayyangar@gmail.com

Department of Zoology, Andhra University, Andhra Pradesh (530003), India

Abstract: In the ongoing quest to discover potent antimicrobial agents from natural sources, *Kappaphycus alvarezii*, a red seaweed, has been heralded for its promising bioactive properties, particularly in solvent-extracted forms. Yet, our investigation charts an unorthodox course, by passing traditional extraction methods to employ pure *Kappaphycus alvarezii* powder directly against Gram-positive bacteria, specifically *Bacillus subtilis* and *Staphylococcus aureus*. Despite the rich phytochemical profile associated with *Kappaphycus alvarezii*, our findings reveal a striking absence of significant antimicrobial activity in its powdered form when compared to the established efficacy of Ciprofloxacin as a positive control.

This unexpected outcome challenges the prevailing narrative of *Kappaphycus alvarezii*'s antimicrobial potential, raising critical questions about the role of extraction processes in unlocking the bioactivity of marine-derived compounds. The inert response observed in Gram-positive bacteria suggests that the pure powder's bioactive constituents may remain latent or inaccessible without the intervention of solvent extraction, which typically serves to solubilize and concentrate these compounds. This phenomenon invites a deeper exploration into the structural integrity and bioavailability of the algal constituents, positing that the antimicrobial efficacy of *Kappaphycus alvarezii* is not inherent but highly dependent on the method of preparation.

Our research underscores the necessity of rethinking the methodologies used to evaluate the antimicrobial properties of natural products, particularly in the context of microbial therapeutics and the growing challenge of

antimicrobial resistance. By confronting the limitations observed in this study, we pave the way for future investigations that could elucidate the complex dynamics between extraction methods and bioactivity, ultimately refining our approach to harnessing the therapeutic potential of marine algae.

Keywords: *Kappaphycus alvarezii*, Antimicrobial resistance, Gram-Positive bacteria, Pure powder, Bioactive compounds, Marine therapeutics

MTAMR-23 (Poster)

Surveillance of fungi, their antimicrobial resistance and biofilm formation ability in Intensive Care Unit (ICU)

Saloni Taparia, Sumana MN and Umamaheshwari
*umamaheshwari@jssuni.edu.in

Department of Microbiology, JSS Academy of Higher Education & Research, Mysuru, Karnataka, India

Abstract: Intensive Care Unit (ICU) acquired infections are a serious health care concern since patients admitted are severely ill and immunocompromised. Microbes shed by them can cross-contaminate the ICU environment, and the dominating organism may be resistant to stick to the surface as well as the current equipment. As per reviews, bacterial screening was always focused so here we are trying to screen and characterize fungi particularly yeast. To do so swab samples were collected which were plated onto the Sabouraud Dextrose Agar with Chloramphenicol (SDAC) media and was incubated at 37♂ C for 1 week. A total of 83 samples were collected, out of which 33 (39.75%) showed growth. The isolates were subjected to microscopic observation using Lactophenol cotton blue (LCB) stain for identification of yeast and moulds which revealed 15 (45.45%) yeast in which 1 (3.03%) was identified as *Rhodotorula* and 18 (54.54%) moulds. The yeast was then subjected to morphological and biochemical test followed by its virulence attributes for Haemolytic, phospholipase and esterase along with their susceptibility towards some antifungal, and the ability to form biofilm using 96-well plates for its identification. Moulds were then identified by slide culture and temperature tolerance test. The Germ tube test revealed that one was *Candida albicans* (6.66%) and the other fourteen isolates were non-*Candida albicans* (93.33%) . CHROM agar and corn meal agar revealed two *C. parapsilosis*, five *C. krusei* and one *C. tropicalis*. When tested for its virulence attributes one (6.66%) was virulent and the rest 14 (93.33%) was non-virulent. Three isolates were biofilm formers, while they were sensitive to all antifungal drugs and was able to ferment different sugars. Slide culture revealed the presence of *Aspergillus flavus, A. fumigatus, A. niger* as well as *Penicillium sp.* Out of all 5 yeast and rest moulds are yet to be identified. The result thus revealed that despite proper cleaning fungal forms may still be prevalent posing an impact on patients and health care workers. Efforts are thus needed to increase and to maintain the hygiene with minimal pathogen shedding.

Keywords: Intensive Care Units (ICU), yeasts, Moulds, Opportunistic, Multi Drug Resistance Organism (MDRO)

MTAMR-24 (Poster)

High Prevalence of Cotrimoxazole Resistance Genes among Uropathogenic Isolates of Bacteria

Mohammad Saif, Shayan Ahmed, Qazi Mohd. Rizwanul Haq*
*qhaque@jmi.ac.in

Microbiology Research Laboratory, Department of Biosciences, Jamia Millia Islamia, New Delhi, India

Abstract: Cotrimoxazole, (a synergistic ratio of trimethoprim and sulfamethoxazole), has been widely used as an empirical treatment for urinary tract infections (UTIs) caused by uropathogenic bacteria. However, increasing resistance to cotrimoxazole among these pathogens poses a significant challenge to effective UTI management. The aim of this study was to investigate the prevalence of co-trimoxazole resistance among clinical isolates of bacteria causing UTI and molecular detection of *dfr* and *sul* genes. Phenotypic resistance to co-trimoxazole was screened using Kirby-Bauer disc diffusion assay. Furthermore, Multiple Antibiotic Resistance (MAR) and Minimum Inhibitory Concentration (MIC) was used to analyse multi-drug resistance (MDR) bacteria. Molecular

detection of resistance genes (*sul* 1,2 & *dfr*A1, A5, A7, A12 and A17) were carried out by PCR using plasmid DNA isolated from resistant isolates and gene specific primers. Phenotypic screening of bacterial isolates causing UTI were found to be highly resistant (81%) to co-trimoxazole. Of the total 94 phenotypically positive isolates screened, *sul*1 and *sul*2 genes were detected in 77% and 32% isolates respectively. Furthermore, *dfr*A1, *dfr*A5, *dfr*A7, *dfr*A12, and *dfr*A17 were successfully amplified in 22%, 23%, 56%, 66% and 14% among isolates respectively. Resistance to co-trimoxazole was found to be very alarming among uropathogenic bacteria. Genetic analysis confirmed the presence of *sul* and *dfr* genes among resistant isolates. Thus, this study provides useful data on prevalence and distribution of co-trimoxazole resistance and resistant genes among bacteria causing UTI in humans.

Keywords: Cotrimoxazole, Antibiotic resistance, Urinary tract infection, Multidrug resistance

MTAMR-25 (Poster)

Screening and Characterization of *Candida* Species in Paediatric Patients with Dental Caries

Sinchan HG[1], Seema Deshmukh and Umamaheshwari S*
umamaheshwari@jssuni.edu.in

Department of Microbiology, JSS Academy of Higher Education & Research, Mysuru, Karnataka, India

Abstract: Dental caries is a most prevalent chronic multifactorial infectious disease that can begin at an early age causing early childhood caries or anywhere in lifetime. The disease is characterized by progressive destruction of the crowns and roots structures which develops due to the complex interaction of cariogenic oral microflora that metabolize carbohydrates, leading to acid production that demineralizes the tooth structure. Most of the studies have proven that the destruction of tooth or biofilm formation is predominantly by bacterial colonisation. In this regard, an attempt here was made to screen yeast such as *Candida* a predominant oral thrush pathogen in paediatric patients as they are sensitive due to undeveloped immune systems, insufficient oral hygiene practices and biofilm formation. The plaque samples were aseptically collected from 35 patients aged 6-8 with an informed consent. The samples were then inoculated onto Sabouraud dextrose agar with Chloramphenicol plates and incubated at 37°C for 72 hours. The isolated yeast colonies were tested for germ tube, followed by morphological biochemical characterization. The isolates were then tested for virulence and subjected to antifungal susceptibility test. Of the 35 samples processed we were able to isolate 3 (8.57%) Candida isolates. Germ tube test revealed, one was *Candida albicans* (33.33%) and other two (66.67%) non-*Candida albicans*. Morphological-CHROMagar, Cornmeal agar and biochemical study-Sugar fermentation revealed that non-*albicans* were *C. tropicalis* and *C. parapsilosis.* All isolates were strong biofilm formers but were sensitive to all antifungal drugs tested. Virulence test revealed that isolated *Candida albicans* was haemolytic and was negative for esterase and phospholipase activity. With this we conclude that both *C. albicans* and non-*Candida albicans* were isolated from paediatric cases and they had the capacity to ferment sugars that could produce acid and causes rampant tooth decay. This necessitates the choice of therapeutic for effective oral hygiene.

Keywords: Dental caries, Paediatrics, *Candida albicans,* Non-*albicans,* Virulence

MTAMR-26 (Poster)

The Transcriptome Response of *Enterobacter* sp. S-33 is Modulated by Low pH-Stress

Kiran Kumari[1*] and Rajnish Prakash Singh[2]
*kirankumarikk121@gmail.com

[1]*Department of Bioengineering and Biotechnology, Birla Institute of Technology, Mesra, Ranchi, Jharkhand, India*
[2]*Department of Biotechnology, Jaypee Institute of Information Technology, Noida, India*

Abstract: Acidic environments naturally occur worldwide and uncontrolled use of agricultural practices may also cause acidification of soils. The development of acidic conditions disturbs the establishment of efficient

microbial populations in their natural niches. The survival of *Enterobacter* species under acidic stress remains poorly understood. This study aimed to investigate the survival of an environmental isolate *Enterobacter* sp. S-33 under acidic stress and to identify the various genes involved in stress protection at the global gene transcription level. The obtained results provide new targets that will allow understanding the in-depth mechanisms involved in the adaptation of bacteria to environmental pH changes. We used the next-generation sequencing (NGS) method to analyze the expression (up-regulation & down-regulation) of genes under varying pH conditions. A total of 4214 genes were differentially expressed under acidic conditions (pH 5.0), with 294 up-regulated and 167 down-regulated. At pH 6.0, 50 genes were significantly expressed, of which 34 and 16 were identified as up-regulated and down-regulated, respectively. Many up-regulated genes were involved in carbohydrate metabolism, amino acid transport & metabolism, and the most down-regulated genes were related to post-translational modification, lipid transport & metabolism, etc. The observed transcriptomic regulation of genes and pathways identified that *Enterobacter* reduced its post-translational modification, lipid transport & metabolism, and increased carbohydrate metabolism, amino acid metabolism & transport, energy production & conversion to adapt and grow in acidic stress. The present work provides in-depth information on the characterization of genes associated with tolerance or adaptation to acidic stress of *Enterobacter* bacterium.

Keywords: *Enterobacter,* RNA-Seq, pH stress, Transcriptomic analysis, Gene ontology

MTAMR-27 (Poster)

Multi-Drug Resistance in Diarrhoeic Newborn Calves: A Growing Threat to Bovine Health

Sarishti and Kiran Nehra*
*nehrakiran@gmail.com

Deenbandhu Chhotu Ram University of Science and Technology (DCRUST), Murthal, Sonipat, Haryana (131039), India

Abstract: Neonatal diarrhoea is one of the most common diseases reported in calves upto 3 months old. Due to global increase an antibiotic-resistance in bacteria causing this disease, it has become a serious problem in the control of infection in neonatal calves. Many of the isolates in newborn calves have multiple resistance to beta-lactams, including extended-spectrum cephalosporins. Current treatment for faecal infections caused by MDR bacteria which form a biofilm layer and Extended Spectrum beta lactamase (ESBL) behaviour, mainly constitutes the antibiotics; but, more recently it has been observed that bacteria which exhibit resistance against most of the available antibiotics due to the development of mutant strains. In the Present study, the author collected multidrug- resistance (MDR) pathogens from diarrhoeic new born calves, obtained from the State Disease Diagnostic Laboratory, Haryana. According to Antibiotic Susceptibility test (AST), it has been found that neonatal calf diarrhoea within initial month of life accounts for approximately 65% antibiotic resistance. Thus, based on the present study, the emergence of multidrug-resistant bacteria in diarrhoeic newborn calves has become a significant threat to bovine health, hence creating a need to investigate alternative therapeutic options.

Keywords: Biofilm-formation, ESBL-producing bacteria, Multiple Drug Resistance (MDR), Antibiotic Susceptibility Test (AST)

MTAMR-28 (Poster)

Green Synthesis of Nanoparticles against Biofilm forming Multi - Drug Resistant Pathogens

Dimple Khatri and Kiran Nehra*
*nehrakiran@gmail.com

Deenbandhu Chhotu Ram University of Science and Technology, Murthal, Sonipat, Haryana, India

Abstract: The spread of antibiotic resistance and increasing prevalence of biofilm associated infections is driving demand for new means to treat bacterial infections. In recent years the use of antibiotics has been accompanied by the rapid emergence antimicrobial resistance. Development MDR pathogens is currently

considered as a big threat to global health. Biofilm is a complex structure of microbiome having different bacterial colonies or single type of cells in a group, adhere to the surface. These cells are embedded in extracellular polymeric substances, a matrix which is generally composed of eDNA, proteins and polysaccharides, showed high resistance to antibiotics. Nanoparticles have unique chemical and physical properties, granted by their high surface area to volume ratio. Nowadays, there is a growing need to develop eco-friendly processes, which do not use toxic chemicals in the synthesis protocols. To encounter the rise and spread of MDR pathogenic strains, nanoparticles are viable approach to treat biofilm-associated infections. Due to increase of Multi Drug Resistant pathogens the alternate solution is to synthesize nanoparticles by using metals like Fe, ZnO2, TiO2, etc. These nano-materials are least toxic to human beings and do not affect the normal flora of human body. This approach will reduce the burden of economy and infections on mankind and can significantly control the rise of MDR strains and also reduce the minimum required dose of antibiotics.aai

Keywords: Biofilm, Nanoparticles, Antibiotics

MTAMR-29 (Poster)

Regulatory Networks Reconstruction in *Streptomyces coelicolor* A3 using Microarray Data Analysis

Parul Sharma*, Varun Jaiswal, Shailja Bains, Puneet, Megha Sharma, Subhash Chand and Sunita Devi
*paruls91@gmail.com

Microbiology Laboratory, Department of Basic Sciences, College of Forestry, Dr. YS Parmar University of Horticulture and Forestry- Nauni, Solan, Himachal Pradesh (173230), India

Abstract: Soil-dwelling bacteria called *Streptomyces coelicolor* have a complicated life cycle that culminates in the production of spores and aerial mycelia. Because *Streptomyces coelicolor* bacteria have enzymatic pathways that allow them to break down complex debris from dead plants, animals, and fungi and produce a wide variety of bioactive secondary metabolites, they are a valuable source of natural products for the pharmaceutical and agricultural industries. The genes pertaining to disease resistance and secondary metabolite biosynthesis remain unknown despite several investigations in this area. The current understanding gaps are crucial since they could lead to a deeper comprehension of the bacterial pathogen's drug resistance mechanism. Discovering the genes and gene networks involved in the biosynthesis of secondary metabolites could lead to methods for increasing the production of these pharmacologically active compounds in industrial settings. In the current study, available genomic and expression data were utilized, along with clustering analysis, to identify genes involved in secondary metabolite biosynthesis and disease resistance. Gene annotation information was utilized to identify genes crucial for transportation and drug resistance. Network analysis revealed that some neighbouring genes were shared among the predicted genes. These predicted genes, along with their common neighbouring genes, may play a role in drug resistance and secondary metabolite biosynthesis.

Keywords: Regulatory networks, Gene network, Annotation information, Secondary metabolites, Network analysis, Clustering

MTAMR-30 (Poster)

Endophytic Bacterial Community Reveals Antimicrobial Resistance in Response to Poultry-Manure Application

Animesh Tripathi* and Suresh Kumar Dubey
*animesh.t.0498@gmail.com

Molecular Ecology Laboratory, Department of Botany, Institute of Science, Banaras Hindu University (BHU), Varanasi, Uttar Pradesh (221005), India

Abstract: The widespread administration of antibiotics in poultry farming raises serious concerns about poultry manure, often utilized as fertilizer in agriculture and could potentially contain antimicrobial resistance genes

(ARGs). Studies have indicated that the introduction of poultry manure to fields may increase the levels of ARGs linked to resistance to several antibiotics, such as aminoglycosides, bacitracin, tetracyclines, sulfonamides, fluoroquinolones, and macrolide-lincosamide-streptogramin. Comprehending the microbial communities containing these ARGs is essential since some of these microbes may find their way into human diets. This study tests the hypothesis that environmental exposure to poultry manure elevates antimicrobial resistance (AMR) in plant endophytes using selective culture, phenotypic Antibiotic Susceptibility Testing (AST), phylogenetic analysis, and whole genome sequencing (WGS). *Bacillus* sp., *Pseudomonas* sp., and *Pantoea* sp. were the most common endophytes. Bacterial endophytes from *Sorghum bicolor* (L.) Moench plants treated with poultry manure showed increased resistance to multiple antibiotics compared to untreated controls. WGS analysis revealed multi-drug resistance (MDR) profiles in all 21 endophytes. *Priestia* sp. encoded multiple ARGs like *arlS*, *vanR*, *bcrA*, *tetA*(*58*), *AcrAB-TolC*, *soxS*, and *marA*. The analysis revealed MDR endophytes, highlighting the importance of genomic surveillance to detect emerging drug-resistant pathogens. The rise in ARGs in plant endophytes exposed to poultry manure underscores the urgent need for responsible antibiotic use in animal farming to prevent ARGs contamination of ecosystems and the plant microbiome. Ensuring the therapeutic value of antibiotics for usage in human and veterinary medicine and additionally tackling the growing problem of AMR necessitates continuous monitoring and surveillance.

Keywords: Agroecosystem; Antimicrobial resistance; Bacterial endophytes; Poultry manure; Resistome; Whole genome sequencing

MTAMR-31 (Poster)

A Study on the Prevalence of Carbapenem Resistance among Bacterial Isolates from Wastewater Systems in New Delhi

Shayan Ahmed, Mohammad Saif and Qazi Mohd. Rizwanul Haq*
*qhaque@jmi.ac.in

Microbiology Research Laboratory, Department of Biosciences, Faculty of Natural Sciences, Jamia Millia Islamia, New Delhi (110025), India

Abstract: Carbapenems were considered one of the last resort antibiotics against multidrug-resistant bacteria; unfortunately, resistance against carbapenems has been extensively documented in recent years. Carbapenem resistance, which was long considered a clinical challenge, is becoming a significant concern in the environment. The emergence of carbapenem-resistant bacteria poses a substantial risk to global public health, with wastewater systems serving as potential reservoirs and facilitators for antibiotic resistance. This study investigates the prevalence of carbapenem resistance among bacterial isolates from wastewater systems across New Delhi. Wastewater samples were collected from multiple sites, including open and sub-surface drains around residential, hospital, and industrial effluent zones. A total of 40 carbapenem-resistant isolates were obtained through antibiotic susceptibility testing using the Kirby-Bauer disk diffusion. These isolates were then subjected to the determination of minimum inhibitory concentration (MIC). Additionally, the Multiple Antibiotic Resistance (MAR) index was determined to evaluate multidrug resistance among these isolates. The study highlights wastewater systems as critical hotspots for the propagation of carbapenem resistance in urban environments. These findings underscore the urgent need for enhanced monitoring, stricter wastewater management protocols, and strategies to mitigate the dissemination of antimicrobial resistance from environmental reservoirs. Addressing this issue is crucial for safeguarding public health and preventing the further spread of resistance in clinical and community settings.

Keywords: Antibiotic resistance, Carbapenem resistance, Multidrug resistance, MIC, Wastewater, Public health

MTAMR-32 (Poster)

Bdellovibrio bacteriovorus: A Potential Predatory Bacteria against Multidrug Resistant Pathogens

Dhanyashree Rai, Jenal Weona Pereira, Divyashree M*
*divyashree.m@nitte.edu.in

1.Nitte University Centre for Science Education and Research, Nitte (DU), Deralakatte, Mangaluru, Karnataka (575018), India

Abstract: *Bdellovibrio bacteriovorus* is a gram-negative predatory bacterium present in various environment and are able to predate wide range of bacteria including human pathogens. In the rising era of antimicrobial resistance (AMR), multidrug-resistant bacterial pathogens have become a major global problem. Being generalist predator *Bdellovibrio* overviews the concept of live antibiotic. The objective of the present study is to isolate *Bdellovibrio* from environment water samples and evaluation of their predatory efficacy against biofilm forming human pathogens *Escherichia coli, Salmonella* Typhimurium and *Pseudomonas aeruginosa.* A total of *Bdellovibrio* strains (n=5) were isolated by double layer agar method using dilute nutrient broth using *E.coli* as prey. *Bdellovibrio* strains were observed under phase contrast microscope, scanning electron microscopy and further confirmed by Polymerase Chain Reaction and sequencing (GenBank accession number: OR501397). The antibiotic susceptibility tests and biofilm forming ability of the prey cells were determined. *In vitro* predatory efficacy of *B. bacteriovorus* (LBD1) was tested against *E. coli* (ATCC 25213), *S.* Typhimurium (ATCC 14028) and *P. aeruginosa* (wound isolate P1). The reduction in optical density (OD at 600nm) from 0.5 to 0.1 was observed at specific interval of time from 0 to 72 hours of co-culture incubation at 30°C at an initial concentration of 10^6 PFU/mL. Biofilm removal ability of LBD1 was tested on preformed biofilms in 96 well micro titre plates using crystal violet assay. LBD1 strain showed 40.5, 26.3 and 50.6% biofilm reduction while ATCC *Bdellovibrio Stolp and starr* (ATCC 15143) showed 72.4, 48.0 and 67% reduction among *E. coli, S. Typhimurium* and *P. aeruginosa* isolates respectively. We observed that a titter of *B. bacteriovorus* 10^6 PFU/well is sufficient to reduce the preformed biofilm. Our data suggest *B. bacteriovorus* could be a promising therapeutic agent for treating MDR gram negative infections, highlighting the importance of developing alternatives, which is crucial in the fight against global crisis of AMR.

Keywords: *Bdellovibrio bacteriovorus,* Multidrug-resistant bacterial pathogens, LBD1

MTAMR-33 (Poster)

Prevalence of Virulence amongst Carbapenem-Resistant Clinical Isolates of *Acinetobacter baumannii* from Ahmedabad Gujrat

Varsha Kaushik and Seema Rawat*
*seema.rawat@cug.ac.in

Microbiology lab, School of Life Sciences, Central University of Gujrat, Gandhinagar, Gujarat (382030), India

Abstract: An *ESKAPE* category opportunistic pathogen *Acinetobacter baumannii* is the leading causative agent for widespread nosocomial infections which are becoming difficult to treat. Over the period due to bacterial evolution and exploitation of classical antibiotics, resistance in *A. baumannii* is gradually increasing. Since the first discovery of oxacillinases in 1993, Carbapenem resistance has become more challenging. With the reduced effectiveness of second-line antibiotics like tigecycline and colistin against Carbapenem-resistant *A. baumannii* (CRAB) isolates, there is an urgent need for alternative treatment options. The pathogenesis of CRAB is notable for its ability to express various virulence factors and phenotypes, such as robust biofilm formation, AHL production, and surface motility. These factors contribute significantly to the enhancement of antimicrobial resistance. In the current study, 60 clinical strains of *A. baumannii* were analyzed for their carbapenem resistance, biofilm-forming potential, surface motility, and virulence potential. All isolates of *A. baumannii* were found to be *blaoxa-51* positive. Crystal violet assay reflected that 50 isolates were strong-biofilm formers, 9 were moderate-biofilm formers, 2 were non-biofilm formers and 1 was weak-biofilm former. Surface motility assay depicted 3 highly-motile, 14 intermediately-motile, and 42 non-motile *A. baumannii* isolates. These data indicate that all clinical isolates of *A. baumannii* were carbapenem-resistant. The majority of them exhibited

strong biofilm-forming potential and few isolates also showed pronounced twitching motility. Therefore, a novel and potent antimicrobial compound effective against CRAB is needed urgently.

Keywords: Carbapenem-resistant, Biofilm formation, *blaOXA-51,* Surface motility, Multidrug-resistant, Virulence

MTAMR-34 (Poster)

Preliminary Characterization of a Trans-Editing Protein from *Escherichia coli* Involved in Maintaining Translational Fidelity

Smit Shah, Jaykumar Jani and Anju Pappachan*
*anju.p@cug.ac.in

School of Life Sciences, Central University of Gujarat, Gandhinagar, Gujarat (382030), India

Abstract: Trans-editing proteins have evolved to maintain translation fidelity by cleaving misacylated aminoacyl tRNA, thereby protecting cells from protein misfolding. Through our *in silico* studies we identified a putative trans-editing protein from *E. coli*. This protein was cloned in pET28avector and the protein was expressed in *BL21*DE3Cells and purified using Ni-NTA affinity chromatography. Initial studies showed that the protein can bind serine, threonine, and lysine with similar low dissociation constants (Kd), highlighting their role as versatile multi-ligand effectors. Docking studies identified Asn137 as a key residue for ligand binding. Circular dichroism (CD) spectroscopy revealed that the Apo protein predominantly adopts α-helical conformation, which is further stabilized upon binding threonine, serine, and lysine and proline.Thermal melting assays revealed that the Apo protein melts at 52°C. The protein is stable between pH 6 and 9. Incorporation of serine, threonine, proline, and lysine lowered the melting temperature by 3-6°C. Denaturation studies using fluorescence spectroscopy revealed that 1 M urea fully unfolded the protein, while 2.5 M guanidine hydrochloride is required for complete denaturation. Urea caused a 23 nm shift in emission maxima, compared to a 10 nm shift with guanidine hydrochloride, suggesting higher α-helical content. Our study also revealed that *E. coli* strains lacking this protein exhibited strikingly diminished growth, underscoring its crucial role in cellular function compared to wild-type strains. The halo assay showed that wild-type *E. coli* strains exhibited significantly higher resistance to streptomycin compared to null strains, depicting some connection between this protein and antibiotic resistance. Future research will use structural studies to elucidate ligand binding sites and explore therapeutic applications.

Keywords: Trans-editing proteins, Translation fidelity, Multi-ligand effectors, Circular dichroism (CD) spectroscopy, Antibiotic resistance, *E. coli*

MTAMR-35 (Poster)

Phage Therapy as a Viable Solution to Combat Multi-Drug Resistant Pathogens Causing Dental Infections

Nishu Rawat and Kiran Nehra*
*nehrakiran@gmail.com

Deenbandhu Chhotu Ram University of Science and Technology,
Murthal, Sonipat, Haryana (131039), India

Abstract: The overuse of antibiotics has led to the emergence of multi-drug-resistant bacteria (MDR) which complicates the treatment of many infections including dental infections. In both industrialized and developing countries, dental caries and periodontal diseases are the leading causes of tooth loss and are estimated to afflict 20–50% of the world's population. The scientific community is thus compelled to search for an alternative treatment or an approach of empirical antibiotic therapy. Bacteriophage or phage therapy is a viable alternative approach in this direction. Phages have the potential to be effective anti-bacterial agents because they are host-specific, easy to isolate, do not harm the normal flora of the oral cavity, have the unique ability to self-dose and self-limit. Phage therapeutics includes monophage therapy, polyphage therapy or phage cocktails, and phage-derived proteins. The phages act by binding to the receptor proteins present on the pathogenic microbes, modify

them and lyse these microbes. In the present study, the authors collected dental pathogens, which were tested for antibiotic susceptibility and MDR (Multi-Drug-Resistant) isolates were selected. Bacteriophages were isolated against these by using sewage water. Clear plaques of varied morphology were observed on a lawn of bacterial isolate which were purified to obtain a single phage which exhibited lytic activity against bacterial isolates. Thus, based on the present study, the authors concluded that phages can be used as an effective therapeutics for multi-drug-resistant dental microbes.

Keywords: Bacteriophages; MDR; Dental infections; Phage cocktail; Receptor proteins; Lytic activity.

MTAMR-36 (Poster)

Exploring Bioactive Potential of *Streptomyces* spp. against Diverse Pathogenic Fungi

Harsha[1], Munendra Kumar[2], Prateek Kumar[3], Renu Solanki[4] and Monisha Khanna Kapur[1*]
*monishakhanna@andc.du.ac.in

[1]*Microbial Technology Laboratory, Acharya Narendra Dev College, University of Delhi, New Delhi (110019), India*
[2]*Department of Zoology, Rajiv Gandhi University, Doimukh, Arunachal Pradesh (791112), India*
[3]*Department of Zoology, University of Allahabad, Prayagraj, Uttar Pradesh (211002), India*
[4]*Department of Zoology, Deen Dayal Upadhyaya, University of Delhi, Sector 3, Dwarka,Opp. NSIT, New Delhi (110078), India*

Abstract: Pathogenic fungi and the mycotoxins they produce are deadly challenges for human health and the environment. Fungi cause diverse human diseases, ranging from allergic syndromes to superficial, disfiguring, and life-threatening invasive fungal diseases, which affect more than a billion people and the environment worldwide. These pathogens are rapidly getting resistant to all the available drugs. Most antifungal compounds currently in use target the biosynthetic pathway of ergosterol by acting upon the enzyme lanosterol demethylase (CytP450). However, a major drawback to this approach is that it leads to the accumulation of methylated sterol and causes drug resistance. So, there is a consequential need for the discovery of novel bioactive compounds against pathogens. Natural compounds serve as a good source having a broad range of bioactivities like antimicrobial, antifungal, and anti-cancer. During our previous studies, different *Streptomyces* strains were isolated and taxonomically characterized using the 16S rRNA gene and screened for the production and identification of bioactive compounds using GC-MS, LC-MS, and NMR techniques. Upon these considerations, extraction of bioactive molecules from *Streptomyces* strains and detection of antifungal activity will be verified against diverse fungi through MIC determination, disc-diffusion assay and spot assay. Furthermore bacterial strain with well potential activity will be used for synthesizing of silver nanoparticles. Characterisation of nanoparticles will be done like UV-Vis, zeta potential, DLS, XRD, FTIR. Moreover *in-silico* studies would be performed to get information about the binding modes of ligands to the fungal enzyme active site and ADMET studies to show pharmacokinetics. In a nutshell, findings from the present study using *Streptomyces* spp. may help to control the pathogenic and crop-destroying fungi.

Keywords: *Streptomyces* spp., Natural compounds, Pathogenic fungi, MIC determination, Nano-particles synthesis, Molecular Docking, ADMET

MTAMR-37 (Poster)

Dihydroorotate Dehydrogenase Inhibitors have Anti-*Theileria equi* Activities as Evidenced by Molecular Docking and in vitro Analysis

Mamta Tirdia[1,2], Lalita Gupta[1], Geetanjali Sharma[2], Rajender Kumar[2] and Sanjay Kumar[2*]
*kumarsanjay66@yahoo.com

[1]*Deparment of Zoology, Chaudhary Bansi Lal University, Bhiwani, Haryana, India*
[2]*ICAR-National Research Centre on Equines, Hisar, Haryana, India*

Abstract: Equine piroplasmosis, caused by *Theileria equi*, is an economically important illness that affects horses and other equids across the globe. However, no safe and effective medicine is presently available to treat

T. equi. Novel active compounds with specific actions are urgently needed for control of theileriosis in equines. This study investigated to find the pharmacological compounds that might work as effective anti-theilerial drugs. Here we targeted the dihydroorotate dehydrogenase (DHODH) enzyme which is important in the *de novo* pyrimidine production pathway of apicomplexean parasites. This enzyme has been the therapeutic target for plasmodial parasites. There is no PDB structure available for this enzyme in *T. equi*, Homology modelling is done to predict the 3D structure of *Te*DHODH. Using the bioinformatics approaches, we tested molecular docking properties of two drug molecules: artemisinin and dihydroatemisinin on modelled structure of *Te*DHODH. Both drugs showed high potential docking interaction with *Te*DHODH enzyme with binding affinity of -8.4 and -8.5kcal/mol respectively, suggesting potential target for *T. equi*. Further *in vitro* studies were carried out to find the IC_{50} of these drugs against *T. equi*. The *in vitro* results showed that the half maximal inhibitory concentration of artemisinin and dihydroatemisinin against *T. equi* were approximately 11.3µM and 10µM respectively. Our result indicated that these drugs interacted with the *Te*DHODH enzyme. Further research is going on to evaluated their beneficial pharmacokinetic features towards the development of anti-theilerial therapy.

Keywords: *Theileria equi*, Dihydroorotate dehydrogenase, Homology modelling, Molecular docking, Artemisinin, Dihydroartemisinin

MTAMR-38 (Poster)

Biosynthesis of Selenium Nanoparticles with Antimicrobial, Anti-Inflammatory and Antidiabetic Activity

Prayrna Kulkarni, Neha Kalvit and Kedar Ahire*
*kedar_ahire@unipune.ac.in

Department of Zoology, Savitribai Phule Pune University, Ganeshkhind, Pune, Maharashtra (411007), India

Abstract: The present study focuses on the synthesis, characterization and antimicrobial properties of selenium nanoparticles (SeNPs). The green synthesis of SeNPs was carried out using the aqueous extracts of medicinal plant *Bryophyllum pinnatum*. SeNPs were characterized using UV-Vis spectroscopy, SEM, XRD, Zetasizer and FTIR. The peak at 260 nm in UV-Vis spectra confirmed the formation of SeNP. SEM data revealed that SeNP were in the size range of 30-100 nm. The zeta potential value of SeNP was -38.05 mV, confirms the stable colloidal solution of nanoparticles. The biomolecules of *B. pinnatum* responsible in the reduction and further capping of SeNPs were analysed using FTIR. Further, the XRD analysis revealed that the synthesized SeNPs were crystalline in nature. The synthesized SeNP also showed a potent antidiabetic and anti-inflammatory property with an IC_{50} of 33.45 µg/mL and 34.92 µg/mL respectively. Furthermore, cytotoxicity assays revealed that the synthesized SeNPs were non-toxic to the mouse fibroblast cell line 3T3L-1. The antimicrobial activity of SeNPs was evaluated against Methicillin Resistant *Staphylococcus aureus* (MRSA). The results indicated a strong antibacterial (MIC of 10 µg/mL) and antioxidant activity (IC_{50} 40 µg/mL) of SeNP.

Keywords: Selenium nanoparticles, SEM, XRD, Cytotoxicity assays

MTAMR-39 (Poster)

Naringenin-loaded Chitosan-Coated Silver Nanoparticles Exhibit Potent Antibacterial, Anti-Biofilm, and Anti-Inflammatory Properties against Drug-Resistant Urinary Tract Infections

Ashu Devraj* and Pramod Kumar Kushawaha**
*ashudevraj499@gmail.com, **kpramodk82@gmail.com

Department of Microbiology, School of Basic Sciences, Central University of Punjab, VPO Ghudda, Bathinda, Punjab (151401), India

Abstract: The increasing emergence of drug-resistant UTI pathogens warrants the discovery of new antibiotics. Therefore, the present study was carried out to synthesize Naringenin (N) loaded chitosan-capped silver

nanoparticles (N_C@AgNPs) to evaluate its antimicrobial, antioxidant, and anti-inflammatory potential. The synthesized N_C@AgNPs were characterized by UV-Spectra, DLS, FTIR, and SEM. It showed MIC between 1.55 µg/ml to 12.5 µg/ml and MBC between 3.12 µg/ml to 25 µg/ml against drug-resistant UTI pathogens, *Escherichia coli*, *Pseudomonas aeruginosa*, *Klebsiella pneumoniae*, and *Enterococcus faecalis*. Moreover, the antibiofilm activity of the synthesized N_C@AgNPs was also assessed against *Klebsiella pneumoniae* and *Pseudomonas aeruginosa*. In the pre-treatment method, concentration-dependent significant inhibition of the biofilm development was reported against *Pseudomonas aeruginosa* (70.30%) and *Klebsiella pneumoniae* (75.26%) at 30µg/ml compared to individual bacterial control. Similarly, in the post-treatment method, the highest inhibition was observed at 100µg/ml against *Pseudomonas aeruginosa* biofilm (85.51%) and *Klebsiella pneumoniae* biofilm (84.03%) compared to individual bacterial control. Further, the fluorescence staining test for live/dead bacterial viability confirmed that N_C@AgNPs at 100µg/ml effectively inhibit the biofilm formed by these drug-resistant UTI pathogens. Moreover, no cytotoxicity of N_C@AgNPs was observed in the THP-1 cell line. N_C@AgNPs also exhibited anti-inflammatory activity by inhibiting the expression of proinflammatory cytokines (IL-6, IL-12b, and IFN-Y) in lipopolysaccharide-treated THP-1 differentiated macrophages. This study concludes that N_C@AgNPs exhibit solid antimicrobial, antioxidant, anti-biofilm, and anti-inflammatory activity and may be developed as a promising antimicrobial agent for treating UTI pathogens.

Keywords: *Pseudomonas aeruginosa*, THP-1 differentiated macrophages, N_C@AgNPs, UTI pathogens

MTAMR-40 (Poster)

Isolation and Characterization of Novel Bacteriophages fMTSA1 and fHBSA8 that Effectively Infects *Shigella flexneri*

Anshu Singh, Aaina, Tushar Midha, Ishita Gulati, Simran Sharma, Krishna P. and Somesh Baranwal*
hostel159866@gmail.com, *somesh.baranwal@cup.edu.in

Department of Microbiology, Central University of Punjab, VPO-Ghudda, Bathinda, Punjab, India

Abstract: *Shigella flexneri*, a pathogenic bacterium, is the primary cause of shigellosis, a highly contagious infection marked by severe diarrhoea, abdominal pain, and fever, often transmitted through contaminated food, water, or direct person-to-person contact. As antibiotic resistance continues to rise, bacteriophages have emerged as a promising and safe alternative for controlling bacterial infections. In this study, we report the successful isolation and characterization of two bacteriophages, fMTSA1 and fHBSA8, from wastewater, both of which showed effective inhibition of *S. flexneri* growth. Phage fMTSA1 exhibited stability over a temperature range of 4°C to 65°C and a pH range of 3 to 11, while fHBSA8 remained stable from 4°C to 60°C within the same pH limits. Complete phage adsorption was observed within 25 minutes, with latent periods ranging between 0 to 30 minutes. The generation times were determined to be 60 minutes for fMTSA1 and 30 minutes for fHBSA8. Transmission electron microscopy revealed that fMTSA1 belongs to the Myoviridae family, with a head width of 72 ± 0.5 nm and a contractile tail of 128 ± 20 nm, while fHBSA8 measured 150 ± 10 nm. Randomly amplified polymorphic DNA -PCR analysis revealed significant genetic diversity between these phages, suggesting they belong to different families. Both bacteriophages showed lytic activity against *Shigella* strains with Multiple Antibiotic Resistance Index (MARI) ranging from 0.125 to 0.75 and were effective against several members of enterobacteriaceae. The Genomic characterization was also performed for these two phages. To summarise, our findings suggest that bacteriophages fMTSA1 and fHBSA8 possess strong potential to counteract antimicrobial resistance in *Shigella flexneri*, offering a promising alternative treatment for shigellosis.

Keywords: *Shigella flexneri*, Shigellosis, Antimicrobial Resistance (AMR), Multidrug resistance, Bacteriophage

MTAMR-41 (Poster)

Therapeutic Potential of Bioactive Molecules from Seaweed against Biofilms on Urinary Catheter

Krishna Vaniya*, Ashok Kumar Bishoyi, Kantha Deivi Arunachalam
*krishna.vaniya128906@marwadiuniversity.ac.in

Department of Microbiology, Marwadi University, Rajkot, Gujarat (360003), India

Abstract: Urinary tract infections (UTIs) are the second-most frequent disease and women are morelikely to contract UTIs once in their life. Urinary tract infection (UTI) is the most common nosocomial infection. The high prevalence of nosocomial infections is related to the contamination of intravenous catheters implicated in hospitalized patients with biofilm forming pathogens. Biofilms are communities of microorganisms that adhere to surfaces and present considerable risks in clinical environments, resulting in heightened morbidity and increased healthcare expenditures. To tackle biofilm-related infections linked to urinary catheters the therapeutic potential of fucoidans and fucoxanthin, bioactive compounds from seaweeds, offers a promising approach. Current review articles described the effectiveness of fucoidans and fucoxanthin, especially in conjunction with nanoparticles, in inhibiting biofilm formation on urinary catheters. Different bioactive compounds such as carotenoids, polysaccharides, and fucoidans demonstrate significant anti-inflammatory, antibacterial, and antiviral properties, whereas fucoxanthin is well known for its antioxidant activity. This method seeks to develop a dual-action strategy by utilizing natural compounds in conjunction with innovative nanoparticle technology to inhibit pathogenic bacterial growth and improve the biocompatibility of urinary catheters. Incorporating marine-derived substances into catheter design may significantly decrease the occurrence of catheter-associated urinary tract infections (CAUTIs), thereby enhancing patient outcomes and alleviating healthcare burdens. The current literature survey highlights the significance of investigating sustainable and biocompatible methods in the development of medical devices, which aligns with societal welfare objectives by enhancing healthcare safety and mitigating antibiotic resistance through natural alternatives. The outcomes of this review may help to design innovative treatment strategies using natural bioactive compounds to address current or future medical challenges.

Keywords: Fucoidans, Fucoxanthin, Nanoparticle, CAUTIs, Seaweeds, Biofilm, Urinary catheter

MTAMR-42 (Poster)

Isolation, Characterization, and Application of a Novel Bacteriophage fBSPA 4 against *Salmonella enterica* in Dairy Products

Aaina*, and Somesh Baranwal
*aainachoudhary1995@gmail.com

Department of Microbiology, School of Basic Sciences, Central University of Punjab, VPO Ghudda, Bathinda, 151401, India.

Abstract: Non-typhoidal Salmonella (NTS), a zoonotic veterinary pathogen, is associated with food-borne illness in human. Contaminated food of animal origin such as poultry, milk and meat are frequent sources of *Salmonella enterica*, a foodborne pathogen that is associated with Salmonellosis in human.
In this work, we have isolated and characterized a broad-spectrum lytic bacteriophage (fBSPA4) from chicken intestine that inhibits growth of antibiotic resistance NTS strain from several Indian poultry farm and target *Salmonella enterica* infection in dairy products. fBSPA4 shows large burst size, a very short latent period, a strong tolerance to high temperatures (5-65ºC) and unnatural pH (3.0–11.0). TEM analysis revealed a polyhedral head (77 nm in diameter) and non-contractile tail (120 nm in length), which belongs to family Caudovirales. fBSPA4 showed single contig of 87,179 base pairs with an average G+C content of 38.91% as revealed by whole genome sequencing experiments. The fBSPA4 has 123 codon-determining sequences (CDS) and does not harbor any genes related to lysogeny, antibiotic resistance, virulence factors, or toxins. Further, fBSPA4 significantly decreased *Salmonella enterica* levels in the milk and yoghurt as determined by *ex-vivo* infection model.
In summary, our research highlight the potential use of fBSPA4 as a disinfecting agent to prevent contamination of food products.

Keywords: *Salmonella,* Bacteriophage, Phage Therapy, Poultry, Dairy products, AMR

MTAMR-43 (Poster)

Identification of a Putative Metallo β-lactamase (MBL) Gene in a Multidrug Resistant Emergent *Salmonella* Infantis Isolated from Seafood

Jerusha Stephen*, Manjusha Lekshmi, Binaya Bhusan Nayak, and Sanath Kumar H.
*jeruselva@gmail.com

QC laboratory, Department of Fish Processing Technology, ICAR-CIFE, Mumbai, Maharashtra (400061), India

Abstract: Carbapenem resistance in *Salmonella enterica* subsp. *enterica* is relatively rare when compared with other Enterobacterial pathogens. Most carbapenem resistance mechanisms involve β-lactamases or porin modifications. However, recent findings suggest the presence of chromosomally encoded metallo-β-lactamase (MBL) genes in specific serovars, particularly in emergent *Salmonella enterica* subsp. *enterica* serovar Infantis. In this study, the whole genome sequence (WGS) of an emergent *S*. Infantis carrying pESI plasmid was derived. Comprehensive genomic analysis of WGS revealed a putative MBL gene sharing significant homology with SPR-1 and SER-1. This gene, characterized by the HARLDQ motif, is predicted to encode a metallo β-lactamase enzyme. The gene was cloned and expressed in *Escherichia coli* without signal peptides, and its role in carbapenem resistance was investigated. However, the recombinant *E. coli* carrying the cloned MBL gene did not exhibit a significant increase in carbapenem resistance, suggesting the presence of mechanisms that regulate the functioning of the gene. Further analysis suggested that upstream and downstream regulatory elements, including promoters and membrane transporters, might be crucial for the expression and functioning of the MBL gene. Also, in-silico modeling of MBL protein revealed that the molecule was highly unstable, pointing to possible post-transcriptional or post-translational modifications. Gene expression studies were carried out to elucidate the precise role of each element in carbapenem resistance.

Keywords: Carbapenem, *Salmonella enterica,* β-lactamases, pESI plasmid, MBL protein

MTAMR-44 (Poster)

In silico and *In vitro* Evaluation of Bicyclic Monoterpenoid as a Potential Antifungal Agent against *Candida albicans* Cell Membrane

Parveen* and Nikhat Manzoor
*parveenchaprana1@gmail.com

Medical Mycology Laboratory, Department of Biosciences, Jamia Millia Islamia, New Delhi (110025), India

Abstract: Yeast from the *Candida* genus is a normal component of the human microbiota, playing a role in maintaining its balance and overall health. However, when this balance is disrupted, a condition known as *Candida* spp. dysbiosis can occur, leading to candidiasis. This condition can manifest with symptoms ranging from mild, localized rashes to serious, widespread infections. The standard treatment for candidiasis typically involves azole-class antifungal medications, which target the fungal cell membrane. However, increasing antifungal resistance has created an urgent need to explore alternative therapeutic options, as candidiasis is becoming a major medical concern. Plant-derived compounds, especially monoterpenoids, have shown potential as antifungal agents. While acyclic and monocyclic monoterpenoids have been extensively studied, less attention has been given to bicyclic monoterpenoids. This study aimed to explore the antifungal effects of a bicyclic monoterpenoid Nopol, against *Candida albicans*. Broth microdilution assays demonstrated fungal growth inhibition, with minimum inhibitory concentrations (MIC) of 146 µg/ml. Scanning electron microscopy, fluorescence microscopy, fluorescent-assisted activated cell sorting (FACS), H+-extrusion, and ergosterol quantification were employed to evaluate their impact on membrane integrity. *In silico* studies were used to further validate their action on the cell membrane. The findings suggest that Nopol is a promising, safer natural antifungal agent, primarily disrupting membrane integrity.

Keywords: Bicyclic Monoterpenoids, *Candida albicans*, Natural antifungal, Cell membrane, Nopol, Candidiasis

MTAMR-45 (Poster)

Novel Antimicrobial Formulation for *Pseudomonas aeruginosa* Infection in Burn Wound Injuries

Avleen Kour[1*], Sundeep Jaglan[2], Sarika Sharma[3] and Sandeep Sharma[1]
*kouravleen949@gmail.com

[1]*Department of Medical Laboratory Science, Lovely Professional University, Phagwara, Kapurthala, Punjab, India*
[2]*Fermentation and Microbial Biotechnology Division, CSIR- Indian Institute of Integrative Medicine, Jammu & Kashmir, India*
[3]*Department of Sponsored Research, Division of Research & Development, Lovely Professional University, Phagwara, Kapurthala, Punjab, India*

Abstract: *Pseudomonas aeruginosa,* an important nosocomial bacterial pathogen, is highly involved in burn wound infections. Due to its emerging multi-drug resistance (MDR) complicates the traditional treatment approaches, highlighting the present need for potent and innovative anti-infective strategies. Burn injuries significantly disrupt body tissues, damage the immune system, and cause hinderance in the biological process of wound healing. The compromised skin barrier and impaired immune response aggravates the infection risk, leading to higher mortality rates and prolonged hospital stays. We propose a unique antimicrobial cocktail which includes an antibiotic, a natural molecule, and a probiotic strain. The combination so formulated aims to effectively manage *P. aeruginosa* infections, boosting patient's weakened immune system and accelerating the wound healing process by inducing anti-infective and anti-inflammatory activities. In-vitro investigations have revealed that the antimicrobial cocktail effectively reduces *P. aeruginosa* load, enhances bacterial clearance, inhibits biofilm formation, and lowers the probability of development of resistant bacterial mutants. We are firm in our belief that the formulation could be a powerful approach to target *P. aeruginosa* infections in burn wounds.

Keywords: *Pseudomonas aeruginosa*, Burns, Wound infections, Antibiotic, Probiotic, AMR

MTAMR-46 (Poster)

Bacteriophage Therapy for Multidrug-Resistant Avian Pathogenic *Escherichia coli*

Tushar Midha[**], and Somesh Baranwal[*]
*somesh.baranwal@cup.edu.in, **midhatushar@gmail.com

[1] *Department of Microbiology, School of Basic Sciences, Central University of Punjab, VPO Ghudda, Bathinda, (151401), India*

Abstract: Avian pathogenic *Escherichia coli* (APEC) causes diverse local and systemic infections in the poultry farm with potential zoonotic transfer of antimicrobial resistance (AMR). Due to the indiscriminate use of antibiotics, most *E. coli* strains found in poultry are multidrug-resistant, making the treatment unsuccessful. Bacteriophage therapy emerges as a safe alternative to contain the spread of AMR genes from animal to human. Using *E. coli* O135 as a host, we isolated seven highly lytic bacteriophages from poultry fecal samples collected from several Indian states. Transmission electron microscopy analysis revealed that phages belong to the myoviridae or podoviridae family and were stable at pH 4-10 and temperatures up to 50-60ºC. One-step growth curve and adsorption experiments confirmed the lytic development of phages. Whole genome sequencing revealed none of the phages carry toxic or AMR genes. Spot assay and lytic efficiency with phage combination revealed a strong efficacy against several antibiotic-resistant strains of APEC isolated from poultry farms across India.
In summary, our research highlights the potential use of phage therapy and lays the groundwork for future research aimed at developing a prophylactic and therapeutic approach with direct implications for drug-resistant APEC infections causing Colibacillosis and loss of flocks in the Indian poultry sector.

Keywords: Avian Pathogenic *Escherichia coli* (APEC), Multidrug resistance, Bacteriophage therapy

MTAMR-47 (Poster)

Targeted Genome Editing using CRISPR-Cas9 Approach to Decipher the Functional Role of MCC Genes in Survival of *Mycobacterium kansasii*

Indu Rani[1,2], Rakesh Kumar[2] , Shanmugasundaram K.[1*], Harisankar Singha[1], Riyesh Thachamvalley[1], Rajesh Kumar Vaid[1] and Tarun Kumar Bhattacharya[1]
*shanmuga02@gmail.com

[1]*ICAR-National Research Centre on Equines, Hisar, Haryana, India*
[2]*Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana, India*

Abstract: Non- tuberculous mycobacteria (NTM) are the group of mycobacterial species that cause infections in humans and animals. *Mycobacterium kansasii* is the third most frequently isolated NTM globally, primarily affecting immunocompromised individuals and person with preexisting pulmonary disorders. *M. kansasii* rely on host for its survival and pathogenicity. Due to lack of genomic studies there is research gap in understanding the role of various genes in its adaptation, survival and pathogenicity. While methylcitrate cycle (MCC) linked with bacterial survival by detoxifying propionate, a byproduct of odd fatty acid chain degradation, however, further investigation is required to elucidate its role in persistence and virulence in the host. Thus, this study aimed to determine the role of MCC genes in survival of *M. kansasii* using CRISPR-Cas9 technique. Three sgRNAs were designed for MCC (*PrpC*) genes, cloned them into pC9L5 plasmid, via electroporation plasmid was transformed in *M. kansasii* cells and successful transformants were verified through sequencing. Wild type and MCC deficient mutants were subjected to different in vitro culture conditions and their growth curve were subsequently analyzed. Isolates were grown at 37°C (i) in Middlebrook 7H9 broth supplemented with 10% OADC (ii) M9 minimal media with 0.1% glycerol or 0.01% cholesterol or 0.1% glycerol + 0.01% cholesterol or 0.01% cholesterol with vitamin B12 or 0.1% propionate or 0.1% propionate with vitamin B12. Growth curve was plotted with the $OD_{600\ nm}$ values measured at an interval of 3 days successively up to 30 days. Results indicated that MCC deficient mutant were unable to proliferate in media with cholesterol or propionate as primary carbon source. Whereas supplementation with vitamin B12 activated alternative pathway methylmalonyl pathway (MMP), successfully restored the growth of MCC mutants on media containing cholesterol or propionate. Thus, to maintain intracellular lifestyle and survival, *M. kansasii* require MCC genes to mitigate the toxicity of propionate and it can acts as promising drug target.

Keywords: *Mycobacterium kansasii,* Methyl citrate cycle, Growth curve, CRISPR-Cas9 approach

MTAMR-48 (Poster)

Investigation on Phytoconstituents, Antimicrobial and Antioxidant Activity of *Prinsepia utilis*

Suraj Prakash* and Radha
*surajprakash.botany@gmail.com

School of Biological and Environmental Sciences, Shoolini University of Biotechnology and Management Sciences, Solan, Himachal Pradesh (173229), India

Abstract: *Prinsepia utilis* Royle, known for its diverse applications in traditional medicine (Chinese and Indian folk medicines), has garnered substantial attention within the field of phytochemistry and bioactivity exploration. *P. utilis* is a deciduous shrub from the family Rosaceae which is predominantly distributed within the Himalayan mountain range at altitudes ranging from 1000 to 3000 meters above sea level. This study is mainly focused on the investigation of phytochemical constituents, antimicrobial activity, and antioxidant activity of hydroethanolic extracts obtained from leaves of *P. utilis*. Anti-microbial studies were carried using disk diffusion method while the DPPH, FRAP and ABTS method was employed for investigating antioxidant activity. Extract were tested against four different bacterial strains comprising two species from gram-positive bacteria i.e., *Staphylococcus aureus* and *Streptococcus pyogene*s and two species from gram-positive bacteria i.e. *Pseudomonas aeruginosa* and *Klebsiella pneumonia*. Results showed among the three extracts, maximum phenol content was found in PSH (39.57 ± 1.678 mg Gallic acid/g dry extract weight) and maximum flavonoid

content was found in PSH (16.75 ± 1.0 mg Quercetin/g). Further, results showed significant antibacterial and antioxidant activity by all three hydroethanolic extracts.

Keywords: Bioactivity, *P. utilis*, Antimicrobial, Antioxidant, Medicinal plants

MTAMR-49 (Poster)

In Silico Analysis of Phytoconstituents from *Tinospora cordifolia* (Giloy) on Uropathogenic Bacteria using Network Pharmacology and Molecular Docking

Sanover Khan[1,2], Uzma Jabeen[1,2], Qazi Mohd. Rizwanul Haq[1], Sayeed Ahmad[2]
qhaque@jmi.ac.in

[1]*Department of Biosciences, Faculty of Natural Sciences, Jamia Millia Islamia, New Delhi (110025), India*
[2]*Bioactive Natural Product Laboratory (BNPL), Department of Pharmacognosy & and Phytochemistry, School of Pharmaceutical Education and Research, Centre of Excellence in Unani Medicine, Jamia Hamdard, New Delhi (110062), India*

Abstract: Urinary tract infections (UTIs) are highly prevalent affecting approximately 150 million individuals worldwide annually, largely caused by uropathogenic microorganisms like *Escherichia coli* (80%–90%), *Klebsiella pneumoniae, Proteus mirabilis* and *Staphylococcus aureus* leading to rise in antibiotic resistance. The rising prevalence of antibiotic resistance among bacterial pathogens highlights the need for medicinal plants as an alternative treatment to control resistant infections. *Tinospora cordifolia* a well-known medicinal plant with a long history of use in traditional medicine is recognized for its wide range of pharmacological activities, including anti-inflammatory, antimicrobial, and immunomodulatory effects. This study aims to evaluate the potential of phytoconstituents from *Tinospora cordifolia* as novel therapeutic agents against uropathogenic bacteria using *In silico* methods. Network pharmacology is used to map the relationships between phytoconstituents and their biological targets, providing insights into the mechanisms of action and potential efficacy. Molecular docking further evaluated the binding affinity of these compounds with bacterial proteins, aiming to identify promising candidates for combating urinary tract infections. Our findings highlight the therapeutic potential of Giloy's phytoconstituents, suggesting their role in developing alternative treatments for antibiotic-resistant uropathogenic bacteria.

Keywords: Urinary tract infections (UTIs), Antibiotic resistance, Medicinal plants, Network pharmacology, Molecular docking, Antibacterial activity

MTAMR-50 (Poster)

A Study on Co-trimoxazole Resistance in Environmental Bacteria

Syed Ahmed Rizvi, Vikar Ahmad and Qazi Mohd Rizwanul Haq*
*qhaque@jmi.ac.in

Department of Biosciences, Faculty of Natural Sciences, Jamia Millia Islamia, New Delhi, India

Abstract: Antibiotic resistance, a natural phenomenon, is the ability of microorganisms to resist the effect of an antibiotic to which they were once sensitive, which could cause around 300 million premature deaths and a loss of up to $100 trillion (£64 trillion) to the global economy by 2050 [1]. Resistance to first-line antibiotics and, more recently, last-line treatments, and even combination drugs could be fatal in case of minor infections. Co-trimoxazole, a combination of two antifolate compounds - sulfamethoxazole and trimethoprim, is effective against Gram-negative and Gram-positive bacteria, and a drug of choice in treating urinary tract infections and respiratory infections associated with pulmonary fibrosis. The antibiotic is listed as highly important antimicrobials for human medicine in WHO handbook and thus the study of resistance against co-trimoxazole is of major importance. The wastewater sample was collected and spread on co-trimoxazole amended LA (Luria Agar) plates for the isolation of morphologically distinct bacterial colonies. The selected bacterial isolates were screened for phenotypic resistance against co-trimoxazole using Kirby-Bauer disc diffusion test. Furthermore,

the phenotypically resistant bacterial isolates were screened for the genes (*sul* and *dfr*) conferring co-trimoxazole resistance using gene specific primers. Moreover, the selected bacterial isolates were phenotypically screened for ESBL production followed by PCR based detection of different ESBL genes (*bla*-CTX-M, *bla*-TEM, and *bla*-SHV) using specific primers. The phenotypically positive bacterial isolates were found to be having more than one co-trimoxazole and ESBL genes. Further studies are in progress.

Keywords: Antimicrobial Resistance (AMR), Co-trimoxazole, Expended spectrum beta-lactamases (ESBLs), Trimethoprim/ Sulfamethoxazole

MTAMR-51 (Poster)

Sweet and Sour: How Glucose and Gentamicin Influence Swarming and biofilm in *Pseudomonas aeruginosa*

Saurav Kumar Saha and Tapas K Sengupta*
*senguptk@iiserkol.ac.in

Department of Biological Sciences, Indian Institute of Science Education and Research Kolkata Mohanpur, Nadia, West Bengal (741246), India

Abstract: *Pseudomonas aeruginosa* causes various diseases and has significant medical importance due to being multidrug-resistant in nature. Swarming, a coordinated bacterial movement, and biofilm formation, where bacteria attach to a surface within a protective matrix, are key factors for virulence and antibiotic resistance in bacteria.

The present study explores how glucose and gentamicin influence the swarming and biofilm formation by *Pseudomonas aeruginosa* HRW.1-S3. We observed that swarming was prominent in presence of 0.25% glucose, however, 0.5% or higher glucose restricted the swarming. Interestingly, treatment with 0.75µg/ml gentamicin, a commonly used drug in *Pseudomonas aeruginosa* infections, promoted swarming in presence of either 0.25% and 0.5% glucose, while 1.5µg/ml gentamicin restricted it. However, biofilm formation was found to be increased with increase in glucose and gentamicin although gentamicin had a greater effect on induction of biofilm formation. Increased biofilm formation was observed to be associated with increased secretion of extra polymeric substances. Scanning electron- and confocal microscopy revealed that bacteria undergo transition from swarming to biofilm in presence of higher concentrations of glucose and gentamicin. Thus, bacteria tend to swarm in presence of 0.75 µg/ml gentamicin but prefer to shift to biofilm when the dose of gentamicin increases to 1.5 µg/ml. Atomic-force microscopy results revealed no visible flagella in restricted swarming which may be a possible reason for switching to biofilm mode of survival. Gene expression analyses indicated increased swarming was associated with increased expression of flagellar gene, *fliC* whereas biofilm load increase correlated with increased *pqsA* expression responsible for eDNA secretion. Most strikingly, quorum sensing gene, *lasI* decreased with decreased swarming but increased in higher biofilm highlighting the role of quorum sensing in switching of bacteria from swarming to biofilm as a key player in decision making. Further studies aim to unravel the mechanisms involved in regulating this transition as survival strategies.

Keywords: *Pseudomonas*, Swarming, Biofilm, Glucose, Gentamicin

MTAMR-52 (Poster)

Fusion of Oral Bacterial Metabolite with Green - Synthesized Copper Microparticles to Combat *Streptococcus mutans MTCC 497*: Antibacterial Resistance and *In-Vivo* Toxicity Analysis with *Caenorhabditis elegans*

Shanmugam Nivetha, and Marudhamuthu Murugan*
*murubio2001@gmail.com

Department of Microbial Technology, Madurai Kamaraj University, Madurai, Tamilnadu (625021), India

Abstract: *Streptococcus mutans,* a gram-positive coccus in chains, is a key pathogen responsible for dental caries. Excessive sucrose intake activates the enzyme glucosyltransferase in the glycolysis pathway, leading to

the production of sticky glucan, which facilitates biofilm formation. The resulting lactic acid production contributes to the rupture of tooth enamel. This study aims to inhibit glucan synthesis by targeting glucosyltransferase using a metabolite from the oral bacterium *Enterobacterobacter quasihormaechei,* isolated from healthy individuals, fused with green-synthesized copper microparticles derived from leaf soaked water of *Wrightia tinctoria*. Initially, the metabolite was extracted and tested against glucosyltransferase from *S. mutans MTCC 497*, showing significant inhibitory effects compared to other oral bacterial metabolites. *Wrightia tictoria* leaves, known for their medicinal properties against dental caries, were used to synthesize copper particles characterized by UV-visible spectroscopy, EDX analysis, and SEM for shape and XRD for crystalline structure. The synthesized copper particles were then fused with the oral bacterial metabolite of *E.quasihormaechei* and confirmed through UV visible spectroscopy. Antibacterial activity against *S. mutans MTCC 497* was assessed using the agar well diffusion method, showing a 33mm inhibition zone at 100µL of 1mg/mL concentration. *In vivo* toxicity studies using *Caenorhabditis elegans* showing no toxicity. The results indicated that, the fusion of green synthesized copper particles with oral bacterial metabolites has potent antibacterial properties against *S.mutans* biofim with minimal toxicity, making it a promising therapeutic approach for dental caries.

Keywords: *Streptococcus mutans*, *E. quasihormaechei* Oral bacterial metabolite, Green synthesized copper particles, *Wrightia tinctoria*, *In vivo* toxicity analysis, *Caenorhabditis elegans*

MTAMR-53 (Poster)

Shigella flexneri Derived Extracellular Metabolite Targeting *Acinetobacter baumannii* Mediated Biofilm

Bakyalakshmi Sundararajan[1], Jegan N[2], Murugan Marudhamuthu[*]
murubio2001@gmail.com

Department of Microbial Technology, School of Biological Sciences, Madurai KamarajUniversity, Madurai, TamilNadu (625021), India

Abstract: Bacterial biofilms pose a major threat to public health worldwide. Worrisomely, the prevalence of antibiotic resistant gram-negative bacteria implicated in biofilm formation has increased recently, especially among pathogens connected to healthcare facilities. *Acinetobacter baumannii* is a critically opportunistic pathogen, due to the high rates of antibiotic resistant strains causing healthcare-acquired infections (HAIs). The clinical isolates of *A. baumannii* can form biofilms on both biotic and abiotic surfaces; hospital settings and medical devices are the ideal environments for *A. baumannii* biofilms, thereby representing the main source of patient infections. However, the paucity of therapeutic options poses major concerns for human health infections caused by *A. baumannii* strains. The limited effective antibiotics have encouraged the development of innovative strategies such as using bacterial metabolite and their constitutes. Here, nosocomial *Shigella flexneri* strain was isolated from the gastrointestinal tract of human and extracellular metabolite was extracted. The biofilm inhibition ability of *Shigella flexneri* derived extracellular metabolite (SFEM) was confirmed using crystal violet assay and fluorescence imaging. The results indicate that SFEM is sub-inhibitory at 50 µg/mL against *A. baumannii* biofilm. Moreover, the extracted bacterial metabolite also inhibited the motility of *A. baumannii.* The study provides valuable insights into the potential of bacterial metabolite as an effective agent against *A.baumannii* biofilms, offering promising avenues for developing novel strategies to prevent persistent infectious bacterium that overcome antibiotics.

Keywords: Biofilm, Gastrointestinal tract of human, Secondary metabolite, *Acinetobacter baumannii*, *Shigella flexneri*, Biofilm Dissociation

MTAMR-54 (Poster)

Bacteriophage as a Non-Microbial Antibiotic Solution for *Bovine mastitis*

Naina and Nehra Kiran*
*nehrakiran@gmail.com

Deenbandhu Chhotu Ram University of Science & Technology
Murthal, Sonipat, Haryana (131039), India

Abstract: Bovine mastitis is defined as the inflammation of the tissue of udder, occurring with a high prevalence which ultimately results in the economic losses due to the premature culling, quantitative and qualitative losses in the milk production and the cost of the treatment associated with it. The average cost of the remediation is approximately upto $ 32 billion to the dairy industry globally. It is a polymicrobial disease, which includes causative organisms from *Staphylococcus, Streptococcus, Enterococcus, Escherichiat and Klebsiella* and *Proteus* species. Traditional treatments depend on antibiotics; however, the effectiveness of these therapies is hindered by antimicrobial resistance, reduced development of new antibiotics, and the formation of biofilms. Bacteriophages (phages) are viruses that precisely target and break down bacteria, making them a potentially valuable addition to or alternative for antibiotics in treating bovine mastitis. Phages specifically infect bacteria, leading to either the destruction of the bacterial host through lysis (as seen with lytic or virulent phages) or the integration of phage genetic material into the host's bacterial chromosome (as seen with temperate phages). Phages are highly specific in their targeting, which helps minimize disturbance to the normal microbiomes of animals, thereby preserving beneficial microbial communities. This precise targeting occurs because phages identify and bind to specific receptor proteins on the host bacterium using specialized tail fibers. Once bound, the phage penetrates the bacterium and delivers its genetic material into the host. Hence, bacteriophages are a more promising treatment strategy for bovis mastitis.

Keywords: *Bovine mastitis*, Polymicrobial, Bacteriophage, Biofilms, Premature culling, Microbiome

MTAMR-55 (Poster)

Assessment of Antimicrobial, Antioxidant and Anticancer potential of *Rauwofia serpentina* (L.) Benth. ex Kurz Leaves Extract

Pragati Pandey and Tulika Mishra*
*tulika.mishra.2000@gmail.com,

Plant Tissue Culture Lab, Department of Botany, D.D.U Gorakhpur University, Gorakhpur, Uttar Pradesh (273009), India

Abstract: *Rauwolfia serpentina* (L.) Benth. ex Kurz (Family: Apocynaceae), commonly known as "Sarpgandha," "Chhotachand," "Snakeroot" and "Devil pepper," etc. is a traditional herbal plant that is rich in many secondary metabolites such as alkaloids, flavonoids, glycosides, phenols, resins, saponins, tannis, etc. Medicinal plants are a significant source of numerous therapetutic agents and the emergence of pathogenic bacteria has kindled interest in traditional medicine systems as an alternative approach to overcoming resistance. This study aimed to investigate the antibacterial and antioxidant activity, anticancer activity, and phytochemical screening of *Rauwolfia serpentina* (L.) ethanolic and methanolic extract Antibacterial activities were evaluated against standard bacterial strains, representing both gram-postive and gram- negative types. Furthermore, the minimal inhibitory concentration of the ethanolic leaf extract was observed between 250µg/ml to 2000µg/ml, and a minimal bacterial concentration of ethanolic leaves of *Rauwolfia serpentina* was observed between 500µg/ml to 4000µg/ml against four human pathogens, *Escheriachia coli, Klebsiella pneumonia, Staphylococcus aureus* and *Pseudomonas aeruginosa.* The Plant extracts were characterized by UV-visible spectroscopy, Fourier- transforms infrared spectroscopy, and GCMS. This study concludes that *Rauwolfia serpentina* leaves extract exhibits antimicrobial agent for treating human pathogens.

Keywords*:* Saponins, *Rauwolfia serpentine,* UV-visible spectroscopy

MTAMR-56 (Poster)

AI-designed Antimicrobial Peptide AIG-R4: A Potent Therapeutic Agent against MDR *Acinetobacter baumannii* and *Klebsiella pneumoniae*

Vipasha Thakur[1*], Anvita Gupta[3], Prince Sharma[2] and Neena Capalash[1]
*thakurvipasha311@gmail.com

[1]*Department of Biotechnology, Panjab University, Chandigarh, India*
[2]*Department of Microbiology, Panjab University, Chandigarh, India*
[3]*AINovo Biotech, Sacramento, California, USA*

Abstract: *Acinetobacter baumannii* and *Klebsiella pneumoniae* are ESKAPE group MDR pathogens that possess the ability to form biofilms which greatly enhance their virulence and persistence in clinical environments. The increasing resistance of these pathogens to multiple antibiotics, combined with limited treatment options, is posing a significant challenge in healthcare settings. The limited efficacy of current therapies, coupled with their capacity to rapidly acquire resistance traits, highlight the urgent need for alternative therapeutic strategies. Addressing this critical issue, our study introduces AIG-R4, an antimicrobial peptide (AMP) developed using artificial intelligence (AI). AIG-R4 exhibited strong antibacterial activity against *A. baumannii* and *K. pneumoniae* at MIC of 3µM. The peptide showed membranolytic activity with minimal associated haemolytic and cytotoxic effects. The combination of 1/4×MIC AIG-R4 and 1/4×MIC colistin (1×FIC) was synergistically effective, whereas 1/4×MIC AIG-R4 showed additive effect with 1/2×MIC tobramycin (1×FIC). AIG-R4 inhibited *A. baumannii* biofilm formation by 24% at 1×MIC that increased to 33% when combined with colistin and 37% with tobramycin, at 1×FIC. Pre-formed biofilm eradication improved from 22% with AIG-R4 alone to 28% with colistin and 43% with tobramycin, at 1×FIC. Similarly, it inhibited *K. pneumoniae* biofilm by 27%, rising to 39% in combination with colistin and 37% with tobramycin. AIG-R4 also eradicated pre-formed biofilm by 20%, with eradication surging to 24 and 43% when combined with colistin and tobramycin, respectively, at 1×FIC. The peptide's ability to induce membrane permeabilization likely enhanced the uptake of tobramycin. The administration of conventional antibiotics at reduced concentrations will help attenuate the associated toxicity, thereby augmenting their therapeutic applicability in clinical settings for managing infections associated with these MDR pathogens.

Keywords: AIG-R4, Antimicrobial peptide (AMP), MDR pathogens

MTAMR-57 (Poster)

Combining Molecular Docking and Network Pharmacology Methods to Uncover the Multi-Target Pharmacological Process of *Solanum nigrum* acting on uropathogenic *Escherichia coli*

Uzma Jabeen[1,2], Sanover khan[1,2], Qazi Mohd. Rizwanul Haq,[1*] and Sayeed Ahmad[2**]
*qhaque@jmi.ac.in, **sahmadjh@yahoo.co.in

[1]*Department of Biosciences, Faculty of Natural sciences, Jamia Millia Islamia, New Delhi (110025), India*
[2]*Bioactive Natural Product Laboratory, Department of Pharmacognosy and Phytochemistry, School of Pharmaceutical Education and Research, Centre of Excellence in Unani Medicine, Jamia Hamdard, New Delhi (110062), India*

Abstract: Urinary tract infections (UTIs) are the second most common infectious disease in humans, after respiratory tract infections. The bacteria most commonly linked to urinary tract infections are *Escherichia coli, Pseudomonas aeruginosa*, *Klebsiella pneumoniae*, *Proteus mirabilis*, and *Staphylococcus aureus*. Several different medications were part of the standard treatment for UTIs, but uropathogenic bacteria have been known to become resistant to practically all of the current antibiotics, according to multiple reports. Finding new classes of antibacterial compounds is therefore desperately needed, especially those derived from natural sources. *Solanum nigrum* L., a prominent member of the Solanaceae (nightshade) family, is also referred to as black nightshade. In India and other nations, traditional medicine makes extensive use of it. Research has shown that extracts from *S. nigrum* exhibit antimicrobial properties against common pathogens like *Escherichia coli* and *Staphylococcus aureus*. *S. nigrum* seeds exhibit strong antimicrobial, anti-biofilm properties. The purpose of

this study was to determine the multi-targeted compounds, and their possible mode of action pathways of *Solanum nigrum* against uropathogenic *E. coli* using network pharmacology and docking tools. **Conclusion:** The results of this study not only identified the therapeutic targets of plants but also provided a theoretical framework for the use of these plants as UTI preventatives.

Keywords: UTI, Network pharmacology, Docking, Antimicrobials

MTAMR-58 (Poster)

Development of a Rapid Point-of-Care Biosensor for the Detection of *bla*$_{NDM}$ Gene in ESKAPE group MDR Pathogens

Anandita[1]**,** Prince Sharma[2] and Neena Capalash[1]
chalanaanandita1717@gmail.com

[1]*Department of Biotechnology, Panjab University, Chandigarh, India*
[2]*Department of Microbiology, Panjab University, Chandigarh, India*

Abstract: New Delhi metallo-β-lactamase (NDM) is an enzyme produced by certain Gram-negative MDR pathogens that exhibit resistance against a broad spectrum of antibiotics, including carbapenems, leading to infections challenging to treat. NDM-positive strains are globally prevalent, with the highest occurrence in the Indian subcontinent. Twenty-four NDM variants have been identified so far in more than 60 species from 11 bacterial families. A rapid detection method for bacterial strains harbouring the *bla*$_{NDM}$ gene, responsible for producing NDM, is urgently needed to provide referential information for early and effective treatment. We have developed a gold nanoparticles-oligonucleotide conjugate probe based biosensor that can rapidly and visually detect the carbapenem resistance caused by the *bla*$_{NDM}$ gene, regardless of its variants. In comparison to PCR, the biosensor showed 95% sensitivity for pathogens like *A. baumannii, E. coli, K. pneumoniae*, and *P. aeruginosa*. The biosensor was further validated with clinical samples like tracheal aspirations, bronchial lavage and sputum without any requirement of DNA extraction or its amplification. The biosensor was sensitive (0.5ng DNA) and 95% specific, and could provide results within 40 minutes without the need for complex procedures or expensive equipment like PCR or spectrophotometers. The very affordable early *bla*$_{NDM}$ gene detection will allow prudent use of antibiotics to lessen unnecessary oral and gut microbiota's exposure to them. The goal is to manage the infection, hospital outbreak containment and limit the spread of resistance.

Keywords: New Delhi metallo-β-lactamase, gold nanoparticles-oligonucleotide, PCR, *bla*$_{NDM}$ gene

MTAMR-59 (Poster)

Bioburden Analysis of Commercially Available Probiotic Supplements

Dhimahi Bhatt and Gayatri Dave*
*gayatridave.bt@charusat.ac.in

P D Patel Institute of Applied Sciences, CHARUSAT, Anand, Gujarat, India

Abstract: Probiotics are live organisms which confer health benefits by maintaining a balanced gut microbiota. Imbalance or disruption of this gut microbiota can lead to a number of possible disorders such as irritable bowel syndrome, fatty liver diseases, metabolic disorders and many more. *Lactoabacillus* (LAB) and *Bifidobacterium* are well established probiotic organisms well known to confer health benefits to individuals across multiple disorders. A range of market ready probiotics have boosted their market sales in over a decade for their health benefits, these benefits are only served when the probiotic organism is alive in the products sold. Our study focuses on checking the number of live organisms in a commercially available probiotic products undertaken for survey. The research helps in understanding the quality and efficacy of probiotics in the market today.

Keywords: Probiotic products, Gut health, Viable microorganisms, Health advantage, *Lactobacillus, Bifidobacterium*

MTAMR-60 (Poster)

In Silico Identification and Characterization of Novel Outer Membrane Proteins of *Brachyspira pilosicoli*

Amisha Panda[1], Jahnvi Kapoor[1], B. Hareramadas[2], Ilmas Naqvi[2], Ravindresh Chhabra[3], Sanjiv Kumar[4**] and Anannya Bandyopadhyay[1*]
anannya@zoology.du.ac.in*, drsanjivk@gmail.com**

[1]*Protein Biology Lab, Room No. 115, Department of Zoology, University of Delhi, Delhi, India*
[2]*Department of Zoology, Zakir Husain Delhi College, Jawaharlal Nehru Marg, New Delhi, India*
[3]*Department of Biochemistry, Central University of Punjab, Bathinda, Punjab, India*
[4]*Independent Researcher, Stockholm, Sweden*

Abstract: *Brachyspira pilosicoli* is a pathogenic, Gram-negative, spirochete bacterium responsible for causing intestinal spirochetosis (IS) in birds, pigs, and humans and is globally widespread. This anaerobic intestinal bacterium colonizes the large intestine, potentially leading to colitis, diarrhoea, and decreased growth rate. Outer membrane proteins (OMPs) of Gram-negative bacteria play crucial roles in adhesion and host-pathogen interaction, helping the bacteria to evade the host immune system and enhancing their virulence. However, *B. pilosicoli* outer membrane proteins are yet to be identified and characterized. Here, we report the computational discovery of 43 outer membrane β-barrel (OMBB) proteins in *B. pilosicoli* proteome, predicted using a consensus-based computational framework. β-barrel architectures of the predicted proteins were validated by generating AlphaFold 3-based structural models. Structure-based functional annotation predicted putative functions for the identified OMBB proteins, including the folding and insertion of OMPs, transport of lipopolysaccharides into the OM, efflux pumps, transporters, enzymatic activity, diffusion channels, and porins. Sequence variations across nine strains of *B. pilosicoli* were identified and mapped onto structural models, revealing that many of the variations were present on the surface exposed loop regions of the β-barrel structures. Overall, our *in silico* study has identified OMBB proteins such as BamA, LptD, TolC, TonB-dependent receptor, CsgG and many hypothetical proteins, providing insights into their potential roles in virulence, physiology, disease pathogenesis and vaccine development.

Keywords: *Brachyspira pilosicoli,* Intestinal spirochetosis, Outer membrane proteins, β-barrel structures, Structural models, Sequence variations

MTAMR-61 (Poster)

Comparative Analysis of Antibiotic Resistance Pattern and Extended Spectrum β-Lactamases (ESBLs) among Uropathogenic *Enterobacteriaceae*

Nikita Jangra[1], Hemlata Yadav[1], Aparna Parmar[2] and Pooja Gulati*[1]
*gulatipooja1@gmail.com, *pooja.micro@mdurohtak.ac.in

[1]*Department of Microbiology, Maharshi Dayanand University, Rohtak, Haryana (124001), India*

[2]*Department of Microbiology, Post Graduate Institute of Medical Sciences, Rohtak, Haryana (124001), India*

Abstract: Antibiotic resistance has posed a significant challenge in the treatment of infectious diseases, particularly urinary tract infections (UTI) commonly caused by members of *Enterobacteriaceae*. Over the last two decades, the introduction of third and fourth generation cephalosporins for the treatment of UTI has led to the emergence of Extended Spectrum β- lactamases (ESBLs). The emergence of multidrug resistance in these bacteria to even the "last-resort" carbapenems has further increased the incidence of such infections and limited treatment options. In this context, this study is focused to determine antibiotic susceptibility profiling and ESBL detection in Uropathogenic Enterobacteriaceae collected from Pt. B.D. Sharma Post Graduate Institute of Medical Sciences (PGIMS), Rohtak. In this study, 100 Uropathogenic *Enterobacteriaceae* isolates were isolated and identified using standard biochemical methods and were confirmed using MALDI-TOF and 16s rRNA gene sequencing. Further, antibiotic susceptibility profiling was accessed in accordance with standard CLSI guidelines against eighteen antibiotics belonging to different classes *viz*. β-lactams, sulphonamides, fluroquinolones, aminoglycosides, phosphonic and nitrofuran antibiotics. Antibiotic susceptibility profiling

showed high levels of resistance towards last resort antibiotics viz. imipenem (52%), ertapenem (38%) and meropenem (36%) as well as for cephalosporins: second generation cephalosporin: cefazolin (89%), third generation cephalosporin: cefotaxime (88%) and fourth generation cephalosporin (80%). Out of 100 uropathogenic Enterobacteriaceae, 47 isolates were MDR as per CLSI guidelines and were screened for the presence of ESBL. Of the 47 isolates, 32 were identified as potential ESBL by combination disc method. However, only 23 of 32 were confirmed as ESBL producers by confirmatory E- strip test. The prevalence of ESBL encoding gene viz. *bla*TEM and *bla*CTX-M were also studied in all the MDR uropathogenic isolates and compared with the phenotypic ES.

Keywords: Imipenem (52%), Ertapenem (38%), Meropenem (36%), Uropathogenic *Enterobacteriaceae*

MTAMR-62 (Poster)

Antimicrobial and Antiproliferative Activities of Bacteriocin-like Proteins from *Enterococcus* L12b

Rahul Sharma and Sukhraj kaur*
*drsukhrajkaur@gmail.com

Department of Microbiology, Guru Nanak Dev University, Amritsar, Punjab (143005), India

Abstract: Antibiotics represent one of the most successful forms of therapy in medicine. But the efficiency of antibiotics is compromised by a growing of antibiotic-resistant pathogens. In recent years, antibiotic resistance is a major global health challenge, involving the transfer of bacteria and gene between humans, animals and the environment. The side effects of antibiotic resistance are relapse of the infection after treatment, needing increased usage and dosage of antibiotics and increased spread of antibiotic-resistant bacteria. Thus, there is an urgent need to look for alternative ways for treating antibiotic resistant infections. A promising alternative approach is the use of new natural microbial products such as the use of bacteriocins. Bacteriocins are proteinaceous compounds produced by bacteria that inhibit the growth of similar or closely related bacterial strain. Bacteriocins from lactic acid bacteria (LAB) have been reported to exhibit narrow spectrum antimicrobial activities. Therefore, the aim of the study was to isolate broad-spectrum bacteriocin producing LAB. The ammonium precipitated protein of Enterococcus sp. L12b inhibited the growth of various pathogens viz., Candida albicans, Bacillus subtilis, Listeria monocytogenes, Salmonella enterica, Staphylococcus aureus, and Escherichia coli etc. Further, the ammonium precipitated crude protein was desalted and molecular weight was calculated by SDS-PAGE. A single band was obtained around 3.5/7.5 kDA in size. Cytotoxicity study of purified protein was also done on L929 (normal cell line) and MCF (cancer cell line). IC_{50} value of purified protein against L929 and MCF was observed to be 8.59µg/ml and 8.41µg/ml, respectively. The dual antimicrobial and anticancer activities of bacteriocin-like protein of Enterococcus L12b is a promising candidate that should be further tested for anticancer and antimicrobial activities in in vivo model.

Keywords: Antibiotics, Antimicrobial activity. Antibiotic-resistance, Bacteriocin, Ammonium precipitation, Antiproliferative

MTAMR-63 (Poster)

Artificial Intelligence-Machine Learning (AI-ML) Investigation on the Drug Dose Optimization of Cuminaldehyde, Gentamicin, and Tobramycin for the Efficient Management of Methicillin Resistant *Staphylococcus aureus* (MRSA) Biofilm: an Epidemic Level of Threat

R. Roy* and P. Tribedi**
*ritwikroy096@gmail.com, **tribedi.prosun@gmail.com

Microbial Ecology Research Laboratory, Department of Biotechnology, The Neotia University, South 24 Paraganas, West Bengal (743368), India

Abstract: Methicillin-resistant Staphylococcus aureus (MRSA), a formidable pathogen, poses a significant global health threat due to its inherent antibiotic resistance and ability to develop biofilm. Biofilms are complex

bacterial colonies enclosed in a self-produced matrix that protects them from host immune responses and antibiotics. In this direction, this study explored a combinatorial therapeutic approach to combat MRSA biofilms by combining the aminoglycoside antibiotics namely, tobramycin and gentamicin with a natural phytochemical, cuminaldehyde. Initially, to optimize drug doses from a dataset of 65 in-vitro observations on MRSA biofilm inhibition, advanced AI-driven mathematical models like Multiple Linear Regression (MLR), Polynomial regression (PR), Artificial Neural network (ANN) and Support Vector Regressor (SVR) were employed. Interestingly, ANN-predicted, and experimental values showed strong correlation (R^2=98.07). Furthermore, the most effective AI-driven combinatorial drug doses (cuminaldehyde 40 µg/mL, tobramycin 0.035 µg/mL, and gentamicin 0.5 µg/mL) were selected for this investigation due to their strong antibiofilm activity against MRSA cells, which was verified by a battery of in-vitro assays including CV assay, total biofilm protein estimation, and measurements of the EPS profile. Additionally, upon investigating the fundamental mechanism underlying behind this promising antibiofilm effect, the study demonstrated that the combination of AI-driven combinatorial dosages not only enhanced intracellular ROS accumulation in MRSA cells but also markedly boosted the test organism's cell membrane permeability. Thus, this study emphasizes the significance of investigating novel therapeutic approaches against MRSA biofilms using AI-driven drug dose optimization and in-vitro validation of the AI optimized dataset.

Keywords: Methicillin Resistant *Staphylococcus aureus* (MRSA), Cuminaldehyde, Gentamicin, Tobramycin, AI- driven mathematical models

MTAMR-64 (Poster)

Isolation and Screening of Bacteriocin Producing Lactic Acid Bacteria from Floral Niches

Swadhyay U. Phatangare and Ulhas K. Patil
phatangareswadhyay@gmail.com

Department of Microbiology, Government Institute of Science, Chhatrapati Sambhajinagar, 431004

Abstract: Lactic acid bacteria (LAB) inhabit diverse environments and are known for their antimicrobial activity against a wide spectrum of bacteria as a result of their metabolites. These include molecules like lactate, acetate as well as proteinaceous molecules like bacteriocins. Floral microbiomes, enriched with sugary nutrients and interactions with plant pollinators, harbour various LAB.
In the following work LAB isolated from different flowers were evaluated for their antimicrobial activity against Micrococcus luteus as a primary indicator strain. The antagonistic activity was determined by agar well diffusion assay by utilizing the cell-free supernatant of the isolates. Among the 18 different isolates obtained from various flowers, the LAB isolate CC isolated from cucumber flower was confirmed as a bacteriocin producer by agar well diffusion assay. The proteinaceous nature of the bacteriocin was confirmed by suitable chemical and enzymatic treatment to the cell-free supernatant. The crude bacteriocin shows significant activity against M. Luteus (250 AU/ml). Besides M. Luteus the crude bacteriocin also inhibits Listeria monocytogenes and Lactobacillus plantarum, emphasizing its efficacy to inhibit pathogenic and food spoilage microbes.

Keywords: Lactic Acid Bacteria, Probiotics, Bacteriocins, Antimicrobial activity

MTAMR-65 (Poster)

Antibiotic Resistance of Uropathogenic *Escherichia coli* isolated from Clinical Sample

Sanjay Chavan, Bhagvat Lad and T. A. Kadam*
takadam67@gmail.com

Senior Professor, Department of Biotechnology, School of Life Sciences,
Swami Ramanand Teerth Marathwada University, Nanded (M.S.)- 431 606

Abstract: Urinary tract infections (UTIs) are mainly caused by uropathogenic strains of *Escherichia coli, Klebsiella* and *Enterobacter spp.* UTI infection by *E. coli* in children's and older adults may develop life

threatening form of haemolytic uremic syndrome. Such UTI infections are treated by nitrofurantoin, co-trimoxazole and cephalosporins. These antibiotics are not effective against UTI. It is necessary to investigate the antibiotic resistance of these strains. Therefore, urine samples of patients having UTI were collected from GMC hospital Nanded. Uropathogenic strains were isolated on MacConkey's agar plates. The isolates were evaluated using HiMedia™ discs to assess antibiotic resistance against various classes of antibiotics by disc diffusion test on Muller Hinton agar and resistance was determined as per the guidelines provided by the Clinical Laboratory Standard Institute (CLSI). The MDR strain was identified by biochemical characteristics and 16S rRNA sequence analysis as *Escherichia coli* and designated as *Escherichia coli strain SUC-3* (NCBI Accession No.PP854587). Our investigation revealed that UTI infection due to *E. coli* may be difficult to treat due to high resistance to commonly used antibiotics, indicating the need for routine antibiotic surveillance and monitoring.

Keywords: AntibioticResistance, Urinary tract infection and Uropathogenic *E. coli*.

MTAMR-66 (Poster)

To decode the virulome linked to antibiotic resistance in *Acinetobacter baumannii* using Pan-Genome Approach

Milani Sharma, Anshika Thakur and Khem Raj
khemrajthakur@gmail.com

Department of Microbiology
Basic Medical Sciences Block I, South Campus,
Panjab University, Sector-25, Chandigarh-160014, India

Abstract: *Acinetobacter baumannii* an opportunistic pathogen is often linked to infections in immunocompromised patients and hospital settings. It exhibits genomic flexibility and transmits mobile genetic components by horizontal gene transfer. It also produces variety of virulence factors, including lipopolysaccharides and biofilm-associated proteins, to withstand drugs. Given its prevalence in healthcare settings, research on its genetic diversity and transmission is needed. Whole-genome sequencing (WGS) have enhanced our knowledge about the resistomes, and pangenome approach can reveal hidden genetic changes demonstrating true genetic diversity at species level.

This study aimed to decode the genetic diversity associated with antibiotic resistance and virulence factors in 100 A. *baumannii* strains using pan-genome approach. Reference genomewas downloaded from NCBI and Next Generation Sequencing (NGS) data was obtained using the SRA Toolkit. Data quality was checked using FastQC, aligned using Bowtie2, and the resulting SAM/BAM files were processed using SAMtools. Variant calling was executed through GATK. For variant annotation SnpEff was used. Functional annotation was performed using SPAdes and Prokka, and identification of virulence factors was done using a Python script, with the outcomes visualized using matplotlib.

In our study, *A. baumannii*exhibited high level of genetic variation, including large number of missense mutations indicating evolutionary adaptation. Significant virulence factors were also identified, suggesting unique pathogenic processes. This study contributes in identification of important virulence factors and SNPs in *A. baumannii*, expanding our knowledge about the pathogenic mechanisms of this bacteria. Results may open up the possibilities for the development of efficient methods for controlling infections and targeted treatments.

Keywords: Antibiotic resistance, Virulence factors, Pan-genome analysis, SNPs, Indels, WGS

MTAMR-67 (Poster)

To Decipher the Acquired Resistome of *Pseudomonas Aeruginosa* through Pan-Genome Approach

Kanika Multani, Aryan Bhan and Khem Raj*
*khemrajthakur@gmail.com

Department of Microbiology, Basic Medical Sciences Block I, South Campus, Panjab University Sector-25, Chandigarh-160014, India

Abstract: *Pseudomonas aeruginosa*, a gram-negative opportunistic pathogen causes sub-acute to chronic infections, particularly in individuals with malignancies, chronic disorders, and compromised immune system. Its large "plastic" genome attributes to its adaptability and development of resistance by horizontal gene transfer. The rise of high throughput sequencing has enabled researchers to investigate genomic differences at both species and strain levels. The pan-genome analysis is one approach to study the core genome and the accessory genome of an organism that might be contributing to Antimicrobial resistance, pathogenicity, and adaptive mechanisms.

This study used pan-genome approach to analyze acquired antimicrobial resistance in 100 *P. aeruginosa* strains downloaded using SRA toolkit along with a reference genome from NCBI. The quality of reads was checked using FASTQC and then aligned to the reference genome with Bowtie2, followed by variant calling using GATK to detect genomic variants. Structural annotation was done using SnpEff & SNPs were visualized using IGV. SPAdes and Prokka were used for functional annotation of variants, and pan-genome construction was done to identify core and accessory genomes using Roary. The RGI tool from CARD was used to predict the anti-microbial resistance gene in the sample by matching it with CARD database.

The study identified various SNPs, Indels, and the presence of Multi-drug resistance (MDR) proteins. Pan-genome analysis revealed a large accessory genome, which contributes to its ability to acquire genes and develop resistance. The findings suggest a significant increase in antibiotic resistance among *P. aeruginosa* strains highlighting the need for targeted treatment approaches to address *P. aeruginosa* growing antimicrobial resistance.

Keywords: Pan-genome analysis, Antimicrobial Resistance, *Pseudomonas aeruginosa,* SNPs, MDR, Indels

MTAMR-68 (Poster)

Efficacy of Lactic Acid Bacteria in Managing Hypercholesterolemia: Insights from In Vitro and In Vivo Studies

Siloni Patial[1] and Geeta Shukla[2*]
*geeta_shukla@pu.ac.in

[1]*Department of Microbiology, Panjab University, Chandigarh 160014, India*
[2]*Department of Microbiology, Basic Medical Sciences (Block-1), South Campus, Panjab University Chandigarh 160014, India*

Abstract: Probiotics are gaining attention for their potential in managing hypercholesterolemia, a major risk factor for cardiovascular diseases. The objective of this study was to assess the capacity of isolated lactic acid bacteria to assimilate cholesterol, with a particular emphasis on the reduction of cholesterol levels and establishment of a high-cholesterol diet (HCD)-induced animal atherosclerotic model. Among the screened isolates, *Lactobacillus plantarum* A5 demonstrated the greatest assimilation of cholesterol, attaining 54.10% in MRS media and 50.42% in simulated intestinal conditions. The selected LAB isolates were further assessed for cholesterol assimilation in the presence of isomaltose, demonstrating significantly enhanced cholesterol uptake at 1% and 2% concentrations. *In-vivo* study revealed that animals administered with HCD had significantly higher body weight and BMI. These changes were accompanied by higher levels of dyslipidemia, decreased glucose tolerance, and fasting hyperglycemia. In HCD-fed animals, hepatic steatosis, atheroma development, and adipocyte hypertrophy were confirmed by histopathological investigation. Probiotic supplementation, particularly with *L. plantarum* A5, significantly mitigated these effects, reducing body weight, adiposity, and serum lipid levels while improving glucose tolerance and hepatic function. Additionally,*L. plantarum*A5 and *L.*

pentosus GSSK2 notably reduced oxidative stress markers and enhanced antioxidant levels in liver and arterial tissues.

Keywords: Atherosclerosis, Cholesterol Assimilation, High-Cholesterol Diet (HCD), Lactic Acid Bacteria (LAB), Prebiotics, Probiotics

MTAMR-69 (Poster)

Exploring the Antimicrobial Potential of *Ocimum* Leaf Extracts Against Multidrug-Resistant Bacteria in Hospital Effluent-Exposed Water Bodies

Prajakti and Kunal Mukhopadhyay*
*kmukhopadhyay@bitmesra.ac.in

Department of Bioengineering and Biotechnology, Birla Institute of Technology, Mesra, Ranchi, Jharkhand, 835215, India

Abstract: The rise of antibiotic-resistant microbial communities has emerged as a major concern for global health, driven by the extensive use of conventional antibiotics. This study determines the existence of microorganisms in water bodies contaminated by hospital waste effluents, with a focus on the prevalence of multidrug-resistant bacteria. Isolates displaying multidrug resistance were collected from four different sampling sites across two water bodies and identified as *Aeromonas* species through 16S rRNA sequencing. *In silico* methods enabled to predict the presence of resistance genes within these microbial communities, using the ResFinder Database after analyzing their chromosomal sequences. Leaf extracts derived from *Ocimum tenuiflorum* and *Ocimum gratissimum* were evaluated for their antimicrobial potentiality to inhibit the growth of the identified multidrug-resistant bacteria. High-performance thin-layer chromatography-mass spectrometry (HPTLC-MS) was performed for metabolite profiling of ethanolic and DMSO extracts, followed by mass spectral library search of the analytes. *In silico* methods, such as protein modeling of the determined antibiotic resistance gene (ARG)-encoded proteins using I-TASSER, were employed to supplement *in vitro* research. Molecular docking denoted the interactions between these proteins and the bioactive compounds of the plant extracts. Molecular dynamics simulations between the ligand-protein complexes demonstrated the highest docking scores. By using both experimental along with computational approaches, the study highlights the efficiency of *Ocimum* leaf extracts against antibiotic resistance by elucidating their inhibitory capability against multidrug-resistant bacteria.

Keywords: Antibiotic Resistance Genes, Antibiotic Resistant Bacteria, *Aeromonas*, *Ocimum gratissimum* and *Ocimum tenuiflorum,* Molecular docking, Molecular dynamics simulation

MTAMR-70 (Poster)

Combinatorial Application of Vancomycin and Cuminaldehyde: A Promising Approach to Withstand the Antibiotic Resistance Exhibited by Methicillin Resistant *Staphylococcus aureus* (MRSA)

Saranya Trivedi and Prosun Tribedi*
saranyatrivedi29@gmail.com, *tribedi.prosun@gmail.com

Department of Biotechnology, The Neotia University, South 24 Paraganas, West Bengal (743368), India

Abstract: Antibiotic resistance or multidrug resistance is a state of condition where microorganisms proclaim elevated resistance against antibiotics alongside several other drugs and is well identified as one of the greatest threat imparted to mankind worldwide. As a consequence of exploitation of antibiotics, several bacteria has acquired resistance against a wide range of antibiotics and among them the most threatening and prevalent bacteria lies the MRSA or Methicillin Resistant *Staphylococcus aureus*. MRSA, exhibits high proficiency in manifestation of infections of skin, glands, mucous membrane, inflammation of bones in both humans. It has gradually not only evolved as a nosocomial pathogen but also a community associated pathogen. With expanded

pathogenicity, MRSA, also confers another serious threat to mankind by evincing multi drug resistance since it not only tends to show resistance against the β lactam groups of antibiotics but also to antibiotic groups like lincosamides, tetracycline, fluoroquinolone, macrolides and aminoglycoside limiting the range of convenient therapeutic drugs available against MRSA. Over the years, Vancomycin has been established as the most effective drug against MRSA, however studies have reported emergence of strains of MRSA showing resistance to Vancomycin. Hence, the issue is twofold: narrow range of availability of drugs against MRSA and proficiency of MRSA in acquiring of resistance to newest antibiotics. Towards this approach, a combinatorial strategy has been developed where the prime antibiotic against MRSA, in sub minimal inhibitory concentration can be applied in a combination with natural compound Cuminaldehyde. This strategy explored, shows promising approach for treatment of MRSA in a minimal dosage of application of Vancomycin along with expanding the period of effectiveness and activity of the drug by developing additive interactions with Cuminaldehyde applied on multiple clinical strains of MRSA.

Keywords: Methicillin Resistant *Staphylococcus aureus*, Vancomycin, Cuminaldehyde, Nosocomial infection, Combinatorial strategy, Minimal inhibitory concentration

MTAMR-71 (Poster)

Insilico and In vitro Study of Antimicrobial Activity of Cuminaldehyde in Combination with Tobramycin: An Effective Approach to Curb the Pathogenicity of the Clinical Strains of *Escherichia coli.*

A. Maity, P. Chakraborty and P. Tribedi
maityalakesh.2211.am@gmail.com, polochak12@gmail.com, tribedi.prosun@gmail.com

Department of Biotechnology, The Neotia University, South 24 Paraganas, West Bengal – 743368

Abstract: The emergence of multidrug-resistant pathogens and the limitations of existing monotherapies underscore the urgent need for novel antimicrobial strategies. Combination therapy of compounds thrives great significance for diminishing the risk of biofilm related infectious diseases caused by various bacteria. Towards this direction, we employ a natural compound, cuminaldehyde in combination with an aminoglycoside antibiotic named tobramycin against biofilm forming multidrug resistant (MDR) clinical strains of *E. coli*. To enhance therapeutic potential, exploring effective drug combinations and optimizing properties of both compounds through in silico approaches holds immense promise. To obtain precise in-silico data and insights about compounds, the PASS online and SwissADME tools were used to predict the biological activity and oral bioavailability. The Osiris, SwissADME, and PROTOX tools were used to analyse the compound's possible adverse effects and theoretical pharmacokinetic aspects. SwissADME was used to estimate cuminaldehyde gastrointestinal absorption, blood-brain barrier permeability, and skin penetration. Osiris was used to estimate drug-likeness and score. In silico analysis predicted poor oral bioavailability for tobramycin due to its higher MW, polarity and poor GI absorption, whereas cuminaldehyde likely to cross blood-brain-barrier with high absorption but might have irritant effects if swallowed in LD50 amount. In vitro investigations demonstrated that cuminaldehyde and tobramycin together had an additive impact against drug-resistant clinical *E. coli* strains. The combination showed a substantial decrease in MIC and biofilm formation when compared to each component alone. Biofilm study predicted that the said combination could interfere with established *E. coli* biofilms that could help to control the UTI related diseases.

Key Words: *Escherichia coli*, In-Silico, Cuminaldehyde, Tobramycin, Biofilm, Antibacterial activity

MTAMR-72 (Poster)

Antimicrobial Potential of Bioactive Peptides from the Epidermal Mucus of Walking Catfish

Ahmed Hussain and Shashwati Ghosh Sachan
ahmadhussain10196@gmail.com; ssachan@bitmesra.ac.in

Department of Bioengineering and Biotechnology, Birla Institute of Technology, Mesra, Ranchi, Jharkhand (835215), India

Abstract: The COVID-19 pandemic has led to a marked increase in global antibiotic consumption, exacerbating the emergence of antimicrobial-resistant pathogens. The limited development of new antibiotics underscores the urgent need for alternative antimicrobial compounds. In response to constant exposure to complex microbial environments, fish have developed defense mechanisms, including the secretion of antimicrobial compounds in their epidermal mucus. This study explores the antimicrobial efficacy of acidic extracts from the epidermal mucus of *Clarias batrachus* (Bloch, 1793) against clinically relevant pathogens. The extracts exhibited significant inhibitory activity against both pathogenic and opportunistic microorganisms. The physicochemical stability of the bioactive compounds in the mucus was confirmed under diverse experimental conditions. Protein analysis using SDS-PAGE revealed dominant bands at 11 kDa, which were identified as hemoglobin subunit-like chains (α and β) via LC-MS/MS. Bioinformatic analyses indicated that these peptides possess broad-spectrum bioactivities, including antimicrobial, antiviral, and anticancer potential. Structural modeling with AlphaFold and validation using the SAVES server confirmed the stability of these peptides. Molecular docking studies further demonstrated the peptides' potential efficacy against antibiotic-resistant targets, such as erm proteins and NDM-producing superbugs, underscoring their promise as novel therapeutic agents in the fight against antimicrobial resistance.

Keywords: Antimicrobial Resistance; Epidermal Mucus; Clarias batrachus; LC-MS/MS; Molecular Docking; NDM Superbugs

MTAMR-73 (Poster)

Uncovering a Novel *Streptomyces rochei* Strain from Soil: Insights from Whole Genome Sequencing

Muzammil Sharief Dar[1] and Iqbal Ahmad[1]
darmuzammil2011@gmail.com, ahmadiqbal8@yahoo.co.in

Department of Agricultural Microbiology, Aligarh Muslim University, Aligarh, UP, India

Abstract: Actinomycetes are renowned for their ability to produce a wide variety of bioactive compounds, including antibiotics, antifungals, antivirals, and anticancer agents, making them invaluable in pharmaceutical and biotechnological fields. In our study to discover novel actinomycetes from soil samples, we isolated a new strain (IA22). After isolation, whole genome sequencing was performed using a combination of advanced tools such as Unicycler for primary assembly and MeDuSa for secondary assembly. Quality control (QC) of the reads was conducted using FastQC and MultiQC. This resulted in a high-quality assembly with an average read length of 151 bp and 84.80x coverage of 4.4 million base pairs, 70 percent of which were GC percentage.

Phylogenetic analysis based on whole-genome data positioned the strain as a Novel Strain within the genus Streptomyces with a maximum similarity match with *Streptomyces rochei*. The strain demonstrated broad-spectrum antimicrobial activity and produced unique secondary metabolites, when subjected to antimicrobial assays. Annotation of the whole genome using PROKKA identified several uncharacterized biosynthetic gene clusters like Streptothoricin, Kinamycin, Granaticin, Candicidin, Lysolipin, predicted using antiSMASH, which suggests the potential production of novel bioactive compounds.

Building on our previous work identifying several novel actinomycete strains, this discovery further underscores the biotechnological potential of actinomycetes from underexplored environments. This is particularly important in the search for new antibiotics amidst rising antimicrobial resistance (AMR). These findings expand actinomycete taxonomy and emphasize the importance of exploring microbial diversity for new therapeutic agents.

Keywords: *Streptomyces rochei*, Soil, Whole Genome Sequencing, Biosynthetic Gene Cluster, AMR

MTAMR-74 (Poster)

Green synthesis: Advancement in the synthesis of Nanoparticles

Shivani and Anil Kumar Chhillar*
anil.chhillar@gmail.com

Centre for Biotechnology, Maharshi Dayanand University, Rohtak (124001)-India

Abstract: In recent years, there has been a considerable increase in interest in nanotechnology. Metallic nanoparticles, in particular, have gained attention for their enhanced antimicrobial properties. Compared to the various physicochemical methods commonly used to synthesize nanoparticles, the biogenic reduction of precursors is more environmentally friendly, cost-effective, and making it particularly suitable for medical and biological applications. The excessive and uncontrolled use of antibiotics has led to a significant rise in drug-resistant pathogens. Novel therapeutic approaches that can replace ineffective antibiotics are in high demand to overcome the increasing problem of microbial multidrug resistance. Nanoparticles made of silver, gold, zinc, and copper have garnered significant attention due to their distinctive antimicrobial capabilities.

Keywords: Green Synthesis**,** Biological Applications, Metallic Nanoparticles, Antimicrobial, Nanotechnology

MTAMR-75 (Poster)

Nisin: An Antimicrobial Peptide, Opens a New Axis in Controlling the Biofilm Mediated Threats of ESKAPE Pathogens

D. Ganguly* and S. Sarkar
*gangulydebolina720@gmail.com, sarita.sarkar@tnu.in

Department of Biotechnology, The Neotia University, South 24 Paraganas, West Bengal (743368), India

Abstract: ESKAPE, major opportunistic pathogens, that infect humans with several acute and chronic diseases by developing biofilm. Nonetheless, these biofilm-embedded microorganisms often shown a significant potential for antibiotic tolerance, hence posing an inevitable risk to public health. Several studies have shown that *Lactococcus lactis* (a gram-positive microorganism) produces nisin, an antimicrobial peptide (AMP), notable for it's potential as a well-established food preservative and considerable antimicrobial efficacy against several microorganisms. In this study, the effectiveness of nisin in controlling ESKAPE pathogen's biofilm-mediated threats was investigated. From our experimental observations it was evident that nisin exhibited a strong antimicrobial efficacy against all ESKAPE pathogens including methicillin resistant *Staphylococcus aureus* (MRSA); an epidemic level of threat. In relation to managing the biofilm mediated threats of ESKAPE pathogens, it was evident that sub-MIC dosages of nisin exhibiting most promising antibiofilm effect against the MRSA cells in contrast with other ESKAPE pathogens (*p 0.01*). Further observations revealed that the sub-MIC dosages of nisin may accumulate reactive oxygen species (ROS) generation and altering cell membrane permeability to inhibit the development of microbial biofilm city of MRSA cells. Sub-MIC concentrations of nisin were also tested for their effects on normal cell lines, such as chang Liver and WRL68, and experimental results indicated that these sub-MIC dosages of nisin were not harmful toward normal cells. Taking together, all these key findings indicating that nisin at sub-MIC dosages might be employed to effectively control biofilm mediated risks of MRSA cells.

Keywords: Nisin, Antimicrobial peptide, ESKAPE, MRSA biofilm, ROS

MTAMR-76 (Poster)

Antimicrobial resistance and detection of *Ureaplasma* spp. among tribal women in District Anuppur, Madhya Pradesh

Suraj Kumar Mishra*[1] and Poonam Sharma[1]
*surajphd23@gmail.com,
[1] pnm245@yahoo.com

[1]*Infection Biology and Molecular Reproductive Toxicology lab, Department of Zoology, Indira Gandhi National Tribal University, Amarkantak, Madhya Pradesh (484887), India*

Abstract: Background- *Ureaplasma* spp. are significant sexually transmitted infections pathogen associated with various urogenital infections, respiratory diseases, and adverse pregnancy outcomes such as preterm labor, etc. According to WHO reports 2018, 13% of India's population was infected with *Ureaplasma* spp. The aim of the study is to evaluate the prevalence of *Ureaplasma* spp. using culture- and RT-PCR-based detection methods. Additionally, the study includes antimicrobial susceptibility testing to determine the effectiveness of various antibiotics against *Ureaplasma* Spp. among tribal women.

Methods- Endocervical swab samples (n=110) were collected from women (age group 20 to 55) visiting the OPDs of district hospital Anuppur and Medical College, Shahdol, Madhya Pradesh, India. Initial identification of *Ureaplasma* was performed using traditional culture methods, and positive culture samples were further confirmed through Urease tests. RT-PCR was performed for precise identification, targeting the gene specific to *Ureaplasma* Spp. Antimicrobial susceptibility testing was conducted on identified *Ureaplasma* Spp. using the Kirby-Bauer disk diffusion method.

Results- The culture method identified *Ureaplasma* in 61 (55.45%) out of 110 samples. RT-PCR detection, confirmed the presence of *Ureaplasma* spp. in 65 (59.09%) samples with *Ureaplasma urealyticum* (UU) and *Ureaplasma parvum* (UP) in 37 (33.63%) samples. The combination of UU and UP was detected in 30 (27.27%) samples. RT-PCR detected UU in four culture-negative samples. Antimicrobial susceptibility testing revealed varied resistance patterns among the isolates. A significant number of isolates exhibited maximum resistance to erythromycin (80.32%), followed by ofloxacin (73.77%) and roxithromycin (70.49%), while doxycycline and tetracycline were found to be the most effective, showing high susceptibility rates.

Conclusion- The RT-PCR method serves as an effective and alternative tool for the rapid diagnosis of active *Ureaplasma* spp. across various clinical specimens. The ability to identify species would enable a more accurate selection of antimicrobial drugs. Patients who are positive for *Ureaplasma* can get treatment without delay.By enabling the detection of resistant strains and facilitating more exact pharmacological therapies, targeted therapy also contributes to reducing the risk of antibiotic resistance. This approach benefits both physicians and patients by reducing the need for repetitive testing and eliminating the waiting period associated with traditional lab results.

Keywords: *Ureaplasma* spp., Real-time PCR, *Ureaplasma parvum, Ureaplasma urealyticum,* Antimicrobial susceptibility testing, & Resistance.

MTAMR-77 (Poster)

Phytochemical Analysis, Antimicrobial and Antioxidant Activity of Endophytic Fungi Associated with the Roots of C*apparis Decidua*

Swati Jaast, Mohit Kumar, and Anil Kumar*
*bhankhar@gmail.com

Department of Biotechnology, Guru Jambheshwar University of Science and Technology, Hisar, Haryana, India

Abstract: Endophytic fungi residing symbiotically within plants constitute a latent source of bioactive compounds. This study aimed to evaluate the phytochemical profiles, antimicrobial and antioxidant potential of 70 endophytic fungi isolated from the ethno-medicinal plant *Capparis decidua*. The ethyl acetate extracts of these fungi were preliminarily evaluated for their phytochemical content, revealing the presence of alkaloids, flavonoids, phenols, terpenoids, and saponins. The antimicrobial efficacy was assessed against *Staphylococcus*

aureus (MTCC-3160), *Escherichia coli* (MTCC-16521), *Bacillus subtilis* (MTCC-421), *Pseudomonas aeruginosa* (MTCC-647), *Aspergillus niger* (MTCC- 281), and *Aspergillus fumigatus* (MTCC-2508). These results revealed that 13 extracts inhibited *S. aureus*, 12 inhibited *E. coli*, 25 inhibited *B. subtilis*, and 20 inhibited *P.aeruginosa*. Notably, 80-90% of the fungal extracts demonstrated significant antifungal activity. Furthermore, 15 extracts exhibited inhibitory effects on all tested microbial strains. Over 80% of the fungal extracts exhibited 50–95% antioxidant activity in DPPH assays, with IC_{50} values varying from 52.8 to 297.14 µg/ml. These findings suggest that endophytic fungi associated with the roots of *Capparis decidua* represent a promising source of novel antimicrobial and antioxidant agents.

Keywords: *Capparis decidua*, Endophytic fungi, Phytochemical, Antimicrobial, Antioxidant

MTAMR-78 (Poster)

Antibiotic Resistance Patterns in Bacterial Isolates from the Kshipra River in Ujjain and their Public Health Implications

Sakshi Sardana[a], Shweta Agrawal[a*] and Paromita Sarbadhikary [b*]
[*]shweta.agrawal24@gmail.comparomitas@uj.ac.za

[a]*Department of Life Science, Shri Vaishnav Institute of Science, Shri Vaishnav Vidyapeeth Vishwavidyalaya, Indore (M.P.), India*
[b]*Laser Research Centre, Faculty of Health Sciences, University of Johannesburg, P.O. Box 17011, Doornfontein 2028, South Africa*

Abstract: The unchecked industrial, agricultural, and human activities, coupled with the overuse of antibiotics in both medical and commercial settings, have significantly altered river water's physicochemical properties and contributed to the rise of antibiotic-resistant bacteria, posing severe treatment challenges and life-threatening risks. In recent times, there has been a significant rise in antibiotic-resistant bacteria in aquatic environments which has become a major health concern and is recognized as a health hazard to the community. In the present study, samples from Kshipra River, Ujjain, Madhya Pradesh, India were collected from the various sites of Kshipra river. The physio-chemical study of water samples was carried out followed by bacterial isolation. A total of 13 multidrug-resistant (MDR) bacteria were isolated. The isolated bacteria were biochemically identified as *E.coli, Klebsiella sp.,* and *Staphylococcus sp.* The isolated 13 MDR bacteria were tested for antibiotic sensitivity test (ABST) and observed to be resistant to several antibiotics like ceftazimide, cefotaxime, ceftriaxone, aztreonam erythromycin, ciprofloxacin along with variable sensitivities towards gentamicin. Among the 13 isolated MDR bacterial species, 8 were identified as Extended-spectrum beta-lactamase producing strains and 4 as Methicillin- resistant. According to this study, the Shipra River has a higher prevalence of bacterial species exhibiting notable multidrug resistance to antibiotics, frequently prescribed to treat different infections. Further studies using 16s RNA and whole genome sequencing will provide key genomic insights into microbial identification, origins, and antimicrobial resistance.

Keywords: ABST; ESBL; MDR; MRSA; VRSA; Genomic insights

MTAMR-79 (Poster)

Biocontrol of *Salmonella Typhimurium* using predatory bacteria *Bdellovibrio*: *In vitro* predation and *in vivo* non toxicity tests in Zebrafish

Dhanyashree Rai[1], Andrea Emilia Lobo[1], Anirban Chakraborty[1] and **Divyashree M**[1*]
divyashree.m@nitte.edu.in

Nitte University Centre for Science Education and Research, Nitte (DU), Deralakatte, Mangaluru, Karnataka (575018), India

Abstract: *Bdellovibrio* are gram-negative, motile predatorydeltaproteobacteria present in nature and kills wide range of other bacteria including a wide range of human pathogens. Antibiotic resistance is a serious concern, necessitate the development of new approach to minimize the risk. One such approach is live predatory

Bdellovibrio. The objective of present study is to check the predatory efficacy of *Bdellovibrio* isolates against *Salmonellain vitro* and to evaluate the non-pathogenic attribute of *Bdellovibrio* in zebrafish model. In the present study, two *Bdellovibrio* strains were isolated from stagnant water using *Escherichia coli* as prey by double layer agar technique. Isolates were confirmed by polymerase chain reaction (PCR) using 16S rDNA gene and further characterized by scanning electron microscopy. *In vitro* predation of isolated *Bdellovibrio* (FBd1, FBd2) were tested against *Salmonella* Typhimurium (ATCC 14028) and *Bdellovibrio* Stolp and Starr (ATCC 15143) as control. The strain FBd2 exhibited better predation activity by observing the reduction in optical density at 600nm at specific intervals up to 72 hours and prey cell viability was decreased to 2x107 CFU/mL. ATCC 15143 strain showed 48% biofilm removal ability, while FBd2 showed 26.3% removal on preformed biofilms in 96 well microtiter plates using crystal violet assay. Administration of *Bdellovibrio* and *Salmonella* to the zebrafish larvae performed by bath immersion method. LD_{50} for *Salmonella* in zebrafish larvae could not be estimated at CFU of 1 x 10^{10} /mL level. However, the behavioral signs of the infected larvae showed sluggish movements, slower response and circular motions compared to the control. Survivability of zebrafish larvae after administration of FBd2 (~1 x 109cells) alone indicates their non-toxicity, non-pathogenic nature. *Bdellovibrio* could persist *in vivo* sufficiently long enough in the presence of prey. Increased number of plaques by FBd2 after homogenizing zebra fish larvae indicate their effective predation inside the zebrafish.

Keywords: predatory bacteria, *Bdellovibrio bacteriovorous*, antibiotic resistance, *Salmonella* Typhumurium

MTAMR-80 (Poster)

Cloning and Expression of Sserratiopeptidase Gene from *S. marcescens* AD-W2 in *E. coli*

Devtulya Chander[1,2] and Asha Chaubey[1,2]*
*achaubey@iiim.res.in

[1]*Fermentation and Microbial Biotechnology Division, CSIR-Indian Institute of Integrative of Medicine, Canal Road, Jammu (180001), India*
[2]*Academy of Scientific and Innovative Research CSIR- Human Resource Development Centre, Campus Ghaziabad (201002), India*

Abstract: Serratiopeptidase, a proteolytic enzyme with various therapeutic applications, is traditionally sourced from the bacterium *Serratia marcescens*. However, the pathogenic nature of this bacterium poses safety risks in production. Recombinant DNA technology offers a safer alternative by expressing the serratiopeptidase gene in a non-pathogenic host like *Escherichia coli*. During the present study, this approach was successfully employed. Cloning of serratiopeptidase gene from *S. marcescens* AD-W2 was carried out into pET28a vector and transformed into *E. coli* KRX cells. The protein expression was optimized with respect to temperature, Point of induction, and concentration of inducers. The final yield of 475 mg protein per litre of culture was obtained at 37°C, 5 OD of cell density at induction, 6 hours of induction incubation, mM of IPTG and 5% of L-Rhammnose. This achievement lays the foundation for further investigation into the production and characterization of recombinant serratiopeptidase, addressing the safety concerns associated with traditional isolation methods.

Keywords: Serratiopeptidase, Anti-inflammatory Enzyme, In-Fusion cloning, Protein expression

MTAMR-81 (Poster)

Identification of Potential Therapeutic Target of *Salmonellaenterica*

Minal Bhalerao[1,2], Aishwarya Davkhar[1,2], Sachin Agawane[1,2*] and Chiranjit Chowdhury[1,2]*
*c.chowdhury@ncl.res.in

[1]*Biochemical Science Division, CSIR- National Chemical Laboratory, Pune, India*
[2]*Academy of Scientific and Innovative Research (AcSIR), Ghaziabad 201002, India*

Abstract: *Salmonella enterica* is a major causative agent of gastroenteritis accounting for more than 20 million deaths globally every year. Recent emergence of multidrug resistant variants attracts novel infection control

measurements. It is revealed that *Salmonella* gains unique metabolic capability to utilize ethanolamine (EA) and demonstrate its fitness and virulence in the host contributing to intrinsic resistance by the pathogen. It is proposed that *Salmonella* deploys ethanolamine utilization microcompartments (Eut MCP) to metabolize EA in the gut. This metabolic machinery bestows a competitive growth advantage to this pathogen over another microflora that lack MCP. Eut MCP comprises of five shell proteins i.e. EutS, -M, -N, -L and EutK that foster EA metabolism by sequestering metabolic partners within MCP shell. In this study, it has been observed that knock out mutants of the *eut* shell protein genes corresponding to EutKLMNS result in growth defects in *Salmonella*. The HPLC study reveals almost 50% loss of certain metabolites in these mutants. Ultrathin section TEM analysis reveals the formation of MCP in the wild type and the *eut* shell protein mutants. Intriguingly, the *eut* shell protein mutants exhibit more susceptibility towards some antibiotics. Wild type shows biofilm production as observed by FE-SEM and surprisingly, the mutants show reduced biofilm formation than the wild type as evident from the crystal violet assay. Congo red assay provides evidence for the effect of disruption of ethanolamine metabolism on the curli expression and exopolysaccharide secretion. The current study indicates the indispensable role of Eutshell proteins in MCP formation and ethanolamine metabolism. This study puts forward a new hypothesis to disrupt the Eut MCP, target the ethanolamine metabolism and sensitize *Salmonella* against antimicrobials.

Keywords: *Salmonella,* Microcompartment, Ethanolamine metabolism, Intrinsic resistance biofilm, Antimicrobials

MTAMR-82 (Poster)

Antimicrobial Resistance: An Emerging Health Concern

Shreya Maheshwari[1], Kanika[1], Raj shayama[2], Shashwat kumar[3] and Shagun Chaudhary[4]
shreyamaheshwari270203@gmail.com

[1]*Guru Jambheshwar University of Science & Technology, Hisar, Haryana*
[2]*Jawahar Lal Nehru University*
[3]*TERI School of Advance Studies*
Goswami Ganesh Dutta Sanatan Dharma College,India

Abstract: Not all microbes are harmful for health. Current day scenario we are using microbes for the treatment of disease as medicinal purpose and chemotherapies and much more The utilization of microorganisms for medicinal purposes is known as microbial therapeutics scientists have developed multiple microbial therapeutics as bacterial vaccines probiotics and faecal microbiota transfer(FMT) to cure diseases and provide protection Microbial therapeutics are applied to remove tumours, prevent infections, and for the treatment of metabolic disorders Microbial therapeutics are applied to remove tumours, prevent infections, and for the treatment of metabolic disorders AMR occurs when bacteria, viruses, fungi and parasites change over time and no longer respond to medicines making infections harder to treat and increasing the risk of disease spread, severe illness and death with introduction of antibiotics we thought we won the battle against microorganisms but thus was not the case with pathogens like bacteria viruses and fungus developed a resistance against the medical therapeutics and with current day scenario it has become a major issue these days fighting against the diseases antimicrobial agents can be divided into groups based on the mechanism of antimicrobial activity. The main groups are: agents that inhibit cell wall synthesis, depolarize the cell membrane, inhibit protein synthesis, inhibit nuclei acid synthesis, and inhibit metabolic pathways in bacteria current day scenario sometimes second or third line of drugs are given initially then the bacteria or pathogens gets more prone to particular drug and leading to increase AMR cases. **Antimicrobial resistance** (AMR) is one of the most serious global public health threats in this century

Keywords: AMR, FMT. Therapeutics, Chemotherapies

MTAMR-83 (Poster)

Phage therapy: A Solution to AMR

Menal Jain[1] and Vanshika Agrawal[2]
23menal.jain@gmail.com

[1]Guru Jambheshwar University of Science & Technology, Hisar, Haryana
[2]Department of Biotechnology
[2]Banaras Hindu University, Varanasi, Uttar Pradesh
Department of Botany

Abstract: Human microbiome is a very complex yet favorable ecosystem for micro-organisms. It serves as an optimal environment for the growth of various kinds of micro-organisms including pathogens, which compromises the human health. Microbial therapeutics is introduced to counter such infections using various approaches based on the complex microbial signatures or bio-markers and develop ways to harness the microbial potential for the treatment. This approach leverages the natural microbial properties and their ability to interact within the host body in a therapeutically beneficial way.
In 2017, WHO has highlighted the potential treat of Gram-negative pathogens which are resistant to multiple antibiotics. The major cause of increasing AMR pathogens is due to the widely available antibiotics and mis- and over-use of antibiotics in day-to-day life. With the current rise in AMR microbes, there is a need to look for ways to lower the death trends due to AMR and effectively treat the infections. One of such approaches is the use of bacteriophages. As we know, bacteriophages are the viruses that naturally predates on the bacteria, so their lytic phase can be used to counter AMR pathogens and yield significant results. Over the recent years, many studies and clinical trials are being conducted on phage therapy leading to the identification and production of phages with their efficacy in treatment being tested for various infections including gastro-intestinal infections, pulmonary infection etc. Although it is unlikely that phages will entirely replace antibiotics, but with the ongoing research, this holds a huge potential in treatment and in exploring new ways in the near future.

Keywords: AMR, Microbial Therapeutics, Phage Therapy, Antibiotics, Bacteriophages, Infections

MTAMR-84 (Poster)

Comprehensive Analysis of Etiological Agents and Drug Resistance Patterns in Ventilator-Associated Pneumonia

Harendra K. Thakur[1,2*], Bansidhar Tarai[2] and Manoj Kumar Jena[1*]
manoj.20283@lpu.co.in; harendra.41900685@lpu.in, bansidhar.tarai@maxhealthcare.com,

[1]Department of Biotechnology, School of Bioengineering and Biosciences, Lovely Professional University, Phagwara, Punjab– 144411, India.
[2]Department of Microbiology & Molecular Biology, Max Super Speciality Hospital, Saket, New Delhi- 110017, India.

Abstract: VAP, a common hospital-acquired infection among mechanically ventilated patients, poses significant risks due to microorganisms invading the lower respiratory tract. This study aimed to examine antibiotic use, VAP incidence, etiology, and resistance trends in nosocomial bacteria within a clinical-surgical intensive care unit. Over 2.5 years, 70 VAP cases were identified in three Max Healthcare branches. Patients with diabetes, immunocompromise, cancer, heart disease, respiratory failure, and other medical conditions were included. The study analyzed causative pathogens and their resistance patterns associated with VAP. *Klebsiella pneumoniae*, *Acinetobacter baumannii*, and *Pseudomonas aeruginosa* were the most prevalent pathogens in ventilator-associated pneumonia (VAP) cases. Other pathogens included *E. coli*, *Ralstonia insidiosa*, *Stenotrophomonas maltophilia*, *Burkholderia cepacia*, *Staphylococcus aureus*, *Serratia marcescens*, *Elizabethkingia meningoseptica*, *Candida tropicalis*, and *Candida albicans*. Notably, *Pseudomonas aeruginosa*, *Acinetobacter baumannii*, *Klebsiella pneumoniae*, and *Staphylococcus aureus* exhibited significant drug resistance. Heatmap analysis revealed a cluster of pathogens, including *Serratia marcescens*, *E. coli*, *Klebsiella pneumoniae*, *Ralstonia insidiosa*, and *Ralstonia mannitolytica*, with moderate to high antibiotic resistance. However, some

pathogens, like *Serratia marcescens* and *E. coli*, showed lower resistance to specific antibiotics. These findings highlight the urgent need for tailored antibiotic regimens to effectively manage VAP in hospitalized patients.

Keywords: Ventilator-associated pneumonia; Etiological agents; Drug resistance; Microbiological culture; AMR; Pathogens.

MTAMR-85 (Poster)

Repurposing of Anti-Fungal Drug -Nystatin- against Multi-Drug Resistant Bacterial Pathogens

Manya[1], Neena Capalash[2] and Prince Sharma[1]
manyaaggarwal001@gmail.com

[1]*Department of Microbiology, Panjab University, Chandigarh, India*
[2]*Department of Biotechnology, Panjab University, Chandigarh, India*

Abstract: The escalating prevalence of MDR and XDR bacterial pathogens in community and hospital ICUs is posing alarming threats to global health. This study explores the potential of repurposing nystatin, a known FDA-approved antifungal drug in market, as a novel antibacterial drug against MDR strains of *Acinetobacter baumannii*, *Klebsiella pneumoniae* and *Pseudomonas aeruginosa,* the priority ESKAPE pathogens in WHO list. Molecular docking analysis identified nystatin (out of 1615 FDA approved drugs) as a promising candidate based on its high affinity for essential outer membrane proteins of *A. baumannii* and *K. pneumoniae*. *In vitro* assays highlighted nystatin's multifaceted mechanism of action against MDR bacteria including targeting of inner membrane thus inducing significant permeability changes while also triggering ROS generation. The plasmid fragmentation assays confirmed DNA damage, enhancing the understanding of its antibacterial properties. Combination therapy demonstrated additive effects with ciprofloxacin, aceclofenac, and ibuprofen, enhancing Nystatin's antibacterial efficacy by reducing effective drug concentrations and lowering the selective pressure, thereby potentially delaying resistance development. Adaptive laboratory evolution studies revealed varying resistance patterns among *A. baumannii*, *P. aeruginosa*, and *K. pneumoniae*, with *A. baumannii* developing resistance most rapidly. Combining nystatin with aceclofenac delayed resistance emergence, especially in *A. baumannii*, while *P. aeruginosa* and *K. pneumoniae* showed no resistance development within the tested passages, emphasizing the effectiveness of combination therapy in curbing drug resistance. This study underscores the promising potential of nystatin as a repurposed antibacterial agent, offering a strategic approach to overcome the growing threat of multidrug-resistant infections.

Keywords: *Pseudomonas aeruginosa*, Nystatin, Molecular docking, ESKAPE pathogens

MTAMR-86 (Poster)

Harnessing Lactic Acid Bacteria for Bioactive Peptide Production: Enhancing Antioxidative Properties in Fermented Sheep and Goat Milk

Pudke Payal Udelal[1], Maitri Goel[1], Harsh Panwar[1], Manvesh Kumar Sihag[2] and Vikas Sangwan[1]
payalpudke@gmail.com

[1] *Department of Dairy Microbiology*
[2]*Department of Dairy Chemistry, College of Dairy and Food Science Technology, Ludhiana, India*

Abstract: Bioactive peptides derived from milk have garnered significant attention for their potential health benefits, including antioxidative properties. In this study, we investigated the production of bioactive peptides through the fermentation of goat and sheep milk with lactic acid bacteria (LAB) isolated from various milk samples. Goat and sheep milk were chosen due to their unique biotherapeutic properties and protein composition. A total of 50 bacterial isolates were screened, with 25 identified using MALDI-TOF mass spectrometry, among which 10 were confirmed as LAB. The proteolytic activity of these isolates was assessed through agar well diffusion and spot-on-lawn assays, selecting cultures with zone diameters ranging from 12-14 mm for further fermentation trials. The selected LAB cultures were employed to ferment goat and sheep milk

over varying time intervals. The resulting fermented milk samples were analyzed for protein content using the Lowry method, degree of hydrolysis through the o-phthaldialdehyde (OPA) method, and antioxidative activity using the ferric reducing antioxidant power (FRAP) assay. The molecular weight of the protein was estimated using SDS-PAGE. Additionally, gene expression analyses after cell line studies provide insight into the modulatory effects of these peptides on oxidative and antioxidative biomarkers. Results demonstrated promising proteolytic and antioxidative activities, particularly in the LAB cultures of *Lacticaseibacillus rhamnosus* and *Lactiplantibacillus plantarum* when fermenting sheep and goat milk, compared to other strains. These findings suggest that these LAB species are potent candidates for producing bioactive peptides during the fermentation of sheep and goat milk. Our research highlights the significant role of LAB in enhancing the functional properties of dairy products, particularly through the generation of bioactive peptides. The study underscores the potential of microbial fermentation in developing functional dairy products with improved nutritional and health benefits, paving the way for novel applications within the dairy industry.

Keywords: Bioactive peptides, Antioxidative potential, Microbial hydrolysis, SDS PAGE, MALDI-TOF MS, Oxidative and antioxidative biomarkers

MTAMR-87 (Poster)

Optimization of Submerged Fermentation Process for Enhancement of Lignocellulolytic Enzymes Production and Red Gram Stalk Degradation

Pratima S B[1*], Nagaraj M. Naik[1], Saroja N. Rao[1], Veeresh H[2],Pampanagouda[3], and Yallappa M[3]
*sbpratima696@gmail.com

[1]*Pesticide Residue and Food Quality Analysis Laboratory, University of Agricultural Sciences, Raichur-584104, Karnataka, India.*
[2]*Department of Soil Science and Agriculture Chemistry, University of Agricultural Sciences, Raichur-584104, Karnataka, India.*
[3]*Department of Microbiology, University of Agricultural Sciences, Raichur (584104), Karnataka, India.*

Abstract: Lignocellulose is the most abundant biomass on the planet, including wood and agricultural byproducts like paddy straw, maize cobs and red gram stalks. Lignocellulolytic enzymes are vital and central to develop an economical, eco-friendly, and sustainable biological method for degradation of lignocellulosic biomass. This study aimed to isolate fungal strains from the termite gut and red gram stalk capable of degrading cellulose and lignin. Upon screening qualitatively, through enzyme plate assay, nineteen fungal isolates were positive for cellulase and eleven fungal isolates were positive for lignin peroxidase and laccase. The fungal isolates LCR6 and LCT8 showed the best combination for cellulase, lignin peroxidase and laccase enzyme production. Further optimization for enhancement of lignocellulolytic enzyme production was carried out by submerged fermentation along with fungal consortia and red gram stalks as carbon sources at three different temperatures (25°C, 30°C and 35°C) and pH (3, 4, and 5) respectively. Results revealed that at 7th day of incubation consortia with pH 5 and 30°C on red gram stalks recorded the highest cellulase activity (18.99 µmoles/min/mlof enzyme) and lignin peroxidase activity (4.35 µmoles/min/ml of the enzyme). Whereas on 14th day of incubation the cellulase activity was (24.84 µmoles/min/ml of enzyme) and lignin peroxidase activity (8.39 µmoles/min/ml of enzyme). Further on 21st day of incubation the cellulase activity found to be reduced (5.60 µmoles/min/ml of enzyme) and lignin peroxidase activity (6.54 µmoles/min/ml of enzyme). The highest percent degradation of cellulose after 21 days of submerged fermentation was (50.30%), hemicellulose (51.60%) and lignin (25.88%). Images captured by the SEM depicted large cracks and high fungal spores on the surface of red gram stalks indicating the efficiency of the consortia in degradation.

Key words: Termite gut, Red gram stalk, Cellulase, Lignin peroxidase, Laccase.

MTAMR-88 (Poster)

Anti-Diabetic Potential of Microbial Hydrolysis Derived Goat Milk Protein Hydrolysates

Maitri Goel[a], Payal Pudke Udelal[a], Vikas Sangwan[a], Manvesh Kumar Sihag[b]and Harsh Panwar[a#]
[*]harshpanwar@gadvasu.in

[a]*Department of Dairy Microbiology, College of Dairy and Food Science Technology, Guru Anagd Dev Veterinary and Animal Sciences University, Ludhiana – 141004, Punjab.* [b]*Department of Dairy Chemistry, College of Dairy and Food Science Technology, Guru Anagd Dev Veterinary and Animal Sciences University, Ludhiana – 141004, Punjab, India*

Abstract: Type 2 Diabetes (T2D) is a chronic metabolic disorder with steadily increasing prevalence, impacting almost all the sections of the society. Halting the spread of diabetes is one among the globally agreed target. Safe and cost-effective interventions are sought to reduce the global burden of T2D. Milk proteins are unique in their nutritional and functional properties and are being investigated for therapeutic purposes. In recent years, goat milk has gained interest due to superior functional properties. This study aimed to explore goat milk protein hydrolysis for generating bioactive peptides with higher anti-diabetic functionality. A total of 39 lactic acid bacteria strains were screened for their proteolytic potential. *Lacticaseibacillus zeae* IF5,*L. plantarum GM6*, *Limosilactobacillus fermentum D10*, *Mammaliicoccus sciuri S4*, *Streptococcus infantarius R4*, *Enterococcus faecalis G12*, *L. fermentum*, *L. acidophilus*, and *L. plantarum* were shortlisted for goat milk fermentation on basis of promising proteolytic activity. Milk fermentation derived supernatant was neutralized (pH7) and another fraction was targeted for protein extraction. The two preparations were screened for alpha-glucosidase and DPP4 inhibition potential. The results demonstrated functional peptides that could inhibit α-glucosidsase from 29-100%. *L. plantarum & L. plantarum GM6* exhibited most promising α-glucosidsase inhibition. However, mild DPP4 inhibition was recorded with tested samples. The bioactive peptides from the screened fractions will be further validated for their anti-diabetic potential and safety under *in vitro* cell line models.

Keywords: Milk protein hydrolysis, Anti-diabetic functionality, Bioactive peptides, Lactic acid bacteria

MTAMR-89 (Poster)

Isolation and Comparison Between Poultry Litter Isolated Bacteria in Terms of Antibiotic Sensitivity

Madhushree Ghorui, K Rajendra r Roy and Rajib Bandopadhyay*
[*]rajibindia@gmail.com

Microbiology Section, Department of Botany, The University of Burdwan, Burdwan, West Bengal (713104), India

Abstract: Antimicrobial resistance is one of the major threats to public health throughout the world. Emergence of resistant superbugs is not only due to the uses of antibiotics in clinical fields, but also due to over and inappropriate use of antibiotics in non-clinical field such as poultry farms. This study casts the characterization of 3 poultry farm (Harihar, Rahimpur, Aligari, Hooghly district of West Bengal, India) isolated bacteria. Depending on antibiotic susceptibility test 2 bacterial strains were selected out of 24 isolates. The strainMHPL4 is found to be most sensitive and while MRPL10 is resistant against 18 antibiotics from different groups. Characteristically both these isolates are Gram positive. The MHPL4 is rod shaped and MRPL10 is a coccus. Both the strains are susceptible to carbapenems, 3rd and 4th generation fluoroquinolone, but similar resistant pattern observed only against bacitracin. XRF analysis of Rahimpur poultry litter exhibit less counts (164 counts) of Cd peak than Harihar litter (385 counts), other metals like molybdenum, manganese, iron, copper, and zinc are also present. The quantity of biofilm is found to be higher in the resistant strain in comparison to the sensitive one at 577nm. Biofilm formation was studied in different media to study the impact of nutrient in biofilm formation. The quantity of biofilm is found to be higher in the resistant strain in comparison to the sensitive one. SEM analysis revealed that biofilm of MRPL10 is more thick, messy, and sticky than MHPL4. Standard CLSI and EUCAST protocols were utilized to reveal the MIC and MBC of both the strains for

different antibiotics. CFU are counted for the resistant strain in both control and different antibiotic stress environments to point out the MDR/PDR possibilities.

Keywords: Antibiotics, Resistance, Biofilm, Non-clinical settings, MDR, XRF

MTAMR-90 (Poster)

Exploring Wheatgrass Phenolic Compounds as Promising Antimicrobial Agents in Understanding the Microbial Therapeutic Solutions

Manju Rani[1], Jayanti Tokas*[1], Shivangi[1] and Sujeeta [2]
manju.hsr97@gmail.com

1. Department of Biochemistry, CCSHAU, Hisar (Haryana) India
2. Department of Microbiology, CCSHAU, Hisar (Haryana) India

Abstract: Wheatgrass is a young grass (10-14th day) from the wheat family, has attracted considerable attention for its broad spectrum of health benefits, including antimicrobial properties. Our studies have shown that wheatgrass phenolics exhibit broad-spectrum antimicrobial effects against Gram-positive and Gram-negative bacteria, including *Staphylococcus aureus*, *Bacillus cereus*, and *Pseudomonas aeruginosa*, as well as antifungal effects against species like *Candida albicans* and *Aspergillus niger*. Seeds from 4 wheat genotypes viz; WH1063, HPYT-481, P40017, and P40005 were sown for 14 days. Wheatgrass was extracted using different solvents including ethanol, methanol, acetone and water. The antimicrobial activities of these extracts were assessed using agar well diffusion assays. Results indicated that wheatgrass extracts in ethanol and methanol exhibited the highest antimicrobial activity compared to those in water and acetone. Notably, wheatgrass exhibited a minimum inhibitory concentration (MIC) of 50 to 200 mg/mL against these pathogens. Ethanol extract demonstrated significant inhibition of both Gram-positive and Gram-negative bacteria, as well as fungi, with inhibition zones averaging 11-20 mm. Methanol extract showed slightly lower but still substantial activity, particularly against Gram-positive bacteria. Water and acetone extracts displayed minimal antimicrobial effects. Further, the phenolic profiles of the extracts were analyzed using UPLC, which allowed for precise quantification of individual phenolic compounds responsible for antimicrobial activity corresponding to chlorogenic acid, gallic acid, catechol, Catechin, Caffeine, vanillin, taxifolin, trans-p coumaric acid, trans-sinapicacid, rutinhydrate, trans-cinnamic acid, quercetin dehydrate, apigenin, Naringenin, syringic acid.

Keywords: Wheatgrass, Antibacterial, Antifungal, MIC, UPLC, Phenolic content

MTAMR-91 (Poster)

Preclinical Evaluation of Encapsulated Bile Salt Hydrolase Consortium in Reducing Serum Cholesterol and Managing Weight Using in vitro and in-vivo Models

Pratisha P. Nair [1] and Uday S. Annapure [1*]
us.annapure@ictmumbai.edu.in

[1]*Department of Food Engineering and Technology, Institute of Chemical Technology, Matunga, Mumbai, Maharashtra, India*

Abstract: Cardiovascular diseases (CVDs) remain a leading cause of mortality worldwide, with hypercholesterolemia as a major risk factor. Although statins are the standard treatment for high cholesterol, they are often associated with serious side effects. This study explores bile salt hydrolase (BSH) consortium, a probiotic biomarker, sourced from two different lactic acid bacteria, as a potential alternative to statins. The research assessed its efficacy and safety in improving lipid profiles and managing weight, while potentially reducing the necessary dosage of statins. BSH consortium was encapsulated in chitosan–coated alginate beads to enhance gastric stability and ensure targeted release in the intestines. The beads were characterized by microscopy for size and morphology, and texture profile analysis for integrity. In vitro studies evaluated BSH release in simulated gastric and intestinal fluids, while in vivo studies measured lipid profiles, weight changes, and side effects in hypercholesterolemic rat models. It was observed that although BSH was effective as a preventive measure for hypercholesterolemia, it was less potent than statins for therapeutic purposes. However,

when combined with statins, BSH significantly enhanced the reduction of serum cholesterol, triglycerides, and LDL, while increasing HDL levels. Notably, liver function tests and histopathology revealed no adverse effects. In conclusion, BSH offers a promising and safer adjunct to statin therapy, allowing for reduced statin dosages and minimizing associated side effects. This combination presents a promising direction for future therapeutic strategies, aiming to minimize the risks of statin therapy while enhancingcholesterol management.

Key words: Cardiovascular diseases (CVDs), Bile salt hydrolase (BSH), Cholesterol, Statins, Probiotics, Side-effects

MTAMR-92 (Poster)

Emerging Challenges in Treating Neonatal Sepsis: Antimicrobial Activity and Pathogen Resistance

Vijay Laxmi[1], Sheetal Verma[1], Vimala Venkatesh[1], Amita Jain[1], Shalini Tripathi[2], and Manoj Kumar[3]
vl121182@gmail.com

Department of Microbiology, King George's Medical University, Lucknow (226003), India
Department of Paediatrics, King George's Medical University, Lucknow (226003), India
CSIR-Indian Institute of Toxicology Research (IITR), Lucknow (226001), India

Abstract: Introduction: Neonatal sepsis is a life-threatening condition caused by systemic infections in newborns, typically occurring within the first 0 to 28 days of life. It is a significant cause of morbidity and mortality, particularly in preterm and low-birth-weight neonates. The condition is characterized by an overwhelming inflammatory response to pathogenic microorganisms, which can lead to organ dysfunction and septic shock if left untreated. Despite advances in neonatal care, the diagnosis and treatment of neonatal sepsis remain challenging clinical symptoms and the increasing prevalence of antimicrobial resistance among causative pathogens.
Material & Methods: Blood samples were collected from neonates with clinical symptoms of sepsis and incubated in a BacT/ALERT system for automated detection of bacterial growth. Upon a positive culture result, the samples were cultured on Blood agar and MacConkey agar and incubated 37^{o}C overnight. The bacterial colonies were then identified using MALDI-TOF MS (Matrix-Assisted Laser Desorption/Ionization-Time of Flight Mass Spectrometry), and antimicrobial susceptibility testing (AST) was performed to determine resistance profiles.
Results: Out of the 171 neonates with suspected sepsis, 135 (78.94%) had confirmed bloodstream infections, while 36 (21.05%) had sterile blood cultures. The most frequently identified pathogens were *Klebsiella pneumoniae (52), Staphylococcus haemolyticus (25), Staphylococcus hominis (12), Staphylococcus epidermidis (12), Escherichia coli (6), and Acinetobacter baumannii (7) and Staphylococcus aureus (1), Bacillus (3), Burkholderia spp. (4) etc*. Most commonly Gram-Negative Bacteria resistance rates to antimicrobial agents were Cefuroxime (31.57%), Gentamicin (28.07%), Amikacin (31.57%), Ampicillin (12.28%), Ciprofloxacin (14.03%), Piperacillin-Tazobactam (29.23%), Amoxicillin-Clavulanate (29.82.%) Ertapenem (25.73%), TOB Tobramycin (22.80%), Ceftriaxone (32.16%). Most commonly Gram-Positive Bacteria resistance rates to antimicrobial agents were Gentamicin (4.09%), Cotrimoxazole (11.11%), Ciprofloxacin (16.37%), Vancomycin (0.58%), Erythromycin (12.86%), Penicillin (21.05%), Polymyxin (12.28%), Ceftriaxone (11.69%). These findings highlight the high prevalence of bloodstream infections among neonates and the concerning levels of resistance to multiple antibiotics.
Conclusion: The findings show a high prevalence of bloodstream infections (78.94%) among neonates with suspected sepsis, with Klebsiella pneumoniae being the most common pathogen. There is significant resistance to multiple antibiotics, particularly among Gram-negative bacteria, with high resistance to Ceftriaxone, Cefuroxime, and Amikacin. Gram-positive bacteria showed lower resistance overall, but still notable resistance to Penicillin and Ciprofloxacin. These results highlight the urgent need for targeted antibiotic use and the development of new treatments to manage neonatal sepsis effectively.

Keyword: Neonatal sepsis, Septic shock, Systematic infection, Clinical symptoms, Resistance profile

MTAMR-93 (Poster)

Bacteriophage and Antibiotic Combinations Effectively Inhibit *Escherichia coli* Biofilms

Damini Thakur[1], Sushant Kumar Pal[1], Juhi Prasad[1] and Lokender Kumar[1*]
[*]daminithakur18@gmail.com

[1]*School of Biotechnology, Faculty of Applied Sciences and Biotechnology, Shoolini University, Solan, Himachal Pradesh (173229), India*

Abstract: Biofilm formation by *Escherichia coli* pose a significant challenge in clinical and environmental settings due to its role in antibiotic resistance and persistent infections. The rise of multidrug-resistant *E. coli* strains necessitates alternative strategies for biofilm control. Bacteriophages, viruses that specifically target bacteria, offer a promising approach when combined with conventional antibiotics like ampicillin.
This study evaluates the efficacy of bacteriophages, both alone and in combination with ampicillin, in inhibiting biofilm formation. Bacteriophages targeting *E. coli* were isolated from environmental sources and characterized based on plaque morphology, host range, and morphology. The Minimum Inhibitory Concentration (MIC) of ampicillin was determined using microbroth dilution assay. The anti-biofilm efficacy of phages, alone and in combination with sub-MIC concentrations of ampicillin, was assessed over 1, 3, and 5 days on glass and polystyrene surfaces, as well as on urinary catheters. Biofilm formation was quantified using crystal violet staining, and bacterial load reduction was also measured in terms of $\log_{10}$ CFU/µL. Microscopic analysis of biofilm inhibition was conducted using light and fluorescence microscopy for coverslips, and field emission scanning electron microscope (FESEM) was utilized for analyzing the urinary catheters.
The isolated bacteriophages demonstrated strong lytic activity against *E. coli* and effectively inhibited biofilm formation on glass and polystyrene surfaces. The combination of bacteriophages with ampicillin showed a synergistic effect, significantly enhanced biofilm inhibition compared to either treatment alone. On urinary catheters, the combination treatment achieved a marked reduction in biofilm formation, as indicated by lower $\log_{10}$ CFU/µL values across all time points. Microscopic analysis corroborated these findings, revealing minimal biofilm biomass with combined treatment.
The study shows that phage-antibiotic synergy significantly enhances the inhibition of *E. coli* biofilm formation, offering a potent strategy for managing biofilm-associated infections, especially with multidrug-resistant *E. coli.*

Keywords: *Escherichia coli*, biofilm, bacteriophage, ampicillin, antibiotic resistance, phage therapy

MTAMR-94 (Poster)

Endophytic bacterial diversity associated with the roots of endemic *Viola odorata*

Richa Salwan[a] and Vivek Sharma[b]
richaihbt332@gmail.com

[a]*College of Horticulture and Forestry (Dr. YS Parmar University of Horticulture and Forestry), Neri, Hamirpur 177 001*
[b]*University Centre for Research and Development, Chandigarh university, Gharuan, Mohali (PB.) 140 413*

Abstract: *Viola odorata*, popularly known as “Banafshah” is well known for its pharmaceutical importance including anti-inflammatory, diuretic, expectorant, and antipyretic properties. The endophytes associated with the roots of *Viola odorata* were raised in pure cultures and evaluated for antibacterial against *Bacillus cereus*, *Escherichia coli*, *Listeria monocytogenes*, *Pseudomonas aeruginosa*, *Staphylococcus aureus* and *S. epidermidis*. Antioxidant activity based on DPPH activity revealed 50-85% scavenging inhibition by the endophytes. Half maximal inhibitory concentration (IC_{50}) of these isolates ranged from 57.65- 2317 µg/ml, suggested strong antioxidant potential in comparison to the ascorbic acid used as standard. Different isolates showing both antimicrobial and antioxidant activity were characterized for intergenic and intragenic variability based on amplified ribosomal DNA restriction analysis (ARDRA) and enterobacterial repetitive intergenic consensus (ERIC) types. Dendrogram based on ERIC pattern showed one group of 40 isolates, and two groups of two isolates each and rest as independent branches at 1.5% distance. Similarly, the purified PCR products of 16S rRNA gene revealed diverse banding pattern i.e., 12 with *Alu*I, 13 with *Hinf*I, 9 with *Rsa*1 and *Hpa*1 and 10 with *Taq*1 restriction digestion forming different clusters in dendrogram at 1.25% distance. Identification of

promising endophytic bacteria showed affiliation to different species of the genus *Enterobacter*, *Microbacterium*, *Pseudomonas*, *Rhizobium* and *Streptomyces*. The present study demonstrates that the endophytes associated with *V. odorata* have immense bioactive potential and can be explored to develop various drugs in the field of pharmaceutical industries.

Keywords: *Viola*, Ribotypes, Bioactive, Antioxidant, Antimicrobial

MTAMR-95 (Poster)

Structural Differences in Superoxide Dismutase Enzyme of Chilling Tolerant & amp; Chilling Sensitive Isolates of Arthrospira using in-silico Approach

Kanu Priya[1,2] and Namita Singh[1*]
[*]namitasingh71@gmail.com

[1]*Lab No. 202, Microbial Biotechnology Laboratory, Department of Biotechnology, Guru Jambheshwar University of Science & Technology, Hisar, Haryana (125001), India*
2Ssafe agro producer Company Limited, Mohil Farm,Village Dabra, Hisar (125004), India

Abstract: The study aimed to characterize oxidative stress induced gene in Arthrospira isolates. Superoxide dismutase gene was chosen for the study and amplified & and sequenced in all the seven Arthrospira isolates. Phylogenetic analysis grouped the isolates into four groups. In-silico characterization of SOD was done using computational tools. The proteins were helices & and coil dominated and differed on the basis of physico-chemical properties. The binding site composition grouped SOD into two groups constituting histidine, aspartate and tryptophan amino acids binding to the metal ion.

Keywords: Arthrospira, SOD, Phylogenetic analysis, Physico-chemical properties, Tertiary structure, Binding site

MTAMR-96 (Poster)

Optimization of Bacteriophage Dosing against Multidrug-Resistant *Klebsiella pneumoniae*: Insights from MOI and Time-Kill Curve Assays for Therapeutic and Prophylactic Applications

Prexha Kapoor[1]*, Bhupendra Kumawat[2], Karan Bhutani[1], Rinku Chaudhary[1], Priya Sharma[1], Ruma Rani[1], B.C. Bera[1], R. K. Vaid[1], Nitin Virmani[1] and Taruna Anand[1*]
tanandbt@gmail.com, prexhakapoor@gmail.com

[1]*National Centre for Veterinary Type Cultures, ICAR-NRCE, Hisar, Haryana (125001)*
[2]*Department of Microbiology, Central University of Haryana, Mahendergarh (Haryana), 123031*

Abstract: The global rise of multidrug-resistant *Klebsiella pneumoniae*, a leading cause of hospital-acquired infections, has prompted urgent efforts to develop alternative therapies, including phage therapy. *K. pneumoniae* is responsible for severe infections, such as pneumonia, bloodstream infections, and urinary tract infections, particularly in immunocompromised patients, with high prevalence approximately 11.8% across healthcare facilities worldwide. This study focuses on bacteriophage φKp, targeting *K. pneumoniae*, to optimize phage dosing by assessing the multiplicity of infection (MOI) and performing time-kill curve assays. These assays are instrumental for understanding phage-bacteria dynamics and determining effective dosing regimens, particularly critical for pathogens with complex antibiotic resistance profiles. In our analysis, φKp was tested against multiple *K. pneumoniae* strains, showing effective host lysis at various MOIs. Results indicated that intermediate MOIs provided an optimal balance between rapid bacterial reduction and minimized resistance risk. High MOIs yielded faster bacterial killing rates but correlated with increased resistance, while lower MOIs required prolonged exposure to suppress bacterial populations. Notably, time-kill assays revealed significant bacterial clearance within 2 hours of phage exposure, followed by a plateau phase, suggesting a controlled but effective bactericidal action. However, the emergence of phage-resistant mutants was observed during these

assays, which underscores the need for strategic dosing to limit resistance development. Furthermore, this phage exhibited prophylactic potential, as pre-exposure to the phage significantly reduced bacterial burden upon infection, emphasizing its utility as a preventative measure in high-risk environments. These findings highlight MOI and time-kill assays as essential tools for optimizing phage dosing strategies and underscore the significance of genomic insights in phage selection and therapeutic development. This work supports φKp as a promising therapeutic and prophylactic option against antibiotic-resistant *K. pneumoniae* infections, contributing to the advancement of effective phage therapy protocols in clinical reigns.

Keywords: Bacteriophage, Phage therapy, Time-kill assay, MOI, Antibiotic Resistance, *Klebsiella pneumoniae*

MTAMR-97 (Poster)

Production, Purification, and Application of Bacteriophage Endolysin Proteins against Drug-Resistant Bacteria

Ruma Rani, Prexha Kapoor, Karan Bhutani, Rinku Chaudhary, Priya Sharma, B.C. Bera, R. K. Vaid, Nitin Virmani and Taruna Anand*
*tanandbt@gmail.com

National Centre for Veterinary Type Culture, ICAR-NRCE, Hisar (125001), India

Abstract: The emergence of drug-resistant bacterial strains poses a significant challenge to global healthcare, necessitating novel therapeutic strategies. Endolysins are bacteriophage (phage)-encoded enzymes that can rapidly destroy bacteria by hydrolysing their cell walls. Endolysins are therefore considered as promising alternatives for resolving the issue of growing resistance. This study focuses on the production, purification, and bioevaluation of endolysin proteins from bacteriophage(s) and assesses their efficacy against clinically relevant, drug-resistant bacterial pathogens. Endolysin was produced by cloning endolysin-encoding genes in BL21 *E. coli* from bacteriophage of *Salmonellaenterica.* Following expression in *E. coli*, endolysins were purified using affinity chromatography technique, yielding highly purified proteins with robust lytic activity. Purified endolysin was confirmed by SDS-PAGE having protein size approx. 17 kDa. The bacteriolytic potential of purified endolysin was evaluated against various other isolated drug-resistant bacterial strains of *Salmonella in vitro*. Significant bacterial cell lysis was observed, demonstrating potential for application as an antimicrobial treatment. Furthermore, combining endolysins with low-dose antibiotics may have synergistic effects that enhance the antibacterial effect. These findings underscore the potential of bacteriophage endolysins as effective agents in combating drug-resistant infections, offering an alternative strategy that circumvents traditional antibiotic resistance mechanisms. Future research will focus on optimizing endolysin delivery and assessing safety *in vivo*, paving the way for clinical applications.

Keywords: Bacteriophages; Endolysin; Drug-resistant bacteria; *Salmonella enterica*; Drug-resistant infections; Antimicrobial treatment

MTAMR-98 (Poster)

Targeting Integrase to Improve Phage Therapy Against MDR *E.coli* : A Step Toward CRISPR-Mediated Lysogeny Control

Priya Sharma[1,2], Rinku Chaudhary[1], Prexha Kapoor[1], Ruma Rani[1], Karan Bhutani[1], Jyoti Gupta[2], B.C. Bera[1], R.K. Vaid[1], Nitin Virmani[1] and Taruna Anand[1,*]
priyasharma67797@gmail.com , *tanandbt@gmail.com

[1]*National Centre for Veterinary Type Culture Collection, ICAR-NRCE, Hisar, Haryana (125001)*
[2]*Department of Biotechnology, GLA University, Mathura-Delhi Road, Mathura (281406), Uttar Pradesh, India*

Abstract: In the ongoing battle against multidrug-resistant bacterial infections, bacteriophages are emerging as potential agents in the search for effective treatments. In this study, we successfully isolated a bacteriophage named φEc exhibiting strong lytic activity against multidrug resistant *Escherichia coli*. Following isolation, we

extracted and purified the phage DNA to ensure high-quality material for subsequent genetic analysis. Using advanced Nanopore sequencing technology, we explored the phage genome and found out φEc comprised of linear DNA with a length of ~72512 bp and with a G C content of ~42.87%, and it contains 83 CDS without any tRNA genes. These CDS were classified into functional groups, including DNA replication, transcription, phage packaging, phage structure, host lysis, lysogeny gene and hypothetical proteins. However, a major challenge in utilizing this bacteriophage for therapeutic purposes arises from the presence of an integrase gene, which plays a crucial role in the induction of lysogeny. While this gene gives a probability of enabling the phage to integrate its DNA into the host genome, it poses a significant barrier to effective treatment by potentially allowing *E. coli* to acquire resistance traits, ultimately reducing the phage effectiveness as a treatment option. To address this concern, we plan to utilize CRISPR-Cas9 technology to knock out the integrase gene in future experiments. This strategic genetic modification aims to convert the phage into a strictly lytic agent, thereby eliminating the risks associated with lysogeny and enhancing its safety and efficacy for therapeutic applications. Our research underscores the critical importance of understanding the genetic structure of bacteriophages and highlights the potential of gene-editing tools to refine phage therapy strategies. Ultimately, this work strives to advance the field of phage therapy and provide innovative solutions to combat the challenge of antimicrobial resistance that can effectively address these global health concerns.

Keywords: Bacteriophage, *Escherichia coli*, Antimicrobial Resistance, Sequencing, Integrase, CRISPR-Cas9.

MTAMR-99 (Poster)

Comparative genomic characterisation of multidrug-resistant (MDR) *Escherichia coli* bacteriophages for phage therapy, research and prophylaxis"

Karan Bhutani, Prexha Kapoor, Rinku Chaudhary, Ruma Rani, Priya Sharma, Nitin Virmani, B.C. Bera, .K. Vaid, Taruna Anand*
*tananddbt@gmail.com, karanbhutani909@gmail.com

National Centre for Veterinary Type Cultures, ICAR-NRCE, Hisar, Haryana (125001)

Abstract: The rise of multidrug-resistant (MDR) *Escherichia coli* poses a critical threat to global public health, necessitating alternative approaches such as bacteriophage therapy. In poultry, the prevalence of MDR E. coli can be alarmingly high, with a prevalence rate of up to 57.14% in poultry populations. This study compares the genetic characteristics of two bacteriophages that may be used against MDR *E. coli* for research, therapeutic, and preventative purposes. The two *E.coli* bacteriophages were isolated from poultry sources and accessioned at NCVTC, ICAR-NRCE. They were sequenced using nanopore sequencer MinION and their genomes were analyzed using bioinformatics tools to explore their genetic architecture, virulence factors, and evolutionary relationships. The genomes of the two bacteriophages consist of approximately 86,156 and 50515 base pairs. Genome annotation revealed that both phages possess distinct genes clusters responsible for host recognition, replication, and lysis. Some of the genes of these *E.coli* shows similarity to genes of *Salmonella* phages and *Shigella* phages. Both the phages contain tail proteins, which are responsible for host specificity. No genes associated with antibiotic resistance or lysogeny were identified, confirming their suitability for therapeutic use in poultry. Comparative genomics using Phylogenetic alignment highlighted several conserved regions involved in critical functions, such as tail fibre protein. Unique genes related to tail structure and adsorption mechanisms were found, indicating potential differences in host range between the two phages. The absence of virulence factors and the presence of host-specific genes make these bacteriophages promising candidates for phage therapy against MDR *E. coli* infections. Furthermore, their genomic uniqueness provides a rich resource for further research into bacteriophage-host interactions, enhancing the understanding of phage biology.

Keywords: Poultry, Bioinformatics, *E.coli,* Phage Therapy, Anti-microbial Resistance

MTAMR-100 (Participate only)

Effect of Lactic Acid and Peroxyacetic Acid on Biofilm Formation

Ekta Sehgal[a], **Anju Kumari[a],** Anil Panghal[b], Rakesh Kumar[c] and Ritu Sindhu[a]
anjugaina@gmail.com

[a] *Centre of Food Science and Technology, COBS&H, Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana (125004), India*
[b] *Department of Process Food Engineering, COAE&T, Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana(125004), India*
[c] *Department of Microbiology, COBS&H, Chaudhary Charan Singh Haryana Agricultural University, Hisar (125004), Haryana, India*

Abstract: A syntrophic community of microorganisms known as a biofilm is formed when cells adhere to one another and frequently to a surface. The extracellular polymeric polymers that make up the slimy extracellular matrix surround these adhering cells. Biofilms are frequently found in food and agricultural products and can form on both living (biotic) and non-living (abiotic) surfaces. Biofilms have been found to be involved in a wide variety of microbial infections in the body. These diseases span a wide range as biofilms can become an issue in various food businesses. One of the most popular salad worldwide, cabbage is also vulnerable to microbial adhesion because of its rough surface. In the present study, peroxyacetic acid and lactic acid were compared to control biofilm formation on cabbage. To compare the various preservation methods for mitigation of biofilm formers, cabbage leaves were inoculated with isolated and standard cultures. These samples were subjected to a series of treatment applications with independent parameters as peroxyacetic acid (50, 100, 150, 200 and 250 ppm), lactic acid (50, 100, 150, 200 and 250 ppm), respectively. The effectiveness of treatment was then optimized in response to the microbial log reduction. Overall peroxyacetic acid and lactic acid were most effective at 250 ppm. They were observed as good alternatives to other harsh chemical treatments in mitigation of biofilm formers.

Keywords: Biofilms**,** Living (biotic) and non-living (abiotic), Syntrophic community

MM-1 (Oral)

Waste to Wealth: A Novel Approach to Sustainable *Catla catla* Aquaculture using Probiotics Consortium from Fruit and Vegetable Peels

Nikita Goyat and *Baljeet Singh Saharan
*Baljeetsaharan@hau.ac.in

Department of Microbiology, CCS Haryana Agricultural University, Hisar (125 004), India

Abstract: Aquaculture is becoming more and more demanding every day. In breeding ponds, aquaculture settings cause maximum death of fishes. To overcome this problem we can introduced probiotics directly or indirectly to the water as feed while raising fish. Probiotics are safe bacteria that improve the health of the host animal and provide defense against harmful bacterial diseases. This study was conducted to isolate, characterize and screen the efficient bacteria from different fruits peels, vegetable peels and rhizospheric soils. One seventy bacterial isolates were isolated, screened and identified for bacteriocin production by using different methods. Selected isolates were further examined for their probiotic properties such as tolerance to low pH, temperature, bile salts, phenol, salt concentrations etc. Based on their maximum potential for probiotic characteristics and high antibacterial activity against selected pathogens. Four selected lactic acid bacterial (LAB) isolates were used for compatibility test and all found compatible.Probiotics consortium was prepared by using selected LAB isolates. *Catla catla* fingerlings were distributed randomly into two treatment T1 and T2. Fish tank T1 used as control and 1% v/v probiotics consortium (10^7 CFU/mL) was added in fish tank T2 to check effect on different water parameters, weight gain, length gain , specific growth rate (SGR), feed conversion ratio (FCR) and feed conversion efficiency (FCE) of *Catla catla* fingerlings up to 45 days. The results of this study indicate that probiotics consortium (1% v/v) was positively affect the growth parameters of the *Catla catla* fingerlings and have no negative effects on the water quality parameters.

Keywords: Aquaculture, Probiotics, *Catla catla*, Consortium, Fingerlings, Growth

MM-2 (Oral)

The multi subunit Cascade Protein of CRISPR-Cas System in *Escherichia coli*: The Expendables

Neha Pandey[1,2], Chitra S Misra[1], and Devashish Rath[1,2]
nehapandey@barc.gov.in, devrath@barc.gov.in, chitras@barc.gov.in

[1]*Applied Genomics Section, Bhabha Atomic Research Centre, Mumbai-85*
[2]*Life Sciences, University of Mumbai (400001), Mumbai , India*

Abstract: Among the CRISPR-Cas systems, the Type II system is notably simpler and widely used for genome editing and gene regulation. In contrast, Type I systems, including the Type IE CRISPR-Cas system found in *E. coli*, are more complex due to their multi-component nature, but offer unique advantages. The Type I-E Cascade complex consists of multiple protein components, Cse1, Cse2, Cas7, Cas5, and Cas6e. The complexity of the Cascade protein may limit its practical application. To explore the potential for simplifying this system, we investigated whether any of the Cascade components are dispensable. Cascade was overexpressed with a series of Cascade subunit deletions from a plasmid and the ability of each Cascade deletion variant (p*Δcse1*, *pΔcse2*, p*Δcas7*, p*Δcas5* and p*Δcas6e*) to silence the GFP gene in two *E. coli* strains: BW25113 and BL21DE3 (a natural mutant of the Type-I system) was evaluated. GFP silencing did not occur in absence of Cse1, Cas7 and Cas5 in either of the strains. However, pΔCse2 could still silence GFP 2.6 fold in both the *E. coli* strains, while full length Cascade could bring about 5.8 fold GFP silencing. pΔcas6e in BW25113 could bring about 2.8 fold GFP silencing, but not in BL21DE3 strain. Upon deletion of the chromosomal alleles *cse2* or *cas6e* in BW25113, in which the Cascade is known to be in a repressed state, pΔCse2 continued to bring about GFP silencing (2.6 fold) in the former but the Δcas6e strain did not show GFP silencing in the latter. This suggests that in vivo gene silencing can be achieved in absence of Cse2, but not Cas6e. Findings from this study could pave the way for the development of a 'minimal Cascade' system, potentially simplifying its use in various applications.

Keywords: CRISPR-Cas, GFP silencing, BW25113, BL21DE3

MM-3 (Oral)

Microbiology Applications in Forensic Sciences: A New Paradigm in Investigation

Neetu Sharma* and Jaskaran Singh **
*msneetumehta@gmail.com

**PhD scholar, Department of forensic science, Geeta University, Naultha, Panipat, India*
*** Head, School of Sciences, Geeta University, Naultha, Panipat, India*

Abstract: Biological fluids are the fluids which are present in living organisms. These fluids are sterile in nature or contain autochthonous microorganisms when present inside a living human being. Only in cases of infectious etiology, pathogens may be present in the body fluids. These fluids play an important role in criminal investigations. At times, when enough of physical evidences are not available, biological fluids contribute towards investigative leads. With the help of microorganisms growing in these fluids at different time intervals and different environmental conditions, leads about the time of death, place of death and cause of death can be interpreted. However if the biological fluids are not properly collected and preserved, they may undergo microbial degradation and render the sample useless. Hence, it is very crucial to know the state of biological fluid (Wet/Dry/Semidry) retrieved from crime scene so as the collection and preservation of such fluids can be made accordingly.

It has been observed that proper handling of biological fluid is must otherwise the evidential value and integrity of investigation may be challenged. As biological fluids are rich in nutrients, they attract various microfauna for predation leading to their degradation. In order to avoid such deterioration of forensic samples, biological fluids must be collected, preserved and packaged within specific timeline so that forensic microbiological aspects can be studied for investigation. In this systematic review, an attempt has been made to discuss various forensic cases where microbiological etiology can be utilised for investigations.

Keywords: Forensic Microbiology, Biological Fluids, Microorganisms, Forensic Investigation, Microbial degradation

MM-4 (Oral)

High-risk HPV testing vs Liquid-Based Cytology for Cervical Cancer Screening among Adult Women in Vadodara Region, Gujarat

Gunjan Shrivastava*
*gunjanshrivastava1986@gmail.com

Parul University, Gujrat, India

Abstract: Introduction- Cervical cancer prevention is enhanced by high-risk human papilloma virus (hrHPV) DNA testing, which is more sensitive than cytology screening. The best screening technique for women in their 25–30s is a topic of debate. HPV infection is prevalent and typically temporary at this age. Thus, there is a considerable risk of false-positive results from hrHPV screening in this age range, which could result in more colposcopies and potentially harmful therapies. In this study, our goal was to compare the outcomes of two screening techniques with respect to the rate of high-grade cervical intraepithelial lesion detection in young adults (30–60 years old). Cervical sample were collected using a spatula and endocervical brush and rinsed in a vial containing 20 ml of preserve cyto-liquid solution and sent for assessment. HPV genotyping was performed by commercially available kits with the help of RT-PCR. LBC (Liquid Based Cytology) was performed by using U-PREP system and interpreted as per standard clinical procedures. During the study period, 200 samples were collected & processed. Out of 200 samples, 17 (8.5%) were found positive, including 11 (64.7%) positive for LBC and 06 (35.29%) positive for HR-HPV; whereas only 02 (11.7%) were found positive for both cytology and HPV. In women aged 30–60 years old, primary hrHPV screening was associated with a higher detection rate of CIN 3+ compared with cytology screening and should be considered for primary screening in this age group.

Keywords: HPV (*Human Papilloma* Virus), LBC, VIA, Cervical Cancer.

MM-5 (Oral)

Impact of Mode of Delivery on the Quality and Quantity of Microbial Population Present in Human Colostrum

Riteshkumar Arya*[1] and Komalben Hirani[2]
*ritesharya43@rediffmail.com

Department of Microbiology, Mehsana Urban Institute of Sciences, Ganpat University, Mehsana, Gujarat, India.
Department of Microbiology, Shobhit Institute of Engineering & Technology (Deemed-to-be-University), Meerut, Uttar Pradesh. India.

Abstract: The first thick milk immediately produced after the delivery is called colostrum. It is very rich in all kinds of nutrients such as carbohydrates, proteins, vitamins, immunoglobulins and several minerals. Apart from this, it also contains several lactic acid bacteria which acts as probiotics in infant gut and have a major role in building up immunity in the initial days of life. There are several different factors responsible for the quality and quantity of these lactic acid bacteria in colostrum. Some of them are diet of the mother during pregnancy, hygiene of the lactating mother, mental stress level, physical activeness and most importantly the mode of delivery. With the development of various techniques in modern medical sciences, clinician's general prefers C-Section delivery for extra income whereas mother prefers it for facing less pain. The primary objective of our present study was to differentiate the quality and quantity of microbial population in human colostrum on the basis of their mode of delivery. The results of our study showed that mothers who delivered normally had greater amount of lactic acid bacteria (probiotics) in its colostrum composition whereas the mothers who delivered through C-Section has very less count of microbial population in its colostrum composition. The entire study will highlight the various impacts of mode of delivery on the quality and quantity of microbial population present in human colostrum.

Keywords: Human Colostrum, Lactic Acid Bacteria, Probiotics, Infant Health, C-Section delivery.

MM-6 (Oral)

Mycochemistry, Antioxidant, Anticancer activity and Molecular Docking of Compounds of F12 of Ethyl Acetate Extract of *Astraeus asiaticus* with BcL2 and Caspase 3

[1]***Koushik Pandey** and [2]Swapan Kumar Ghosh
*koushikpandeybiochemistry@gmail.com

[1]*Department of Paramedical and Allied Health Science, Midnapore City College, Midnapore (721129), West Bengal, India*
[2]*Molecular Mycopathology Lab., Biocontrol and Cancer Research Unit, PG Department of Botany, Ramakrishna Mission Vivekananda Centenary College (Autonomous), Rahara, Kolkata (700118), West Bengal, India*

Abstract: The current study focuses on anticancer/antitumor drugs derived from the partial purification of *Astraeus asiaticus* mushroom extract for the treatment of cervical, lung, and breast cancer. The fruit body was extracted in ethyl acetate solvent (AAEA) and quantitative analysis revealed that it contained a significant amount of total phenols, flavonoids, and ascorbic acids. The column chromatography of AAEA extract was performed and the F12 fraction demonstrated the greatest radical scavenging activity with an EC_{50} of 25.65 ± 4.82 µg. mL^{-1}. GC and mass spectrum analysis showed that F12 was a mixture of six important compounds like Hexadecanoic acid, 3,4,5,6 Tetramethyloctane, 9,12-Octadecadienoic acid, 9,12-Octadecadienoic acid, methyl ester, 1-cyclododecyne, cis-9,10-Epoxyoctadecan-1-ol. The chemical properties (Pharmacokinetic, toxicity, medical chemistry) of all six compounds were screened by SwissADME and Admet SAR predictors. Out of them Hexadecanoicacid, 9,12-Octadecadienoic acid and 3,4,5,6 Tetramethyloctane, exhibited suitable properties for drug preparation and they showed anticancer activity and antioxidant activity as per NIST database and library search. After 24 h of treatment, the percentages of cell growth inhibition of HeLa, MCF7, and A549 cell lines by highest concentration (1500 µg. mL-1) of F12 were 92.03 ±6.21 a, 90.38 ± 4.53a, and 87.51 ± 5.36a% respectively and the IC50 values were 701 ± 11.54,728.71 ± 10.53, and 806.88 ± 11.52 µg. mL^{-1}respectively.The mechanism of anticancerous effect of F12 on cancer cell lines included induction of apoptosis, LDH leakage, and up regulation of gene expression levels of Caspase 3, Caspase 9, P53, and down regulation of BcL2 of all three cell lines. Molecular docking studies revealed that there was satisfactory binding affinity of three compounds with Caspase 3 and they could potentially influenced the function of caspase-3, leading to apoptosis. In conclusion, the use of F12 of AAEA extract in cancer treatment will be a novel study for future drug development.

Keywords: Mycochemistry, GCMS, Cytotoxicity, Apoptosis, Gene expression, Molecular docking.

MM-7 (Oral)

Anti-oxidative Activity of Bioactive Peptides Produced from Pearl Millet Fermentation using *Lactobacillus* sp.

Meena Sindhu[1]*, Anil Panghal[2], Sushil Nagar[3] and Ajay Kumar[1]
meenasindhu20@gmail.com

[1]*Dept. of Microbiology, CCSHAU, Hisar, India*
[2]*Dept. of Processing & Food Engineering, CCSHAU, Hisar, India*
[3]*Dept. of Biochemistry, CCSHAU, Hisar, India*

Abstract: Bioactive peptides are low molecular weight protein fragments of 2–20 amino acid residues that benefit human health. During fermentation, microbial enzymes produced by starter culture release peptides from the precursor proteins. Pearl millet (*Pennisetum glaucum*) is a rich source of protein, used in the present study to isolate peptides and to evaluate their functional activity. The antioxidative bioactive peptides were isolated from fermented pearl millet (PMF) using *Lactobacillus* species. Increased protein content (11.6±0.42 to 15.3 ±0.38) was observed in PMF after fermenting with *L. plantarum and L. fermentum.* Pearl millet fermented with probiotic bacteria *L. fermentum* and *L. plantarum* displayed 34% and 32% of peptide content respectively, after 72 h. Electrophoretic separation revealed peptides of different sizes 36kDa, 45 kDa, 59 kDa along with bands of lesser than 27kDa. Maximum DPPH radical scavenging activity (64.58%) was observed in <5kDa peptides

produced during pearl millet fermentation using *Lactobacillus plantarum* followed by<5kDa peptides producedby *L. fermentum* (60.35%) fermented pearl-millet. Maximum ABTS radical scavenging ability (75.74%) was observed in <5kDa peptides produced during pearl millet fermentation using *Lactobacillus fermentum* followed by <5kDa peptides produced by*L. plantarum* (65.40%) fermented pearl-millet. Human lifestyle and pathological state may cause disproportion among free radicals and antioxidants, resulting in oxidative stress including diseases such as cancer and diabetes. These natural anti-oxidative peptides can be used as fermentative nutraceuticals to reduce oxidative damage among humans.

Keywords: *Lactobacillus*, Peptide, Anti-oxidative, Bioactive, Pearl millet, Fermentation

MM-8 (Oral)

Lytic-Lysogenic Switches Cross-Regulation in *Listeria monocytogenes* 10403S

Avijit Das[1]* and Anat A. Herskovits[1]
*ovijit.logy@gmail.com

[1]*The Shmunis School of Biomedicine and Cancer Research, The George S. Wise Life Sciences Faculty, Tel Aviv University, Ramat Aviv, Tel Aviv (69978), Israel*

Abstract: *Listeria monocytogenes* (*Lm*) is an intracellular bacterial pathogen infecting mammalian cells. *Lm* strain 10403S harbors an active prophage in its genome integrated within the *comK* gene. ϕ10403S temperate prophage is associated with *Lm* and is adapted to the pathogenic lifestyle of its host. In the lysogenic state, the phage is silently integrated in the bacterial chromosome as a prophage but can switch into lytic production in response to stress conditions. Notably, prophage excision does not lead to virion production and bacterial lysis in the mammalian environment, suggesting a cooperative phage behaviour. It was shown that the phage early genes are transcribed in the intracellular niche, whereas the late lytic genes are not, thereby preventing the progression of the lytic pathway. This type of adaptive phage behaviour was termed "active-lysogeny", representing cases where prophages cooperate with their hosts. Such an event needs to be balanced in the mammalian niche, as it can lead to the elimination of both the bacteria and the phage in the mammalian environment. This balance is controlled by the two master regulators CI- and Cro-like repressors. We have investigated the genome of *Lm* 10403S and found that the *Lm* genome does not only carry the prophage but also another cryptic phage element. In our studies, we aim to explore the cross-regulatory interactions between the two elements. These studies will provide molecular insights into the mechanism by which *Lm* controls the phage in the mammalian environment and further increase our understanding of how lysogenic phages interact with bacterial pathogens, information that might lead to a better design of phages for the use of phage therapy.

Keywords: *Listeria monocytogenes* (*Lm*), *comK,* CI- and Cro

MM-9 (Oral)

Assessment of Biofortified Compost from Agricultural Residue on Growth of Mungbean (*Vigna radiata* L.)

Kamla Malik* and Shikha Mehta
kamlamalik06@gmail.com

Department of Microbiology, College of Basic Science and Humanities
Chaudhary Charan Singh Haryana Agricultural University, Hisar (125004), Haryana, India

Abstract: Agricultural residues are composed of lignocellulose compounds that cannot be degraded easily. Their direct use causes immobilization of nutrients, so composting arises as a safe option, resulting in the reusability of nutrients contained in these residues. In the present investigation, paddy straw and sugarcane bagasse along with cattle dung and microbial consortia were used for composting. Bacteria were maximum in the mesophilic phase and the fungal count was in the thermophilic phase, while actinomycetes count was maximum in the maturation phase of composting in log (CFU/gm) in treatment (T6) followed by T9. Alkaline phosphatase, cellulase, dehydrogenase (DHA), Fpase and protease were maximum at 30 days of composting in

T6 followed by T9. Total nitrogen increased from 0.65 to 1.88%, same pattern was observed in total Phosphorous, Potassium followed by T9. The quality of compost was tested by as C:N ratio, CO_2 evolution, humic substances and germination index. The C/N ratio was also 22:1, with a pH of 7.4. Among the fortified treatments, T6+ Poultry showed OC-30.40%, C/N ratio-18.54, humic acid-142 mg/gm, Co2 evolution -101 mg per 100 gram of compost, germination index – 90 to 100% (for 100% leachate of compost extract) indicate it don't have any phytotoxic effect on seed germination. According to quality parametersAccording to quality parameters, T-9 served as a good source of nutrients to improve soil structure, enhance organic matter, promote microbial activity, and plant growth and yield of mungbean MH-421under field conditions.

Keywords: Paddy straw, Compost, Microbial consortia, Germination, Humic acid

MM-10 (Poster)

Microplastics in Human Urine Sample: Detection and Implications using Raman Spectroscopy

Suresh Subramanium[1], Sai Karthik[1], and **Nandhini Babu**[1*]
[*]bnandhinibabu@gmail.com

[1]*JSS Academy of Higher Education and Research, Ooty Campus*
[1*]*Assistant Professor, Division of Microbiology, JSS Academy of Higher Education and Research, Ooty Campus*

Abstract: The impact of micro plastics on human health is still an active area of study, research has demonstrated that humans can be exposed to micro plastics through ingestion, inhalation, and absorption through the skin. These particles have been found in various tissues and organs, including the digestive system, liver, kidneys, and even in the placenta of unborn babies. A study was conducted involving a group of individuals of different age groups. The study followed a specific protocol where urine samples were collected and diluted with 10% KOH in a ratio of 1:2 (sample: KOH). The mixture was placed in a glass flask, sealed with aluminium foil, and incubated at 40°C for 48 hours. After incubation, the samples were filtered using syringe membrane filters. The filter membranes were then allowed to dry at room temperature and analysed using Raman spectroscopy at a wavelength of 785 nm. The purpose of the Raman spectroscopy analysis was to identify the presence of Polyvinyl chloride (PVC), Polyethylene terephthalate (PET), and Polyethylene vinyl acetate (PEVA) polymers. To improve the quality of the spectra and reduce noise, baseline correction was performed on all raw Raman spectra. Micro plastics have emerged as a significant environmental concern, and there is increasing interest in understanding their potential impact on human health. Although studies indicate that humans are exposed to micro plastics and these particles can accumulate in various organs, the exact health consequences remain unclear.

Keywords: Micro plastics, Urine sample, Raman spectroscopy, Polyvinyl chloride, Polyethylene terephthalate, Polyethylene vinyl acetate polymers.

MM-11 (Poster)

Public Health Implications of Bacterial Zoonotic Infections from Pigeons in and Around the Nilgiris, Tamil Nadu, India

Nandhini. B, Susmitha S. and **Suresh.B**
sureshb@jssuni.edu.in

Division of Microbiology, JSS Academy of Higher Education and Research (Ooty campus), Longwood, the Nilgiris, Tamil Nadu, India

Abstract: Pigeon, belongs to the order *Columbiformes* and is a plump, rounded-bodied bird in the family *Columbidae*. There are 289 species in the family *Columbidae* globally, with 30 of them species being found in the Indian subcontinent. The present study was conducted to identify and characterize the zoonotic bacterial pathogens in pigeons and assess their potential to spread diseases to humans. This study at Longwood, The Nilgiris, reviled that the pigeons from both home and pet shop showed to harbor more of *E.coil* and

Staphylococcus aureus, then the other pathogens. There are chances of spreading diarrhaea, entrititis, urinary tract infection, skin infections and pyogenic infections to the handlers and the people living nearby. The fecal droppings are having a chance of causing food poisoning. Among the 4 different kinds of samples, the cloacal and foot pad carried most of the pathogens. The home and pet shop pigeons were carry the threatening MDR strains of *E.coli and staphylococcus aureus*. This may lead to the spread of zoonotic disease among the community living nearby. The bacteria *Enterobacter cloacae, Klebsiella pneumonia* and *Staphylococcus aureus* were found to transport from the pegions to handlers through the contact of feces and foot pad samples. *E. coil* isolates were 60% resistant towards Tetracyline and ampicilin and while sensitive to chloramphenicol was 90%. *Staphylococcus aureus* isolates were 48.4% resistant to Ampicillin and *Klebsiella spp.,* showed 100% resistant to tetracycline and amoxicillin.

Keywords: *Columbiformes, Columbidae, Staphylococcus aureus,* MDR, Chloramphenicol

MM-12 (Poster)

Effect of various therapeutic intervention on pulmonary function in individual with *kyphotic osteoporosis*- A systematic review

Kalindi Dev*
kalindiphysio@gmail.com

PhD, Assistant Prof., Dept. of Physiotherapy, GJUST, Hisar, India

Abstract:
Background: The excessive forward curvature of the thoracic spine, known as age-related hyper kyphosis, is a predictor of poor health outcomes and has been linked to challenges with physical function tasks. Acute osteoporosis-related pain episodes can cause periods of limited mobility and serious cardiac dysfunction in the elderly.
Objective: This study's goal is to evaluate the effect of various therapeutic intervention on pulmonary function in individual with kyphotic osteoporosis.
Methods: Following worldwide databases were searched for this systematic review: PubMed, Cochrane Library, and Google Scholar. The keywords "Kyphosis", "Osteoporosis" and "Respiratory function" are utilized. Title abstract phrases, related keywords, and Boolean operators ('OR' and 'AND') were all used in conjunction with the 'Advanced' search'. Duplicate records were eliminated from computerized systems using Mendeley Desktop software.
Result: Total 466 studies were found after doing an advance search in four databases: Google scholar, Cochrane Library, PubMed. Due to duplication, 259 records were eliminated using Mendeley Desktop software. The titles and abstracts of the remaining 207 studies were reviewed based on the eligibility criteria. Following the initial scanning, 104 records were rejected as not satisfying the inclusion requirements. The remaining 103 full-text papers were reviewed and from these articles, 97 articles were removed for the reasons. Total of 6 studies were included in the qualitative analysis.
Conclusion: Because of these results, the review conclude that exercises centred on the complete curvature of the spine can help adolescents with thoracic kyphosis by strengthening and improving the function of the back muscles and enhance pulmonary function.

Keywords: Kyphosis, osteoporosis, physical exercise, rehabilitation

MM-13 (Poster)

Understanding the role of Rv1954A in the Regulation and Activity of *higBA1* toxin-Antitoxin Locus of *Mycobacterium tuberculosis*

Sapna Yadav[1], Aparna Sharma[1], Nidhi Gupta[1], Vijay K. Chaudhary[2] and Amita Gupta[1,2]
aparnasharma@south.du.ac.in

[1]*Department of Biochemistry*
[2]*Center for Innovation in Infectious Disease Research Education and Training (CIIDRET), University of Delhi South Campus, New Delhi (110021), India*

Abstract: Toxin-antitoxin (TA) systems are widespread genetic modules in bacteria that are crucial for various cellular processes like Plasmid stabilization, stress response, persistence, phage resistance and Biofilm formation. They are usually composed of two elements: a stable toxin that inhibits an essential cellular process and an unstable antitoxin that neutralizes its cognate toxin. *Mycobacterium tuberculosis* harbors more than 90 TA systems in its genome and these play essential roles in the survival and pathogenesis of the pathogen in the human host.

TA systems are grouped into several families based on their sequence and structure similarity. To date, three loci belonging to the HigBA Type-II toxin-antitoxin family have been identified in *Mycobacterium tuberculosis*. These are Rv1955-Rv1956 (*higBA1*), Rv2022c-Rv2021c (*higBA2*) and Rv3182-Rv3183 (*higBA3*). Of these, HigBA1 is the most studied, and is a tripartite system, consisting of *higB1* toxin (Rv1955), *higA1* antitoxin (Rv1956) and a molecular chaperone (Rv1957). Another gene, Rv1954A, is present upstream to this tripartite system and also belongs to this operon. Rv1954A has an immunomodulatory role and induces immune response by enhancing TLR4-Mediated Production of Pro-inflammatory Cytokines in Macrophages. The *higBA1* operon has been shown to be upregulated in response to nutrient starvation and streptomycin treatment.

The expression of this *higBA1* operon is regulated by two distinct promoters: P1, located 51 nucleotides upstream of the start codon of HigB1, and P2, located 29 nucleotides upstream of the start codon of the upstream gene Rv1954A. Since Rv1954A is present between these two promoters of the *higBA1* locus, studies are underway to check its involvement in regulation of this operon and the data will be presented.

Keywords: *Mycobacterium tuberculosis,* Toxin-Antitoxin, Type-II HigBA locus, Operon, Promoters, Rv1954A

MM-14 (Poster)

Comparative Eevaluation of Unprocessed and Processed Amaranth Grains in Preventing High Fat Diet Induced Obesity and Gut Dysbiosis

Laxmi. K,[1,2] Bishnoi M,[1] and Kondepudi KK[1]*
lmehta492@gmail.com

[1]*National Agri-Food Biotechnology Institute, S.A.S Nagar, Punjab, 140306, India*
[2]*Department of Biotechnology, Panjab University, Chandigarh, India*

Abstract: Amaranth grain is a highly nutritious pseudocereal valued for its rich protein content of essential amino acids, making it an excellent plant-based protein source. Its high fiber content supports digestion, gut health, and blood sugar regulation, while its antioxidants help reduce inflammation and oxidative stress. This study examines the effects of unprocessed, roasted, and boiled amaranth grain supplementation on high-fat diet (HFD)-induced obesity and gut dysbiosis in C57BL/6J mice.

Mice were fed isocaloric diets supplemented with either unprocessed, roasted, or boiled amaranth at two doses (20% and 40% w/w) for 12 weeks. Body weight, adiposity, lipid profiles, liver health (histology), inflammatory markers, gut bacterial composition, and oxidative stress markers such as superoxide dismutase (SOD), catalase, and glutathione (GSH) were analyzed. HFD feeding increased the body weight, adiposity, adverse lipid profiles, liver inflammation, oxidative stress, and gut dysbiosis. Supplementation with unprocessed and processed amaranth grains prevented these harmful effects, with higher doses showing stronger protective outcomes.

Gut bacterial analysis revealed that amaranth consumption increased beneficial bacteria and reduced the firmicutes-to-bacteroidetes ratio, an obesity marker. The effects were more pronounced at higher doses. Both unprocessed and processed amaranth improved oxidative stress markers, significantly enhancing SOD, catalase,

and GSH activities, indicating higher protective effects. The study concluded that unprocessed amaranth was most effective in reducing obesity, improving liver health, and correcting gut dysbiosis and oxidative stress, followed by roasted amaranth.

Keywords: Pseudocereal, Antioxidants, Superoxide dismutase (SOD), Catalase, Glutathione (GSH)

MM-15 (Poster)

Antimicrobial Activity of L- Asparaginase Producing Fungi

Rani Nisha[1] and Jain Pranay[2*]
[*]pjain2015@kuk.ac.in

[1]*Ph.D. Scholar, Department of Biotechnology, University Institute of Engineering and Technology, Kurukshetra University, Kurukshetra (136119), Haryana, India.*
[2]*Associate Professor, Department of Biotechnology, University Institute of Engineering and Technology, Kurukshetra University, Kurukshetra (136119), Haryana, India.*

Abstract: Twelve fungi were isolated from the rhizo-spheric soil of the two medicinal plants namely *Epipremnum aureum* (Money plant) and *Rauwalfia serpentine* (Sarpagandha). The most commonly found species were *Aspergillus, Penicillium, Alternaria, Rhizopus, Fusarium, Mucor*. All of the isolated fungi were tested for their antimicrobial activity and L- asparaginase enzyme production. There were two test microorganisms were taken for screening of fungi. Out of which, only two fungal isolates show antimicrobial activity against both of the test microorganisms namely *Escherichia coli* and *Staphylococcus aureus*. Only these two fungal isolates also show L- asparaginase activity. The fungal isolates are belongs to *Fusarium* and *Rhizopus* species. This study indicates that the isolated fungi from rhizosphere of the medicinal plants are the potential source of antimicrobial and anticancer agents.

Keywords: Anti-microbial, L- asparaginase, Fungi, Rhizosphere, Medicinal plant

MM-16 (Poster)

Isolation, Characterization and Bioactive Potential of *Micromonospora sp.* from the Cold Desert

Neha Sharma[a,b], Devtulya Chander[a,b], Ravi S. Manhas[a] and Asha Chaubey[a,b$]
achaubey@iiim.res.in

[a]*Fermentation and Microbial Biotechnology Division, CSIR-Indian Institute of Integrative Medicine, Jammu (180001), India*
[b]*Academy of Scientific and Innovative Research, CSIR-Human Resource Development Centre, (CSIR-HRDC) Campus Ghaziabad (201002), India*

Abstract: The widespread antibiotic resistance among bacteria leads to millions of deaths annually. The most serious problem is the ever-increasing number of bacteria developing resistance to commonly used antibiotics, including those considered drugs of last resort. There is a need of the hour to combat these multidrug-resistant bugs. The present work reports a rare actinobacterium isolated from the soil sample using chemical treatment (phenol) from the cold desert of Ladakh in the North-Western Himalayan region of India (34.43°N; 75.751552°E). Polyphasic strategies, including both biochemical and molecular characterization, were employed to determine the taxonomic position of the strain. The strain displayed characteristic features of the genus *Micromonospora*, specifically rod-shaped elements arising from branching substrate hyphae with punctiform colonies. The 16S rRNA gene sequence showed a 99.08% similarity to *Micromonospora palomenae*. Post fermentation the crude extract obtained from the isolate displayed activity against gram-positive bacteria *Staphylococcus aureus*, Methicillin-resistant *Staphylococcus aureus*, and cancer cell lines HCT 116 & MCF-7.

Keywords: Northwestern Himalayas, Multidrug-resistant, Polyphasic, *Micromonospora,* Antimicrobial activity

MM-17 (Poster)

Functional Characterization of Ebfc/ YbaB, a Nucleoid Associated Protein (NAP) in *Escherichia coli*

Shakkhar Saha[1], Parul Pal[2] and Richa Priyadarshini[1*]
[*]richa.priyadarshini@snu.edu.in

[1]*Department of Life Sciences, School of Natural Sciences, Shiv Nadar Institution of Eminence, Gautam Buddha Nagar (201314), Uttar Pradesh*
[2]*Department of Molecular Microbiology, John Innes Centre, Norwich Research Park, Norwich, United Kingdom*

Abstract: Nucleoid-Associated Proteins (NAPs) are small, abundant, basic, low molecular weight DNA-binding proteins present in bacteria that are essential for maintaining the dynamic structure of the nucleoid and genome compaction. They also influence DNA transactions such as replication, transcription, and recombination by altering DNA topology (bending, wrapping, coating, bridging) thereby regulating gene expression. EbfC is an important NAP initially identified in *Borrelia burgdorferi*, plays a crucial role in virulence of the Lyme disease. YbaB, an ortholog of EbfC found in many bacteria including *Escherichia. coli*, *Haemophilus influenzae*, and *Caulobacter crescentus*. Ebfc/YbaB family NAP has a unique tweezer-like structure and binds DNA primarily as a homodimer. Although the Ebfc/YbaB homologs are well conserved across all eubacterial species the physiological role of YbaB in *E. coli* is yet uncharacterized. In this study, we functionally characterized YbaB in *E. coli*. $YbaB_{Ec}$ protects DNA from enzymatic degradation and plays a significant role in surviving cold stress conditions. Unlike EbfC in *B. burgdorferi*, $YbaB_{Ec}$ binds to DNA in sequence independent manner observed during EMSA experiments. The *ybaB* knockout strain of *E.coli* is fitness compromised in antibiotic stress. Overall, $YbaB_{Ec}$ plays a significant role in bacterial stress responses.

Keywords: Nucleoid-Associated Proteins (NAPs), *Borrelia burgdorferiv,* $YbaB_{Ec,}$ EbfC

MM-18 (Poster)

In vivo Acute Toxicity Assessment of Enterocin LD3 Purified from Food-Grade *Enterococcus hirae* LD3 in Mice Model

Pallvi Sharma and Santosh Kumar Tiwari*
*santoshgeneticsmdurohtak.ac.in

Department of Genetics, Maharshi Dayanand University, Rohtak (124001), India

Abstract: Enterocin LD3 is a cationic peptide purified from *Enterococcus hirae* LD3 previously isolated from Dosa batter. Enterocin LD3 displayed antimicrobial activity against broad-range of bacteria such as *M. luteus*, *E. coli*, *Enterobacter cloaceae*, *P. aeruginosa*, *Staphylococcus aureus*, *Salmonella typhi,Vibrio* sp., *E. faecalis* and *Proteus mirabilis,* indicating its potential clinical applications as antibiotics. The present study was conducted to investigate the *in vivo* toxicity of enterocin LD3 in mice model to understand its biosafety level. Male Swiss albino mice received intraperitoneal administration of enterocin LD3 for the acute toxicity assessment. It was observed that no mortality or infections noticed during the experiments. In addition, there were no noticeable alterations observed in serum biochemical markers and histopathological analysis. These findings demonstrate that enterocin LD3 is a safe and non-toxic bacteriocin, indicating its potential for the use in therapeutics as an alternative to clinical antibiotics.

Keywords: Acute Toxicity, Bacteriocins, Non-toxic, Mice model, Antimicrobial

MM-19 (Poster)

Studies on the Epitranscriptomic Regulation of Foot-nd-Mouth Disease Virus Replication

Raja Kumar[#a,b], Riyesh Thachamvally[a], Naveen Kumar[a*]
naveenkumar.icar@gmail.com

[a] *National Centre for Veterinary Types Cultures, ICAR-National Research Centre on Equines, Hisar, Haryana, India*
[b] *Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana, India*

Abstract: Foot-and-mouth disease (FMD) is a highly contagious disease of cloven-hoofed animals, caused by an *Apthovirus* that belongs to the family *Picornaviridae.* FMDV has a broad host range including cattle, pigs, sheep, goats, buffaloes and wild animals. The clinical symptoms of FMD include fever, lameness and vesicular lesions on the feet, tongue and teats. FMDV spreads from animal-to-animal by aerosol. Besides direct production losses, FMD indirectly affects international trade of animals and animal products. In order to generate herd immunity, ~500 million animals need to be vaccinated twice a year as the protective immunity of FMD vaccine lasts only for 6 months. The vaccines cannot provide protection during the time that bridge vaccination and induction of protective immunity (~21 days). An alternative method to control the spread of FMDV transmission during outbreaks is the application of antiviral agents. However, most of the currently available antiviral agents are based on viral targets, repeated use of which leads to the emergence of drug-resistant virus variants due to mutations at the druggable sites. This necessitates the development of appropriate host-directed antiviral agents that do not tend to easily induce drug resistance due to pre-existing selection pressure. In a study conducted at NCVTC, NRCE, Hisar, it was observed that at a non-cytotoxic concentration, EZH2 inhibitor UNC1999 suppresses FMDV replication. Enhancer of zeste homolog 2 (EZH2) is enzymatic catalytic subunit of polycomb repressive complex 2 (PRC2). By using the cofactor SAM, EZH2 catalyzes the addition of methyl groups to histone H3 at lysine 27. FMDV progressively induces the trimethylation of lysine at 27th position in histone H3. This suggests that methylation machinery regulates FMDV replication, and therefore, may be targeted for development of antiviral therapeutics against FMD.

Keywords: FMD, FMDV, Host-directed antiviral, UNC1999, EZH2, H3K27

MM-20 (Poster)

Metaproteomics Characterizes Human Gut Microbiome Function in Ulcerative Colitis

Asha Yadav[1], Pratik Balwant Shinde[1] and Krishna Kant Sharma[1]*
kekulsharma@gmail.com; kksharma.microbiology@mdurohtak.ac.in

[1]*Laboratory of Enzymology and Gut microbiology, Department of Microbiology, Maharshi Dayanand University, Rohtak (124001), Haryana, India.*
**Department of Microbiology, Maharshi Dayanand University, Rohtak (124001), Haryana, India*

Abstract: Ulcerative colitis (UC) is a chronic inflammatory bowel disease (IBD) characterized by remitting and relapsing episodes of colon mucosa. UC pathogenesis starts in the rectum and gradually extends throughout the colon. The objective of the current study was to characterize the changes in protein expression in the host and microbiome as a consequence of UC severity, and understand the host-microbiota communication in terms of synergistic and differential expression. The fecal samples were collected from healthy control (HC) and UC patients for LCMS-MS analysis revealed the presence of 2072 microbial proteins and 243 human proteins. Proteomic analysis revealed increase in proteins for pentose phosphate pathway in UC; whereas, decrease in proteins related to energy metabolism (carbon and nitrogen metabolism), nucleotide metabolism, transmembrane transporters and membrane proteins, RNA binding, and protein folding. Interestingly, significant over-expression of proteins related to iron metabolism and oxidative stress indicates an oxidative gut environment that favors the growth of pathogenic microbes, enteric infections, and intestinal damage. Over-expression of host proteins such as neutrophil defensin 3, protein S100-A9, lactotransferrin, neutrophil elastase, azurocidin, protein S100-A8, and cathepsin G further indicate inflammation, architectural damage, and microbial infection in UC gut. Further, an effort has been made to discover vital hub genes (LTF, PO, TSG,

AZU1 and RETN) and proteins, which can contributes in identifying potential diagnostic or therapeutic biomarkers for UC. The identified proteins have linked function and show association with UC pathogenesis thus they may help to build foundation for the development of targeted therapy for UC treatment.

Keywords: Gut, human, Ulcerative colitis, Meta-proteome, Microbiome, LCMS-MS

MM-21 (Poster)

A Comparative Study on Mycolic Acid Quantification from Various Mycobacterial Strains for Developing Differential Diagnosis and Treatment Strategies

Zeeshan Fatima[1#] , **Meenakshi Chugh[1,2#],** Gaurav Nigam[1] and Saif Hameed[1]
zfatima@ggn.amity.edu

[1]*Amity Institute of Biotechnology, Amity University Haryana, Gurugram, Manesar (122413), India.*
[2]*Amity Medical School, Amity University Haryana, Gurugram, Manesar (122413), India.*

Abstract: Mycobacterium tuberculosis (MTB), the primary cause of tuberculosis (TB), continues to be a significant global health issue, ranking as the second most lethal single infectious agent after COVID-19. The rise of multidrug-resistant TB exacerbates the problem, necessitating more intricate and extended treatment protocols and underscoring the need for improved worldwide initiatives to combat, identify, and treat this persistent epidemic. Mycolic acids (MAs), distinctive lipids found in mycobacteria's dense, lipid-rich cell wall, influence their pathogenicity and drug resistance. MAs are crucial in TB diagnosis due to their species-specific variations, structural diversity, and immunogenic properties. These distinct MA profiles offer valuable information for developing species-specific diagnostic tools and treatment strategies. The analysis and quantification of MAs molecular species using advanced liquid chromatography-mass spectrometry (LCMS) has become an important technique for understanding mycobacterial diversity and developing targeted diagnostic approaches. Statistical analysis through comparative lipidomics enables comprehensive, organism-wide evaluations of lipid alterations among different mycobacterial strains. In this study, we have developed a method using the reversed-phase ultra-high-performance liquid chromatography-high resolution mass spectrometry with the standard addition method employed to identify and quantify the MAs molecular species. Additionally, to validate the developed method we have compared the MAs molecular species such as alpha, methoxy, and keto-MAs with C-24 and C-26 hydrocarbon chains in five strains i.e. Mycobacterium bovis (BCG), Mycobacterium tuberculosis avirulent (H37R a) , Mycobacterium marinum (M. mar), Mycobacterium smegmatis (M. smeg), and Mycobacterium tuberculosis (MTB). This is the first study that quantified and compared the MAs molecular species in different mycobacterial strains. Taken together, we established a reliable and sensitive UPLC-MS/MS method for the simultaneous identification and quantification of MA molecular species in pathogenic and non-pathogenic mycobacterial strains. Overall, this study lays the groundwork for further exploration of MA as a diagnostic biomarker for future medical research and diagnostics related to mycobacterial infections.

Keywords: Tuberculosis, Mycolic acid, Standard addition method, LCMS, *Mycobacterium tuberculosis*, Lipidomics

MM-22 (Poster)

Mycobacteriophages as Therapeutic Agents to treat Drug-Resistant Tubercular and Non-Tubercular Mycobacterial (NTM) Infections

Kanika Nadar, Ritu Arora and Urmi Bajpai*
nadarkanika@gmail.com

Department of Biomedical Science, Acharya Narendra Dev College, University of Delhi, New Delhi, India

Abstract: Tuberculosis (TB) is the second leading cause of death from a single infectious agent globally. The number of new cases of TB per 100,000 people annually has grown by 3.9% between 2020 and 2022. While

active TB disease is curable, the occurrence of bacterial resistance to drugs has become a serious threat to public health. With the global burden of MDR-TB increasing by more than 20% per year over the past several years, drug-resistant TB is estimated to kill 75 million people over the next 35 years, emphasizing the need to develop new alternative anti-tuberculosis therapies (*Global TB Report, 2023*).
With the fast-growing antibiotic resistance crisis, a renewed interest in phages and phage-encoded lysins as an alternative approach is being observed. Mycobacteriophages are genetically diverse viruses that infect mycobacterial hosts, including members from *M. tuberculosis* complex and non-tubercular mycobacterial (NTM) hosts. Mycobacteriophages and the derived lytic enzymes can be explored as non-antibiotic strategies to treat drug-resistant TB and NTM infections, which could shorten the treatment regimen when given with antibiotics. Endolysins are the enzymes bacteriophages use to release their progeny from the bacterial host. Mycobacteriophages encode LysinA and LysinB, which target the peptidoglycan and ester bonds (linking arabinogalactan with the myco-membrane) in the mycobacterial cell wall, respectively. Here we are presenting key characterisitics of mycobacteriophages and encoded endolysins we have isolated and purified from local environment.

Keywords: Antibiotic Resistance, Tuberculosis, Non-Tubercular Mycobacteria, Mycobacteriophages, Endolysins

MM-23 (Poster)

Exploring the Role of Vaginal Microbiome Composition in Idiopathic Infertility

Chitrakshi Chopra[1], Vinay Kumar[2] and Indu Bhushan[1*]
20dbt001@smvdu.ac.in

[1]*School of Biotechnology, Shri Mata Vaishno Devi University, Katra (182320), India*
[2]*Department of Gynecology, Government Medical College, Jammu (180001), India*

Abstract: The underlying causes of idiopathic infertility remain unclear, but microbial factors may play a role. The aim of the present study was to analyze the disparity in the composition of the vaginal microbiome among women experiencing idiopathic infertility and those who have given birth to healthy full-term infants. The study involved 80 female participants among which two cohorts of women were selected: the first cohort of healthy women (n=40) who had a previous term delivery and the second cohort of women (n=40) with an unknown cause of infertility. The diversity and abundance of microbial populations were analyzed using a taxonomic approach. The findings of the study revealed discernible distinctions between infertile women and healthy women who had experienced uncomplicated childbirth in the past. Variations were observed in both alpha and beta diversity, as well as in taxonomic composition. Infertile women exhibited higher levels of *Gardnerella, Prevotella, Atopobium, Sneathia,* and *Enterococcus*, whereas fertile women had a higher abundance of *Lactobacillus iners*. The study suggests that the composition of the vaginal microbiome may significantly influence idiopathic infertility in women.

Keywords: Vaginal microbiome, Idiopathic infertility, *Lactobacillus*

MM-24 (Poster)

Biopolymeric Nano-Formulation of Arginine Deiminase for Targeted Cancer Therapy

Anubhuti Kawatra[a#] and Pooja Gulati[a]*
gulatipooja1@gmail.com, pooja.micro@mdurohtak.ac.in

[a] *Medical Microbiology and Bioprocess Technology Laboratory, Department of Microbiology, Maharshi Dayanand University, Rohtak, Haryana, India*
[*]*Medical Microbiology and Bioprocess Technology Laboratory, Department of Microbiology, Maharshi Dayanand University, Rohtak, Haryana, India*

Abstract: Cancer accounts for one of the most prominent causes of death worldwide. Conventional chemotherapeutics such as cisplatin, paclitaxel, doxorubicin, etc., cannot selectively target cancers. In this context, arginine deiminase (ADI, EC 3.5.3.6) has appeared as a potent biological intervention for the targeted

treatment of cancer. The rapid growth of the cancerous cells results in auxotrophy for amino acids like L-arginine. These arginine auxotrophic cancers are specifically targeted by the amino acid-depleting enzyme ADI, leading to their regression. Presently, a PEGylated formulation of this enzyme in clinical trials has shown limitations like systemic toxicity, reduced permeability, and anti-PEG antibody formation. Nanocarrier-based enzyme immobilization is an intriguing strategy to overcome these bottlenecks. The biopolymeric nano-enzyme conjugates like chitin, chitosan, polylactic glycolic acid systems (PLGA), etc. with large surface areas, non-toxic nature, and controllable morphology have been developed to improve the pharmacokinetics of enzymes. In the present study, PLGA (an FDA-approved biopolymer) was used for improved efficacy, permeability, and stability of ADI in cancer therapy. ADI was cross-linked with glutaraldehyde and nanoprecipitation was employed to encapsulate this immobilized ADI in PLGA nanoparticles for enhanced activity retention. Structural characterization using DLS/ZETA, TEM, and FT-IR indicated the monodisperse, and highly stable nature of PLGA-ADI NPs. The resulting nanoformulation exhibited higher pH resistivity and denaturant tolerance than free ADI. Storage stability assay also showed that PLGA-ADI NPs remained highly active for over 70 days. Therefore, these biopolymeric enzyme aggregates present a novel and efficient approach for establishing ADI as an alternative or combinational nanomedicine in cancer treatment.

Keywords: Arginine deiminase, ADI, PLGA, Nanoformulation, Cancer therapy.

MM-25 (Poster)

Exploration of Bioactive Compounds from Mushroom Species: A Step towards Novel Therapeutics

Shreya
shreyachahal57@gmail.com

Department of Biotechnology, DCRUST, Sonipat, India

Abstract: Mushrooms have moved in the forefront to sustain the extractable bioactive metabolites which may provide therapeutic benefits. The present study aims at extraction of biologically active compounds from number of mushrooms and seeks to determine their activity. By employing modern extraction methods, we extracted a series of compounds from various species of medicinal cultivated mushrooms.
With an addition of mild optimization strategies that involve solvent extraction using probe sonicator and microwave assisted extraction techniques, we were able to obtain various bioactive fractions that were rich in diverse antioxidants, antimicrobials and putative antivirals. Results from the initial screening indicate that some of the fractions which were pure had good antioxidant properties with regards to commercially available standards, giving reasons for the pursuit of such compounds in the fight against diseases associated with oxidative stress. In addition, some of the extracts showed strong activity against pathogenic bacteria and fungal strains which suggest these extracts could be good templates for design of natural antimicrobials.
This work provides a basis for future efforts to describe these extracts and assess their biological activities to a specific class of bioactive compounds. We do a significant 'first step' in the 'fairly long' and 'quite individualistic' process of isolation of active principles from natural raw materials, such as mushrooms, and their subsequent pharmacological evaluation. All of all importance emphasizes on the need for exploiting fungal diversity for novel compound discoveries.

Keywords: Sonicator, Microwave, Antioxidants, Antimicrobials and Putative antivirals

MM-26 (Poster)

Bacteriocins as Anti-Microbial against Uropathogens

Shaoni Ghosh
dearshaoni@gmail.com

Raiganj University, Raigarh, India

Abstract: Bacteriocins, a diverse group of ribosomally synthesized antimicrobial peptides produced by bacteria, have gained significant attention as potent agents against uropathogens. These naturally occurring peptides offer

a promising alternative to conventional antibiotics, particularly in treating urinary tract infections (UTIs), which are often caused by drug-resistant bacteria. This presentation explores the mechanisms by which bacteriocins exert their antimicrobial effects, including membrane disruption and inhibition of essential cellular processes in target pathogens. We will focus on the potential of bacteriocins to combat common uropathogens, such as *Escherichia coli*, *Klebsiella pneumoniae*, and *Streptococcus sp*. Additionally, the presentation highlights the advantages of bacteriocins, such as their narrow spectrum of activity, which reduces the impact on beneficial microbiota, and their ability to inhibit multi-drug-resistant strains. Through an examination of recent research and clinical studies, we will discuss the feasibility of incorporating bacteriocins into therapeutic strategies for UTIs, addressing both their benefits and the challenges associated with their use. Ultimately, this presentation aims to underscore the potential of bacteriocins as a viable antimicrobial solution in the ongoing battle against uropathogens and antibiotic resistance.

Keywords: Bacteriocin, Uropathogens, Antimicrobial effects, *Escherichia coli*, *Klebsiella pneumoniae*, *Streptococcus sp*.

MM-27 (Poster)

Genomic Insights into COVID-19-Associated Fungal Infections in India

Tanushree Saini[1,2], Pawan Kumar[1,2], Renu Chaudhary[1], Himani Singh[1,2], Shukla Das[3], Susan KS[4], Sushil K Chumber[4], Yukti Sharma[4] and Bhupesh Taneja[1,2]
rajtanushree14@gmail.com

[1]*CSIR-Institute of Genomics and Integrative Biology (CSIR-IGIB), New Delhi-110025, India*
[2]*Academy of Scientific and Innovative Research (AcSIR), Ghaziabad-201002, India*
[3]*Department of Microbiology, UCMS & GTB Hospital, Dilshad Garden, Delhi 110095, India*
[4]*St. Stephen's Hospital, Delhi, India*

Abstract: The emergence of the SARS-CoV-2 global pandemic led to a surge in secondary infections, particularly covid-19 associated fungal infections (or CAFI) such as aspergillosis, candidiasis, and mucormycosis, among COVID-19 patients in India. The heavy use of immunosuppressive therapies and antibiotics further exacerbated the problem, including factors such as prolonged hospitalization, corticosteroid therapy, and ventilation support. The surge in CAFI highlighted the lack of information regarding the molecular epidemiology and evolutionary trends of mucorales and other fungal pathogens in India. Bridging these knowledge gaps, our study analyzed the phylogenomic characteristics of mucormycotic strains prevalent in India, through whole-genome sequencing of the clinical isolates. Whole genome relatedness was assessed using ANI (Average nucleotide identity). Further, the SNP-based phylogeny was carried out using the ParSNP tool. This analysis allowed us to identify the species-specific clusters among CAFI pathogenic strains. The antifungal susceptibility test was also carried out to evaluate the in vitro efficacy of available antifungal agents against these pathogens and to understand their response profiles better. The findings of this study hold significant implications for public health, providing valuable insights into the molecular complexities of SARS-CoV-2-associated fungal infections, particularly mucormycosis.

Keywords: Mucormycosis, WGS (whole genome sequencing), SNP-based phylogeny, Phylogenomic analysis, ANI (Average nucleotide Identity), Antifungal susceptibility test (AFST)

MM-28 (Poster)

Response Surface Methodology (RSM) Mediated Optimization of Recombinant Griffithsin (Rgrft) Expression, a Highly Effective Lectin for HIV Prevention

K Haritha[a, b] and Rachna Agarwal[a, b]
rachna@barc.gov.in

[a] *Homi Bhabha National Institute, Anushakti Nagar, Mumbai (400094), India*
[b] *Bhabha Atomic Research Centre, Mumbai (400085), India*

Abstract: Entry level inhibition of the human immunodeficiency virus (HIV) into host cells is a crucial step in preventing the viral infection. Griffithsin (GRFT), a red alga derived lectin, is one of the most potent inhibitors of HIV entry discovered till date. Although GRFT has been produced using a variety of recombinant systems such as bacteria and plants, the absence of an efficient and cost-effective production platform has limited its widespread application. As the prokaryotic *E. coli*-based systems remain most amenable to the genetic tools and there are newer *E. coli* strains available with better protein expression and folding capacities, the aim of the present study was to optimize the expression of recombinant rGRFT in *E. coli*. Four significant culture conditions i.e., cell density prior to induction (OD_{600nm}), IPTG concentration (mM), induction temperature (°C) and induction time (h) were optimization using traditional "One Factor At A Time (OFAT)" method and then subjected to statistical optimization using "Response Surface Methodology based Central Composite Design (RSM-CCD)" for maximum protein production. The OFAT showed that the optimum condition for obtaining maximum rGRFT expression was an OD_{600} at the time of induction of 0.6 and induction with 0.025 mM IPTG concentration at a temperature of 20 °C for 20 h duration. ANOVA analysis confirmed that the quadratic model adequately represented the process and was significant for all responses ($p < 0.0001$). The over-expressed rGRFT was purified by affinity chromatography and characterised further. The purified protein showed single band on SDS-PAGE, multiple bands on native-PAGE, and monomeric mass of ~ 14.696 kDa by ESI-LC-MS. The purified rGRFT interacted with both HIV-gp120 and COVID-19 spike protein as seen through ELISA and also exhibited significant anti-HIV activity (IC_{50}~ 0.25nM) with a minimal cytotoxicity up to 15 µM.

Keywords: Anti-HIV, Griffithsin, Lectin, Response surface methodology

MM-29 (Poster)

Evaluating the Role of Zinc In Growth and Stress Response of Pathogenic *Mucorales*: Plausible Association of Zinc Supplementation with Emergence of Covid-19 Associated Mucormycosis

Jasdeep Kaur, Anjna Kumari and Rachna Singh*
*rachna.singh@pu.ac.in

Department of Microbial Biotechnology, Panjab University, Chandigarh (160014), India

Abstract: Mucormycosis is an opportunistic, rapidly progressing, angioinvasive disease caused by ubiquitous environmental moulds belonging to the class Zygomycetes and order *Mucorales*. The global incidence of this disease has risen significantly in recent decades, especially in developing countries like India. This increase was worsened by a rise in mucormycosis cases during the Covid-19 pandemic, prompting the classification of Covid-19 associated mucormycosis (CAM) as a notifiable disease. Several hypotheses were proposed to explain the unprecedented surge of CAM cases. One of the widely discussed hypothesis was that zinc supplementation used for COVID-19 management triggered the growth of *Mucorales*, causing CAM. As mechanistic studies investigating this hypothesis are lacking, the present study aimed to evaluate the role of zinc in the growth and stress response of pathogenic *Mucorales*, with an emphasis on *Rhizopus arrhizus*, which is the predominant causative agent of mucormycosis. The effect of varying concentrations of zinc on *R. arrhizus* radial growth, spore germination, metabolic activity, and mycelial dry weight; response to pH, cell wall, oxidative and osmotic stress; biofilm formation, along with antifungal susceptibility was elucidated. Additionally, RNA sequencing was performed to determine the effect of zinc enrichment on *R. arrhizus* gene expression. The results suggested that zinc supported *R. arrhizus* growthin pH and dose-dependent manner, with elevated levels of zinc leading to profused fungal growth, especially under less favourable conditions. Similar resultswere noted in other mucoralean fungi but not in *Aspergillus* and *Candida*. Although zinc did not particularly impact the spore

germination and metabolic activity, it promoted prolonged fungal growth. Zinc availability partly alleviated cell wall stress but did not mitigate oxidative and osmotic stress. Antifungal susceptibility remained unaffected. One notable observation across all assays was the morphological alteration of *R. arrhizus* in response to increasing zinc concentration.

Keywords: Zygomycetes, *Mucorales*, Mucormycosis (CAM), COVID-19, *Rhizopus arrhizus*

MM-30 (Poster)

Endophytic Fungal Diversity in Mangrove Ecosystems of Raigadh District

Neeraj Pandey* and Livleen Shukla*
*pandeyneeraj211@gmail.com

**Division of Microbiology, ICAR- Indian Agricultural Research Institute, India*

Absract: Endophytic fungi are microorganisms that live within plant tissues, establishing intricate and often symbiotic relationships with their host plants. These fungi have garnered significant attention due to their potential as sources of chemically diverse bioactive compounds, including antioxidants, antimicrobials, and anticancer agents. The presence of endophytic fungi within plant tissues contributes to enhanced plant resilience, as they can influence gene expression, modulate biosynthetic pathways, and help plants cope with various environmental stresses. This symbiotic association not only strengthens the plant's innate defense mechanisms but also aids in protecting the plant against a wide array of potential pathogens, enhancing overall plant health and productivity.

The focus of our study is on exploring the diversity of endophytic fungi in the mangrove forests of the Raigad district in Maharashtra. Mangroves are unique ecosystems that provide a distinctive environment for microbial diversity, and the endophytic fungi associated with these plants are expected to exhibit unique characteristics compared to those in other ecosystems. By investigating the fungal populations in this specific region, our research aims to uncover how the diversity of these fungi in Raigad's mangrove forests compares to that of other mangrove forests. This comparison could provide insights into regional variations in fungal communities, potentially influenced by factors such as local environmental conditions, plant species diversity, and ecological interactions. Understanding these differences not only enriches our knowledge of fungal biodiversity but also highlights the ecological significance of endophytic fungi in mangrove ecosystems, paving the way for discovering new bioactive compounds with potential applications in various industries.

Keywords: Endophytic fungi, Mangrove forest, Secondary metabolite

MM-31 (Poster)

Plasmid-Mediated Bacteriocin Production by *Enterococcus Hirae* LD3 Isolated from Fermented Food, *Dosa*

Indu Kumari and Santosh Kumar Tiwari
indu.mehra183@gmail.com

Department of Genetics, Maharshi Dayanand University, Rohtak (124001), Haryana, India.

Abstract: *Enterococcus hirae* LD3, previously isolated from fermented *Dosa*batter, produces a new enterocin inhibiting broad-range of bacteria using pore formation, DNA degradation and efflux of ions (Yadav et al., 2019). *E. hirae* LD3 was found to be sensitive to ampicillin, chloramphenicol, erythromycin and tetracycline whereas resistant to gentamycin, kanamycin and streptomycin. Plasmid curing was performed using acriflavine, ethidium bromide, proflavine and sodium dodecyl sulfate (SDS). It was observed that plasmid with > 10 kb was found in wild type which was absent in cured strains. The plasmid cured strains showed 8 mm (acriflavine treated), 9 mm (ethidium bromide treated) and 10 mm (SDS treated) zone of growth inhibition which was lower than wild-type strain LD3 (19 mm) against *Micrococcus luteus* MTCC106. These findings suggest that the bacteriocin gene may be present on plasmid as well as on chromosome.

Keywords: *Enterococcus hirae*, Plasmid curing, Antibiotics, Ethidium bromide

MM-32 (Poster)

Ameliorative Effects of Exopolysaccharides from Endophytic Fungi on Arsenic-Induced Hepatotoxicity in Wistar Rats

[1,2,3]Sangita Saha, [2,3]Sandip Chattopadhyay[1,3] and Debdulal Banerjee*
db@mail.vidyasagar.ac.in

[1]*Microbiology and Microbial Biotechnology Laboratory, Department of Botany and Forestry*
[2]*Biomedical Laboratory Science and Management, India*
[3]*Centre for Life Sciences, Vidyasagar University, Midnapore (721102), India*

Abstract: Endophytic fungi reside asymptomatically within plant tissues, producing secondary metabolites with pharmaceutical potential. This study investigated the effects of exopolysaccharides (EPS) from *Diaporthe arengae* (CleR1), an endophytic fungal isolate from *Clerodendrum infortunatum* (Cle), on arsenic-induced (As^{3+}) metabolic toxicity in female Wistar rats. GC-MS analysis confirmed the presence of hydroxymethyl furfural, while FTIR spectroscopy indicated the potential chelation properties of EPS towards As(III). In liver tissues, EPS demonstrated significant radical scavenging effects and improved antioxidant parameters, including superoxide dismutase (SOD), catalase (CAT), glutathione peroxidase (GPx), and decreased levels of malondialdehyde (MDA). An electrophoretic zymographic approach was used to measure the activities of these enzymes in the liver tissues of both treated and control rats. Results showed that EPS significantly mitigated As^{3+}-induced hepatic lipid peroxidation and reduced the generation of reactive oxygen species (ROS) by restoring the enzymatic activities of SOD, CAT, and GPx. Additionally, EPS exhibited hepatoprotective properties and improved liver function profiles, as indicated by serum biomarkers such as SGOT, SGPT, urea, and creatinine, which were elevated in the arsenic-treated group compared to the control group. Overall, the findings suggest that EPS from *Diaporthe arengae* has the potential to counteract arsenic-induced oxidative stress and liver toxicity, thereby offering a promising therapeutic avenue for the treatment of arsenic-related metabolic disorders.

Keywords: Endophytes, exopolysaccharides, arsenic, oxidative stress.

MM-33 (Poster)

Cadmium and Lead Resistant Plant Growth Promoting Bacteria from Waste Water of Sewage Treatment Plant

Satvir Kaur[1], Shweta Singh[2], and Anil Kumar Singh[3]
kullarsatvir@gmail.com

[1, 2] *Department of Life Sciences and Allied Health Sciences, University Institute of Sciences, Sant Baba Bhag Singh University, Jalandhar (144030), Punja, Inida*
[3] *University Institute of Agriculture, Sant Baba Bhag Singh University, Jalandhar (144030), Punja, India*

Abstract: Plant growth-promoting (PGP) bacteria support plant growth through a variety of direct or indirect processes. The PGP bacteria has potential to support sustainable agriculture practise by replacing or reducing the usage of agrochemical. Available information suggest that majority of the PGP bacteria has been isolated from the vicinity of plants. The present study reports isolation of metal resistant PGP bacterial strains from waste water of Sewage Treatment Plant (STP), Hoshiarpur. The 35 morphologically distinct bacterial isolates were scrutinized for PGP activities and metal resistant traits. PGP traits namely phosphate solubilization, ammonia (NH_3) production, hydrogen cyanide (HCN) production, indole acetic acid (IAA) production and hydrolytic enzyme (catalase, proteases, and amylases) production were considered in the present study. Strain IN11, SW14, SW15, SW16 and SW20 were observed positive for ammonia, and catalase production. Strain IN11, SW14, SW15, and SW20 was showed IAA and amylase production. HCN production was seen in strain IN11, SW14, SW16 and SW20. Phosphate solubilization was observed in SW15 and SW20. Proteases activity was notice in IN11, SW15, SW16 and SW20 strains. Isolated bacterial strain also exhibited cadmium and lead resistance. Morphological, physiological and biochemical characterization suggested strain IN11, SW14 and SW15 to be *Bacillus* sps. Strain SW20 and SW16 was identified as *Pseudomonas* sps. and *Serratia* sps.

respectively. The overall study suggest that strain SW14, SW15, and SW16 can be used as PGP bacteria in phytoremediation of cadmium and lead contaminated sites.

Keywords: Plant growth-promoting (PGP), Hydrogen cyanide (HCN) production, Indole acetic acid (IAA)

MM-34 (Poster)

Biological Activities of Endophytic Fungi Isolated from *Chamaecostus cuspidatus*

Priyanka Mishra, Shreya Verma, Archana Yadav and Manishi Tripathi
mishra.priyank1988@gmail.com

Department of Microbiology
Institute of Bioscience and Biotechnology, C.S.J.M. University, Kanpur (208024)
Uttar Pradesh, India

Abstract: Endophytes are the microorganisms that live inside the host plant tissues which have novel metabolites exhibiting a variety of biological activities against different pathogens. The aim of my study was to isolate and identify the endophytic fungi from medicinal plant *chamaecostus cuspidatus*. *Chamaecostus cuspidatus* is a medicinal plant commonly known as Insulin plant in India for purporated anti-diabetic properties. Eight fungal species of endophytic fungi were successfully isolated named as CL1, CL2, CL3, CL4, from the leaves and CS5, CS6, CS7 and CS8 from the stem of the plant .The ethyl acetate extract of the crude metabolites of all the isolate, showed antagonastic activity against four human pathogens: *Kleibsella pneumonia, Staphylococcus aureus, Escheria coli* and *Shigella* except CL2 and CS6. CL3 shows the highest zone of inhibition (0.8cm ± 0.50) against *Kleibsella pneumonia*. The enzymatic activity of the isolates was also done in which out of 8 fungal endophytes 4 isolates shows protease activity. Also the free radicals of scavenging activities were measure using DPPH and the reaction was visible as a color change from purple to yellow. The result of the present study indicated that the isolates endophytes produced bioactive compounds which might have potential applicatio in pharmaceutical industry.

Keyword: Endophytes, Antimicrobial activity, Inhibition zone, Medicinal plants

MM-35 (Poster)

Molecular Detection of *Wolbachia* Distribution and Its Vertical Transmission in *Phlebotomus argentipes* (Sand Fly) in Bihar, India

Ajay Kumar [1], Sanjay D.[1], Sanjay Kumar Chaturvedi[2], N. K. Sinha[1]
akajaykumar836@gmail.com

[1]*Department of Vector Biology and Control, ICMR-RMRIMS, Patna, India*
[2]*Department of Microbiology, ICMR-RMRIMS, Patna, India*

Abstract: *Wolbachia*, an intracellular bacterium, belonging to α-proteobacteria (Rickettsia), have maternal inheritance and are commonly found in ovaries, intestines, salivary glands and thoraces of insects. These bacteria have the potential to impact their hosts' ability to reproduce through a range of pathways, leading to effects like feminization and cytoplasmic incompatibility (CI), as well as the death of male progeny. Recently, certain *Wolbachia* phenotypes have been used to control a number of vector-borne diseases caused by *Plasmodium* and viruses, including Zika, dengue, and chikungunya. In *Phlebotomus argentipes*, especially in Bihar, India, there no studies on *Wolbachia*. In order to understand the function of *Wolbachia* in sand fly populations, this knowledge gap must be addressed.
Our findings showed the presence of *Wolbachia* in sand flies collected from two VL non- endemic districts, Patna and Nawada, which have a low endemicity for Visceral Leishmaniasis.Sand flies collected in Muzaffarpur and Vaishali, two areas with a high prevalence of visceral Leishmaniasis where the *Phlebotomus argentipes* was negative for *Wolbachia* infection.The consistent presence of approximately 611 base pair (bp) PCR fragments specific to the *wsp* gene in samples from both the F1 generation of sand flies reared in a laboratory and the natural population of sand flies collected from Patna and Nawada suggests the presence of *Wolbachia* and stable

vertical transmission of *Wolbachia* in *Phlebotomus argentipes*. The finding of *Wolbachia* in *Phlebotomus argentipes* F1 generation indicates that *Wolbachia* may survive and be sustainably maintained in wild sand fly populations over a number of generations. For prospective *Wolbachia*-based vector control techniques, this persistence is essential**.**
Moreover, DNA sequencing is required to sequence the amplified wsp gene to reinforce the evidence of a *wsp* gene fragment in the PCR result in this study and to more successfully demonstrate the existence of *Wolbachia* in *Phlebotomus argentipes*. Nevertheless, this work offers important new information on the distribution and effects of *Wolbachia* in Bihar's sand fly populations. It creates new study opportunities and suggests possible vector management methods to lessen the incidence of Visceral Leishmaniasis.

Keywords: *Wolbachia, Phlebotomus*, Sand Fly, Kala-azar, Vertical Transmission

MM-36 (Poster)

Fermentative Production Optimization and Characterization of an Extracellular Gluten-Digesting Protease from *Bacillus Tequilensis* SU-3

Santosh D. Raut* and Ulhas K. Patil
santoshraut480@gmail.com

Microbiology Department, Institute of Science, Chhatrapati Sambhajinagar, Maharashtra (431004), India

Abstract: Celiac disease, an autoimmune condition triggered by gluten found in wheat, lacks an effective treatment, necessitating a lifelong strict gluten-free diet for patients. Addressing this, a fresh strain (SU-3) with gluten-digesting abilities was isolated from decayed wheat and identified as *Bacillus tequilensis* SU-3 via 16S rDNA analysis. Employing Plackett-Burman Design for screening and Central Composite Design for optimization, a significant boost in protease production (283 U/mL) was attained in an optimized medium containing yeast extract,15 g/L; glucose, 5 g/L; KH_2PO_4,1.0 g/L; $CaCl_2$,1.0 g/L; at pH 7.5, using a 3.5% inoculum, at 40°C, and 100 rpm agitation in a 48-hour.
The two-step enzyme purification process resulted in a 10.12-fold purification of the protease, with a specific activity of 2767.99 U/mg and a recovery rate of 18%. The purified extracellular protease from *Bacillus tequilensis* SU-3 has a molecular mass of 39 kDa. It is characterized as a metalloprotease, with an optimal pH of 7.5 and an optimal temperature of 40°C. The purified protease demonstrated notable stability in the presence of Triton X-100 and $HgCl_2$, with its activity being enhanced by the presence of Ca^{2+}, Mg^{2+}, and K^+ ions.
This protease derived from *B. tequilensis* implies its potential for use in biotechnology. The isolation and purification of this novel gluten-digesting protease present opportunities in enzymology with potential medical and industrial applications. Further exploration regarding in-vivo and animal studies is necessary to evaluate its protective efficacy against gluten sensitivity.

Keywords: Gluten, *Celiac disease,* Gluten-digesting protease*, Bacillus tequilensis,* Response surface methodology, Enzyme purification.

MM-37 (Poster)

Molecular Characterization and Genomic Analysis of Extremophilic Bacterium *Priestia Megaterium* CL-*1*, Isolated from Chilka Salt Lake

Ayushi Sinha[1] and Rajnish Prakash Singh[1]*
manasrajnish2008@gmail.com

Department of Biotechnology, Jaypee Institute of Information Technology, Noida, Uttar Pradesh, India

Abstract: Bacteria have intrinsic ability to tolerate and survive in several stress conditions including salt stress. In the present study, we evaluated the stress tolerance ability of salt-tolerant bacterium known as *Priestia megaterium* CL-1 isolated from Chilka salt lake, Orissa by genome analysis. *P. megaterium* is a gram-positive, spore-forming halophilic bacterium that is ubiquitous in various environments. The ability to survive under wide

temperature environment (3 to 45 ℃), salt conditions and utilization of different carbon sources, makes it suitable for industrial applications. A number of *P. megaterium* strains have been developed and characterized for several features including sporulation, auxotrophy, recombination, division, germination, and antibiotic resistance, etc. The cell surface hydrophobicity and co-aggregation assay against different bacterial strains illustrated its putative pathogenic nature. The complete genome size of CL-1 was 4.1 Mb, 1.66% GC-content, and total gene numbers of 6,068 were predicted. The genome analysis of CL-1 unravelled the presence of an open reading frame (ORF) encoding the functions related to environmental stress tolerance, adhesion processes, multidrug efflux systems, and heavy metal resistance. Genome annotation identified the various genes for chemotaxis, flagellar motility, and biofilm production, illustrating its strong colonization ability.The current findings provide the in-depth investigation of *P. megaterium* CL-1 bacterium that possessed various genome features that enable the bacterium to survive under diverse conditions. The strain possesses the strong ability for probiotic application purposes.

Keywords: Gram-positive Bacteria, Intrinsic ability, Salt-tolerant bacterium

MM-38 (Poster)

Biovalorization of Distillery Spent Yeast for Preparation of Essential Oil (EO)-Based Yeast Microcapsules

Aniya Susan George[1], Gurvinder Singh Kocher[1] and Devinder Kaur Kocher[2]
aniyasusangeorge@gmail.com

Department of Microbiology[1] and Department of Zoology[1], Punjab Agricultural University, Ludhiana (141004), Punjab, India

Abstract: Most essential oils (EOs) have insecticidal properties but their use is limited due to their sensitivity to heat, light, and oxidation. Encapsulating the EOs in yeast is a way to overcome this as it stabilizes them. Besides, yeast is a WHO recommended food for rearing mosquito larvae, hence it can serve as a bio-larvicide. For this encapsulation process, Spent yeast, an underutilized predominant by-product of the wine and beer industries, can be substituted for fresh yeast to make the process more economical. The present study was conducted to standardize the preparation of Essential oil-based yeast (*Saccharomyces cerevisiae*) microcapsules. The plasmolysis of fresh yeast cells with NaCl solution followed by encapsulation of eucalyptus oil in plasmolysed yeast cells was optimized initially and then used to prepare microcapsules using spent yeast. The effect of change in the mass ratio of yeast to oil on loading capacity and encapsulation efficiency was also investigated. Fluorescent microscopy and Fourier transform-infrared spectroscopy (FTIR) were used to analyze the process. Citronella oil and neem oil-based spent yeast microcapsules were also prepared. 5% (w/v) of NaCl plasmolysis for 4h followed by encapsulation for 4h with 2:1:4 (yeast: oil: water) mass ratio were the optimal conditions that provided the highest EO loading capacity (LC) and encapsulation efficiency (EE). Fluorescent microscopy and FTIR confirmed the enhancing effect of plasmolysis and encapsulation of oil in yeast cells. Citronella oil-based spent yeast microcapsules had higher LC and EE when compared with eucalyptus oil and neem oil-based spent yeast microcapsules. Thus, spent yeast for the preparation of EO-based microcapsule appears to be a feasible process that effectively stabilizes eucalyptus oil besides providing a potential eco-friendly mosquito larvicide.

Keywords: *Saccharomyces cerevisiae,* Fourier transform-infrared spectroscopy (FTIR), Loading capacity (LC) Encapsulation efficiency (EE)

MM-39 (Poster)

Genomic Insights into COVID-19-Associated Fungal Infections in India

Tanushree Saini[1,2], Pawan Kumar[1,2], Renu Chaudhary[1], Himani Singh[1,2], Shukla Das[3], Susan KS[4], Sushil K Chumber[4], Yukti Sharma[4], and Bhupesh Taneja[1,2]
rajtanushree14@gmail.com

[1]*CSIR-Institute of Genomics and Integrative Biology (CSIR-IGIB), New Delhi- (110025), India;*
[2]*Academy of Scientific and Innovative Research (AcSIR), Ghaziabad- (201002, India;*
[3]*Department of Microbiology, UCMS & GTB Hospital, Dilshad Garden, Delhi (110095), India;*
[4]*St. Stephen's Hospital, Delhi, India*

Abstract: The emergence of the SARS-CoV-2 global pandemic led to a surge in secondary infections, particularly covid-19 associated fungal infections (or CAFI) such as *aspergillosis, candidiasis*, and *mucormycosis*, among COVID-19 patients in India. The heavy use of immunosuppressive therapies and antibiotics further exacerbated the problem, including factors such as prolonged hospitalization, corticosteroid therapy, and ventilation support. The surge in CAFI highlighted the lack of information regarding the molecular epidemiology and evolutionary trends of mucorales and other fungal pathogens in India. Bridging these knowledge gaps, our study analyzed the phylogenomic characteristics of mucormycotic strains prevalent in India, through whole-genome sequencing of the clinical isolates. Whole genome relatedness was assessed using ANI (Average nucleotide identity). Further, the SNP-based phylogeny was carried out using the ParSNP tool. This analysis allowed us to identify the species-specific clusters among CAFI pathogenic strains. The antifungal susceptibility test was also carried out to evaluate the in vitro efficacy of available antifungal agents against these pathogens and to understand their response profiles better. The findings of this study hold significant implications for public health, providing valuable insights into the molecular complexities of SARS-CoV-2-associated fungal infections, particularly mucormycosis.

Keywords: *Mucormycosis,* WGS (whole genome sequencing), SNP-based phylogeny, Phylogenomic analysis, ANI (Average nucleotide Identity), Antifungal susceptibility test (AFST)

MM-40 (Poster)

Anti-Oxidant Content and Activity of Methanolic Extract of *Calocybe Indica* P & C. And Investigation of Molecular Docking

[1]**Arindam Karmakar** and [1]Swapan Kumar Ghosh*
*gswapan582@gmail.com

[1]*Molecular Mycopathology Lab, Biocontrol and Cancer Research Unit, PG Department of Botany, Ramakrishna Mission Vivekananda Centenary College (Autonomous), Rahara, Kolkata (700118), India*

Abstract: Mushrooms which are renowned for their nutritional value and unique flavor, have gained significant attention for their potential health benefits. The objectives of these studies were to detect the antioxidant contents, and antioxidant activity, identify the bioactive compounds of *Calocybe indica* (MEC), and perform a molecular docking of the selected bioactive compounds against enzymes responsible for the generation of free radicals or Reactive Oxygen Species (ROS). The results revealed that MEC consistently exhibited higher antioxidant content (TPC value was 4.303 mg GAEs /g of extract, TFC value was 3.66 mg QE/g of extract, TAC value was 35.00 mg AAE/g of extract). It was also found that MEC showed significant antioxidant activity. The EC_{50} value of MEC against DPPH free radicals was 48.42±1.14 mg/ml of the sample, and the FRAP value was 57.38±0.37 mM Fe2+/mg of the sample. LC-MS analysis showed that MEC was rich in phenolic and flavonoid compounds. Furthermore, the molecular docking assay confirmed that MEC was able to inhibit proteins responsible for the generation of free radicals. In conclusion, these results suggest that *Calocybe indica* has substantial potential as a natural source of antioxidants, which may contribute to its health-promoting benefits.

Keywords: Mushrooms, Antioxidant content, Antioxidant activity, Free radicals

MSD-1 (Oral)

Bioprospecting Xylanolytic Fungi for Conversion of Lignocellulosic Waste to Xylooligosaccharides

Dolamani Amat, Livleen Shukla, Sandeep Kumar Singh and Subham Yadav
dolaamat@gmail.com

Division of Microbiology
ICAR- Indian Agricultural Research Institute, New Delhi (110012), India

Abstract: Agri-residue is a rich source of NPK and Sulphur. One of the most abundant residue corncobs can be used for the production of xylooligosaccharides (XOs) being rich source of xylan. XOs are one of the most sought after oligosaccharides having prebiotic properties and considered as emerging prebiotics which can be produced from lignocellulosic biomasses. Xylanases act on xylan component of the biomass and results in production of XOs. In this study a total of 8 fungal isolates were obtained from degraded corncobs by enrichment techniques using Reese's minimal medium supplemented with Beechwood xylan(1%). Four isolates were screened for xylanase production both by qualitative and quantitative assay. The results showed that CC-17 fungal isolate produced highest xylanase activity after 7 days (1.4 IU/ml) and 15 days (1.5 IU/ml) of incubation under submerged fermentation in Reese's minimal medium supplemented with Beechwood xylan(1%). These isolates will further be screened XOs production to develop an economical process for its production. The enzyme required for XOs production can be grouped into two categories i.e. pretreatment enzymes like cellulases, laccases, lignin peroxidase etc. and production enzymes i.e. endo-β-1,4-xylanases. Due to variability in expression of the entire enzymes in required amount in a single microorganism not possible; hence a consortium will be developed

Keywords: Xylooligosaccharides, Xylanases, Cellulases, Agri-residue

MSD-2 (Oral)

Impact of Chlorantraniliprole Residues on Soil Microbial Ecology

Reena Chauhan*, Sushil Ahlawat and Sumit Kaur
reenavansh82@gmail.com

Department of Chemistry, Chaudhary Charan Singh Haryana Agricultural University,
Hisar (125004), Haryana, India

Abstract: In agricultural fields pesticides are regularly used to save their crop from infestation which will help farmers to increase their crop yield and income. Though pesticides are combating insect pests but they affect the activity and population of beneficial soil microbial communities also. Microorganisms plays a crucial role in decomposition of soil organic matter and degradation of pesticides invaded in soil ecosystem. A laboratorystudy was carried to know the impact of chlorantraniliprole on microbial and fungal count in soil. Three different doses (40, 75 and 150 g a.i. ha^{-1}) of chlorantraniliprole (Ferterra 0.4% GR) were applied in pots having 4 kg soil. Sampling was done on 0 (2h), 3,5,7,14,21,28,35,42,49,56 and 63 days after application of chlorantraniliprole. Total microbial count was significantly decreased from initial day to 7th day in all the three doses 45, 30, 28 cfu × 10^7 g^{-1} soil, respectively in comparison to control (125 cfu × 10^7 g^{-1} soil). Similarly, fungal count was decreased in first week after application 8, 4, 2 cfu × 10^7 g^{-1} soil, respectively in three doses. Recovery of microbial and fungal population was initiated after 14 days of application in treatment T_1. On 21st day after application microbial as well as fungal count was start increasing in treatment T_2 and T_3. As the residues of chlorantraniliprole decreased in soil, total count of microbes and fungus was increased in soil. Thus, there is need to assess the effect of indiscriminate use of pesticides on soil microorganisms, affecting microbial activity and soil fertility.

Keywords: Chlorantraniliprole, Pesticides, Soil sample, Fungal count, Soil organic matter.

MSD-3 (Oral)

Efficacy of Entomopathogenic Fungi and Biorational Insecticides against Shoot and Fruit Borer (*Earias* spp.) in Okra

Deepika Kalkal*, Harish Kumar and Lomash Kumar
deepikakalkal@gmail.com

Department of Entomology, CCS Haryana Agricultural University, Hisar (125004), Haryana, India

Abstract: Studies were carried out at the Research Area of Entomology farm, CCS Haryana Agricultural University, Hisar during *Kharif*, 2022 & 2023, to evaluate the efficacy of selected entomopathogenic fungi and biopesticides against shoot and fruit borer (*Earias* spp.) in okra crop. The crop was sown under randomized block design (RBD) with ten treatments and observations were recorded before the first spray and at 3, 7, and 10 days after each spray. Results revealed that on the basis of pooled data of two years, the per cent reduction over control on number and weight basis was recorded maximum as 83.10 & 83.39 per cent, respectively when the crop was sprayed twice with spinosad 45 SC@ 187.5 ml/ha at 10 days interval and it was followed by treatment comprising two sprays of *Bacillus thuringiensis* @ 1.0 kg/ha resulting 77.94 and 78.69 per cent reduction over control, respectively. Next best treatment were two sprays of *Metarhizium anisopliae*@ 10^9cfu/ml (75.84 and 77.12 % reduction, respectively) and two sprays of *Beauvaria bassiana* @10^9cfu/ml with 70.62 and 72.66 % reduction, respectively. Maximum pooled yield of two years (8491 kg/ha) of okra fruit was also recorded in treatment having two sprays of spinosad 45 SC @ 187.5 ml/ha which was significantly superior over rest of the treatments. Next best treatment was two sprays of *B. thuringiensis* @ 1.0 kg/ha with 7849 kg/ha fruit yield which was followed by treatment having two sprays of *M. anisopliae* @ 10^9cfu/ml with 7817 kg/ha fruit yield and both were at par to each other and found superior over control (5086 kg/ha). The study demonstrates that among microorganism-based insecticide formulations, *B. thuringiensis* and *M. anisopliae* were found effective alternatives and offered a viable, eco-friendly strategy for managing shoot and fruit borer in okra, particularly in integrated pest management (IPM) programs aimed at reducing chemical pesticide use contributing to sustainable agriculture.

Keywords: Biorational insecticides, Entomopathogenic fungi, *Earias* spp., Okra, Pest management

MSD-4 (Oral)

Evaluation of Bio-Rational Insecticides against Brinjal Shoot and Fruit Borer *Leucinodes Orbonalis* Guenee in Brinjal Crop

Lomash Kumar*, Deepika Kalkal and Harish Kumar
lomash.baliyan0510@gmail.com

Department of Entomology, CCS Haryana Agricultural University, Hisar (125 004), Haryana, India

Abstract: Evaluation of different bio-rational insecticides against brinjal shoot and fruit borer, *Leucinodes orbonalis* Guenee in brinjal crop was done at research area of Entomology farm, CCS Haryana Agricultural University, Hisar during *Kharif* 2023-24. The crop was sown under randomized block design (RBD) with eight treatments including different combinations of entomopathogenic fungi, microbial insecticides and botanicals. Observations were recorded before the spray and at 7 and 14 days after the spray and results revealed that all treatments were found effective against Brinjal Shoot and Fruit Borer (BSFB) in reducing shoot infestation and superior over untreated control plot. Though, two spray of Spinosad 45% SC @ 84.15 g a.i./ha recorded lowest mean shoot infestation (6.41%) followed by Spinosad 45% SC @ 84.15 g a.i./ha + *Beauveria bassiana* @10^9cfu/ml (8.71%). However, two spray of *Beauveria bassiana* @10^9cfu/ml and *Metarhizium anisopliae* @10^9cfu/ml were found to be at par with relatively least effective treatments against BSFB with 10.62% and 13.71% mean shoot infestation, respectively whereas in control plot mean shoot infestation was 20.21%. Bio-efficacy of different treatments on fruit infestation and yield of brinjal were found superior over untreated control plot in mean fruit infestation (35.23%). Among the biorationals, two spray of Spinosad 45% SC @ 84.15 g a.i./ha treated plots recorded lowest mean fruit infestation (8.37%) followed by Spinosad 45% SC @ 84.15 g a.i./ha+ *Beauveria bassiana* 10^9cfu/ml (11.47%) and Spinosad 45% SC @ 84.15 g a.i./ha+ *Metarhizium anisopliae* 10^9cfu/ml (13.40%) and which were found statistically at par with each other. The highest marketable

yield was observed with two spray of Spinosad 45% SC @ 84.15 g a.i./ha 253.25 q/ha followed by Spinosad 45% SC @ 84.15 g a.i./ha + *Beauveria bassiana* 10^9cfu/ml, 207.20 q/ha, whereas in untreated control plot least marketable yield was recorded with 101.60 q/ha.

Keywords: Biorational insecticides, Entomopathogenic fungi, *Beauveria bassiana*, *Metarzhizium anisopliae*, *Leucinodes orbonalis*

MSD-5 (Oral)

Efficacy of Biorationals against Citrus Psyllid (*Diaphorina citri*) in Kinnow

Ankit Kumar* and Deepika Kalkal
ankitzood522@gmail.com

Department of Entomology, CCS Haryana Agricultural University, Hisar (125004), Haryana, India

Abstract: Citrus is native to tropical and subtropical regions of South East Asia, particularly India and China. Although a large number of pests attack citrus, but Asian citrus psyllid, *Diaphorina citri* Kuwayama (Hemiptera: Psyllidae) is currently the most important pests of kinnow. Research was carried out at the Experimental Orchard, DDUCE-OF, CCS Haryana Agricultural University, Hisar during rainy season, 2023, to evaluate the efficacy of selected plant origin formulations against citrus psylla in kinnow. The experiment was planned under randomized block design (RBD) with three replication and six treatments and observations were recorded before the first spray and at 5, 10 and 15 days after each spray. Results revealed that on the basis of overall per cent reduction over control after two sprays during rainy season, maximum reduction (82.02 %) was recorded in azadirachtin 1% @ 5ml followed by azadirachtin 0.15% @ 5ml with 72.88 per cent reduction and *Lecanicillium leanii* 1×10^8 cfu/ml @ 5ml/ litre of water (68.12%) and all were found statistically at par with each other. The changed situations require aiming for environmental safety and replacement of chemical molecules with natural ones that preserve the activity of natural enemies of pests demand some close study on identification of better formulation. In continuation to this the experiment was planned to find out the alternative of chemical pesticides for managing psylla.

Keywords: Biorationals, Citrus, Entomopathogenic fungi, Psylla

MSD-6 (Oral)

Eco-Friendly Management of Pod borer, *Helicoverpa armigera* in Chickpea

Harish Kumar*, Tarun Verma and Lomash Kumar
harishkumar78@hau.ac.in

Department of Entomology, CCS Haryana Agricultural University, Hisar (125004), Haryana, India

Abstract: Research work was carried out at the research area of Entomology farm, CCS Agricultural University, Hisar during *Rabi*, 2022-23 & 2023-24, to evaluate the efficacy of different entomopathogens against gram pod borer, *Helicoverpa armigera* in chickpea. The crop was sown under randomized block design (RBD) with ten treatments and three replications. The pod borer larval population was recorded per meter row length (mrl) one day before spray and 3, 7 and 10 days after spray from 3 random spots in a plot. Two sprays were done at 10 days interval. On pooled mean basis of two years (2022-23 & 2023-24), minimum mean larval population of pod borer (1.01 larvae/ mrl) was recorded in treatment when the crop was sprayed with HaNPV @ 500 LE per ha during 1st and 2nd spray and it was found statistically at par with two treatments viz., two sprays of novaluron 10EC @ 375 ml/ha (1.05 larvae/mrl) and spray of HaNPV @ 500 LE per ha followed by novaluron 10 EC @ 375 ml/ha (1.13 larvae/mrl). Maximum gram grain yield (1780.70 kg/ha) was recorded when the crop was sprayed with novaluron 10EC @ 375 ml/ha during 1st and 2nd spray and it was found statistically at par with two treatments viz., two sprays of HaNPV @ 500 LE per ha (1763.79 kg/ha) and spray of HaNPV @ 500 LE per ha followed by novaluron 10 EC @ 375 ml/ha (1753.52 kg/ha). The study demonstrates that HaNPV was found as an effective alternative and offered a viable, eco-friendly strategy for

managing pod borer in chickpea, particularly in integrated pest management (IPM) programs aimed at reducing chemical pesticide use contributing to sustainable agriculture.

Keywords: Eco-friendly, *Helicoverpa armigera*, HaNPV, Nuclear polyhedrosis virus of *Helicoverpa armigera*

MSD-7 (Oral)

Bioplastics from Cyanobacteria: Progress and Future Prospects

Ranjana Bhati*
ranjana.iitkgp@gmail.com

Assistant Professor, Department of Microbiology, Bundelkhand University, Jhansi Uttar Pradesh (284128), India

Abstract: Increasing concern for environmental sustainability has accelerated the research for wide range of biodegradable polymers. Polyhydroxyalkanoates (PHAs) is currently regarded as most promising eco-friendly polymer as it is biodegradable and biocompatible in nature. PHAs, are used as "green" thermoplastics in medicinal, fiber and agricultural field. PHAs are commercially produced by bacterial fermentation and main drawback is high production cost incurred due to expensive substrate and continuous oxygen supply.Important research efforts are being made to make PHAs production economically viable bioprocesses. In this context utilization of cyanobacteria for biopolymer synthesis is emerging as a promising and sustainable solution to reduce the greenhouse gases emission and rapid biomass production. Moreover,Cyanobacteria can accumulate high PHAs (PHB and P(3HB-co-3HV) with various growth conditions, i.e. photoautotrophic, nutrient deficient and chemoheterotrophic with various carbon sources like glucose, fructose. Cyanobacteria can be easily cultivated on non-arable land and wastewater. In agricultural countries, such as India, a large quantity of nutrient waste is generated. The wastewater contains organics that can enhance production rate and cost effective ways to cultivate cyanobacteria through a mixotrophic system and generate a potentially valuable cyanobacterial biomass for PHAs production. Cyanobacteria grow better when fed with carbon dioxide, the major greenhouse gas. Therefore, PHAs production with cyanobacteria and wastewaters utilization seems highly promising as it has the dual advantage of polymer production and wastewaters recycling with photosynthetic utilization of CO_2. Current research presents an overview on the production and characterization of PHAs from cyanobacteria. A detailed insight on various PHAs production strategies in current scenario is given with their future prospects. Thus, N_2 fixing cyanobacterium can be considered as suitable feedstock for PHAs production and opens up the possibilities for low cost production of PHAs polymers.

Keywords: Polyhydroxyalkanotes (PHAs); Cyanobacteria; Biopolymer

MSD-8 (Oral)

Study on the Isolation and Characterization of Ethanologenic Yeast from Diverse Sources

Jasmeen Kaur[1] and **Pardeep Kaur*[2]**
pardeepkaur2108@gmail.com

[1] *Department of Biotechnology, Sri Guru Granth Sahib World University, Faegre Sahib, Punjab (140406), India*
[2] *University Institute of Biotechnology, Chandigarh University, Mohali (140413), India.*

Abstract: Bioethanol has the capacity to replace fossil-derived fuels. The burning of fossil-derived fuels results in less emission of greenhouse gases and other obnoxious gases which are referred to as carcinogenic. So, the current bioethanol research focuses mainly on the production of bioethanol from different renewable feedstocks like municipal soil waste, starchy and agricultural waste, and industrial waste. The samples for the yeast isolation were collected from diverse sources and screened for different sugars. The screened isolates were characterized morphologically and for various stress tolerance factors such as thermotolerance, osmotolerance, and acetic acid tolerance. The fermentation of acid hydrolysate of kitchen waste was carried out to assess its fermentation efficiency.

Keywords: Bioethanol; Ethanologenic; Thermotolerance; Fermentation Efficency.

MSD-9 (Oral)

Dyella Species as an Efficient Biocontrol agent against Fungal Pathogens: *Sclerotium rolfsii* and *Aspergillus niger*

Arti Thakur
arti.thakur@rediffmail.com

Assistant Professor, PIPHS, Faculty of Medicine, Parul University, Vadodara (391760), India

Abstract: Background: Many soilborne fungal pathogens, such as *Sclerotium rolfsii* and *Aspergillus niger*, can cause catastrophic illnesses that result in large yield losses in groundnuts (*Arachis hypogaea*), a key crop. The use of beneficial rhizobacteria as biocontrol agents offers a sustainable alternative to chemical fungicides. In this study, a PGPR isolate of *Dyella* species appeared to be an efficient antifungal agent after screening its activity against the groundnut fungal pathogens *Sclerotium rolfsii* and *Aspergillus niger* in vitro. A total of 50 PGPR isolates were screened for their antifungal activity by dual culture method after the incubation period of 7 days at 28±2 °C. In the dual culture assay, each selected bacterial isolate was co-cultured with the fungal pathogens on Sabouraud dextrose agar (SDA), and the inhibition of fungal growth was evaluated by measuring the distance between the bacterial and fungal growth fronts. The efficient isolate was characterized phenotypically and genotypically. Results demonstrated that the 5 PGPR isolates exhibited a significant antifungal activity against both fungal pathogens in the range of 21.94% to 47.96% against *A. niger* and in the range of 15.91% to 30.67% against *S. rolfsii*. Maximum zone of inhibition was exhibited by GSB 5 (47.96% & 30.67), interpreted through a clear suppression of fungal growth, suggesting the production of antifungal compounds such as extracellular enzymes chitinase, and possible volatile organic compounds (VOCs) such as HCN. Genotypic & phenotypic characterization of most efficient isolates GSB 5, identified it as *Dyella* sp. and is submitted into gene bank with gene bank with accession no. KT462741. Further research is warranted to characterize the active antifungal compounds and to assess the efficacy of these isolates in field conditions.

Keywords: Dyella species; Groundnut; *Sclerotium rolfsii; Aspergillus niger*; Rhizobacteria; Antifungal activity; Biocontrol

MSD-10 (Oral)

Role of Rhamnolipids (Microbial Surfactants) in Formulation of Edible Food Coatings

Deepansh Sharma
deepanshsharma@gmail.com

Department of Life Sciences, J.C. Bose University of Science and Technology, YMCA, Faridabad, Haryana (121006), India

Abstract: Food products, especially fruits and vegetables, have their main source of deterioration from various physical and microbiological origins, mostly by fungi, which results in post-harvest losses to food industries such as undesirable sensory characteristics and change in physical appearance. The key fungal species responsible for food deterioration are from the genera *Aspergillus* sp., *Fusarium oxysporum*, *Rhizopus oryzae*, *Botrydiplodia theobromae* and *Botrytis cinerea*. Post-harvest losses of fruits and vegetables is a matter of great concern for food security and global hunger in many countries whose economy is agriculture based. Edible coating has useful effect to control post-harvest losses of fruits against microbial decay. Different compounds have been used for edible coating such as: aloevera gel, clove oil, neem, turmeric, moringa, and various kinds of essential oils and biological polymers. There is an emergent need of the next generation's antifungal agents due to increasing health concerns and non-green labelling. Biosurfactants produced by a variety of microorganism give unique antimicrobial and functional attributes. Biosurfactants has been adopted for developing the food coatings to control plant pathogens.

Therefore, the development of new antifungal agents is of great importance because, in addition to the excessive use of agro chemicals, there are reports about fungal resistance to these current biocides.Considering the importance of developing new antimicrobial agents against food spoilage fungi this work aimed to use rhamnolipid and evaluate the antifungal activity against ***Botrydiplodia theobromae*****,** (a commonly known fungal pathogen associated with Banana crop) as an eco-friendly alternative with potential application as an

antimicrobial agent in the form of edible coating in food industry. The present study focussed on the determination of the antifungal potential of the rhamnolipid and essential oils as a synergistic preparation with a possible formulation of antifungal coating.

Keywords: Rhamnolipids, Glycolipids, Post-harvest loses, Antifungal, Starch Content

MSD-11 (Oral)

Microbial biosurfactants- Eco-friendly and Economically-viable Adjuvants for Agriculture

Seema Sangwan[1&*], Harpreet Kaur[1], Pankaj Sharma[1], Sushila Singh[2], Mukesh Kumar[1] and Nishu Sehrawat[1]
seema_sangwan80@yahoo.co.in

[1]*Department of Microbiology,*
[2]*Department of Chemistry, CCS Haryana Agricultural University, Hisar (125004), Haryana, India*

Abstract: Biosurfactants are amphiphilic moieties produced by variety of plants and microorganisms. Their extraction from plants lacks practicality considering the issues such as larger space acquisition, longer life cycle and ever growing requirements of agrochemicals. Microbes conveniently produce these secondary metabolites in smallest possible period utilizing cheaper nutrients for the growth. The environment-friendly aptitude of microbial surfactants makes them pertinent molecules advocating their dominance over chemical surfactants. The biosurfactants helps in increasing the bioavailability of hydrophobic substrates and their antiviral, antifungal and antibacterial actions extends their applications in battling diseases particularly in plants. The majority of biosurfactant producers belong to genera *Acinetobacter*, *Pseudomonas*, *Arthrobacter* and *Bacillus*. The production of biosurfactant by yeasts is mainly reported in genera *Pseudozyma, Yarrowia* and *Candida.* Four biosurfactant producing yeasts strains belonging to *Meyerozyma guilliermondii* and three bacteria namely *Klebsiella pneumoniae* ssp. *ozaenae* BK34, *Staphylococcus lentus* BK23 and *S. lentus* BK68 were found producing significant amount of biosurfactants. Among bacteria, *Klebsiella pneumoniae* BK34 (23.5g/L) and among yeasts, *Meyerozyma guilliermondii* YK32 (18.64 g/L) produced maximum biosurfactant, utilizing whey and butter waste as raw materials, respectively. These biosurfactants were found enhancing germination in various crops included chickpea, mungbean, wheat and even cotton. The biosurfactant produced by *K. pneumoniae* BK34 at 0.5% concentration proficiently degraded the single dose chlorpyrifos to below detection limit after 120 days of treatment. The dissipation pattern of chlorpyrifos followed the first order kinetics with a good fit, revealing the efficacy of these eco-friendly agents in bioremediation of contaminated sites. The biosurfactant produced by yeast *M. guillermondii* YK32 was characterized as a sophorolipid with anionic charge and good stability which has a potential of working as adjuvant for pesticide formulations leading to their dose reduction.

Keywords: Biosurfactant; *Klebsiella pneumoniae*; *Meyerozyma guilliermondii;* Chlorpyrifos degradation; Herbicide mobilization; Nanotechnology

MSD-12 (Oral)

Biomass and Lipid Production Potential of Microalgae

Shikha Mehta[1]*, Kamla Malik[1], Monika Kayasth[1] and Sushil Nagar[2]
shikhamehta@hau.ac.in, shikhamicrobio@gmail.com

[1,1*]*Department of Microbiology, COBS&H, CCS Haryana Agricultural University, Hisar (125004), Haryana, India*
[2]*Department of Biochemistry, COBS&H, CCS Haryana Agricultural University, Hisar (125004), Haryana, India*

Abstract: The world's growing population, industrialization and urbanization have created a significant challenge to fulfil the demand for fossil fuels. Therefore, to satisfy our energy needs, alternative and environmentally favourable energy sources are being explored. Solar, wind and biomass are the major

renewable energy sources. Microalgae are also thought to be a viable option for high value metabolites and can substitute renewable energy sources. Microalgae provide various advantages such as rapid growth rate, efficient land utilization, carbon dioxide sequestration and ability to grow in waste water. Several species of microalgae have ability to accumulate lipid which can be converted to fuel offering an alternative to fossil fuels. In the present study, microalgae were collected from ponds of different locations viz. Hisar, Kurukshetra, Ladwa and Pehowa. Microalgae growth medium was enriched using different concentrations of whey (10, 20 and 30%). The maximum biomass was produced by isolate KMA-1 i.e. 4.85 g/L in BG-11 medium supplemented with 30 % whey. High fluorescence shown by KMA-1 as compared to other isolates indicated the presence of lipids. The lipid yield of 1.12% (v/w) was obtained from microalgal biomass of KMA-1 isolate while HMA-1 isolate produced 1.04% lipid. Thus, microalgae cultivation could potentially reduce reliance on fossil fuels and also contributes to environmental sustainability.

Keywords: Fluorescence, Fossil fuels, Microalgae, Microalgae Cultivation, Renewable Energy

MSD-13 (Oral)

Optimization and Evaluation of *Trichoderma-Azotobacter* Interaction to Develop Biofilm Based Biofertilizers

Ajay Kumar*, Rajesh Gera and Meena Sindhu
ajaykumar@hau.ac.in

Department of Microbiology, COBS&H, Chaudhary Charan Singh Haryana Agricultural University Hisar (125004), Haryana

Abstract: Microbial biofilms are gaining importance in agriculture, due to their multifaceted agronomic benefits and resilience to environmental fluctuations. This study focuses on the optimization of the combined growth of *Azotobacter-Trichoderma* and development of the biofilm based biofertilizer (*Az-Tr*). Application of the *Azotobacter* as biofertilizer has been studied and reported as an alternate to chemical fertilizers. *Azotobacter* strains inoculated in the soil improved soil health and crop production. Another microbial strain *Trichoderma* has been used as biocontrol in agricultural crops which works against plant diseases. *Trichoderma* also has been used as a biofertilizer to promote plant growth and development in number of crops. So, co-application of the both *Azotobacter* and *Trichoderma* may enhance the plant growth promoters and diseases suppression. Two groups of microorganisms viz., *Azotobacter* and *Trichoderma* are studied to evaluate their compatibility and optimization. *Trichoderma* and *Azotobacter* were found compatible for their combined growth. Lab experiment was conducted to evaluate the synergistic growth of *Azotobacter* and *Trichoderma* with different combination of media (Jensen's medium and potato dextrose medium). *Trichoderma- Azotobacter* (*Tr-Az*) showed maximum growth in media combination of J25% + P75% and observed maximum biofilm formation at the same ratio. It was observed that combined application of *Azotobacter* and *Trichoderma* showed significantly increases in plant growth promoting traits as compared to individuals. After a thoroughly research, commercial production of biofilm inoculum based on a mixture of *Azotobacter* and *Trichoderma* can be encouraged.

Keywords: Biofertilizer, *Azotobacter*, *Trichoderma*, Biofilm, optimization, Agriculture, Sustainability

MSD-14 (Oral)

Biodiesel Production from Optimized *Aloe vera* Rind Hydrolysate, Lipid Profiling, and Biodiesel Properties Prediction

Ameera Al Shehhi and **Nallusamy Sivakumar***
apnsiva@squ.edu.om

Department of Biology, College of Science, Sultan Qaboos University, PO Box 36, PC 123, Muscat, Oman.

Abstract: Exploring low-cost feedstock for bioenergy production to replace a non-renewable energy source is gaining attention nowadays. *Aloe vera* rind (AVR) is considered a discarded waste in the *A. vera* products industries, which mainly focus on the gel. However, the presence of cellulosic components in AVR makes it an

alternative, renewable bioresource to produce bioproducts. In this study, AVR was used as a novel substrate for biodiesel production by oleaginous yeasts, *Rhodosporidium toruloides* and *Cryptococcus curvatus*, using mono and co-culture methods. Different pretreatments were used in the preparation of the AVR substrate, and different analytical techniques (X-ray diffraction, Fourier transform infrared, and dynamic light scattering) were used to characterize the pretreated AVR. The pretreatment results showed that the H_2SO_4 pretreatment has the highest effect by increasing the saccharification percentage by 14%, followed by HCl. Double pretreatment with Triton X-100 decreases saccharification percentages. The Box-Behnken design was used to optimize the enzymatic saccharification conditions. The predicted optimum conditions for enzymatic saccharification of AVR were 47.91°C, 70 U/g cellulose, and 4.75% substrate loading for a 50 mL working volume. The maximum reducing sugar obtained in the validation experiment was 34.78 g/L with 65.89% saccharification. The increase in saacharification could be explained by the crystallinity reduction, lignin destruction, and particle size decline of AVR after acidic treatment. The result shows that *R. toruloides* produces about 5 g/L (32%) of lipid, which is significantly more than *C. curvatus* and co-culture. The lipid profiles of mono and co-culture were similar and showed the presence of 13 fatty acid methyl esters. The predicted properties of the produced biodiesel, such as cloud point, cetane number, iodine value, and density, met the international standards (EN14214 and ASTM D6751). Consequently, the AVP could be a potential renewable feedstock for producing microbial lipids, which are crucial for biodiesel production.

Key words: *Aloe vera* rinds, Enzymatic saccharification, Reducing sugars, Pretreatments, Biodiesel, lipid profile

MSD-15 (Oral)

Development of Bioinoculants Consortia pre-coated seed – A Ready to Use Agro Input for Effective Nutrient Acquisition in Rice

M Gnanachitra[a]*, D Balachandar[a] and Jerlin[b]
mgc74@tnau.ac.in

[a]*Department of Agrl Microbiology, Tamil Nadu Agricultural University, Coimbatore (3),India*
[b]*Department of Seed Science & Technology, Tamil Nadu Agrl. University, Coimbatore (3), Inida*

Abstract: Rice is the most responsive crop towards application of fertilizers applied for nitrogen, phosphorus, potash and zinc nutrition. The applied fertilizer use efficiency can be enhanced by the action of biofertilizers.These biofertilizers are normally delivered by seed treatment, seedling root dipping and soil application. Among them**,** application of beneficial microbes through seed is an efficient mechanism for deliveringthem into soil for effective colonization. In seed inoculation, pre-coating of seed with biofertilizers and polymer is a new idea which adhere on the seed surface like film coating and effectively delivered into the seed for the purpose for which it is applied. Application of liquid biofertilizers in different combinations as consortia is now becoming an emerging and promising practice among farmers, because of its better performance at field condition in terms of plant growth, nutrient acquisition and reduce biotic and abiotic stresses. In the present study, two different biofertilizer consortia (NPK & NPKZn) were developed using *Azospirillum,* phosphobacteria, potashbacteria and zinc solubilizing bacteria and used for pre-coating of rice seed. The shelf life of both NPK and NPKZn biofertilizer consortia in the liquid formulation and pre-coated rice seed was estimated. In both bioinoculants consortia, population of the individual organism was maintained @ 10^8/ml up to 15 months, whereas in pre-coated rice seed as 10^{3-4} /seed over 3 months shelf life. Of the two, the individual bioinoculant load was found comparatively more in NPK than NPKZn consortia. The effect of NPK than NPKZn biofertilizer consortia pre-coated rice seed was also studied both by paper towel method and in pot culture in comparison with the existing seed treatment. Irrespective of seed treatment and seed coating, NPKZn consortium recorded more germination % (85 &79) & vigour index (2353 & 2314) than control (70% & 1777) respectively. In pot culture experiment also, both biofertilizer consortia (NPK & NPKZn) recorded more plant biomass, grain yield and plant nutrient uptake level than individual application of biofertilizers. Hence, this type of biofertilizer consortia coated seed ensures the right choice of biofertilizers for the farmers as 'Ready to use agroinput'.

Keywords: Biofertilizers, Bioinoculants, NPK, NPZn, Rice, *Azospirillum*

MSD-16 (Oral)

Ectomycorrhizal Bioinoculants for Sustainable Nutrient Management of Tasar Host Tree Plantations

Aparna K.*, S. Das, H. Yadav and N.B. Chowdary
aparna.micro@gmail.com

Central Tasar Research and Training Institute, Piska Nagari, Ranchi (835303), Inida

Abstract: Ectomycorrhiza are fungi which form a mycorrhizal symbiosis with the roots of tree species providing them with an advantage of efficient nutrient acquisition from places which are not reachable for the plant roots. Unlike arbuscular mycorrhizae, the fungal hyphae penetrate only the intercellular spaces and are subject to lesser impact of defence mechanisms of the plants and therefore the symbiosis lasts for longer periods. Tasar sericulture is an agroforestry based activity carried out by the native tribal and rural communities of the states like Jharkhand, Chhattisgarh and Orissa to produce tasar silk. Adaptation of nutrient management practices is low due to the poor economic status of the tasar farmers. In order to develop a sustainable nutrient management practice with minimum intervention of farmers, ectomycorrhizal bioinoculants are evaluated in tasar host plantations which are unconventional hosts. Fungal fruiting bodies from sal forests and from plantations of *Terminalia arjuna* and *T. tomentosa* were collected and the pure cultures of fungi were isolated. The fungi were tested for in vivo efficiency to promote growth of the arjun seedlings and symbiotic efficiency with the roots. Shortlisted fungi with high efficiencies were identified as *Phlebopus portentosus*, *Agaricus* sp., *Agrocybe pediades*, *Amanita* sp., and along with these *Curvularia lunata* was also shown to exhibit plant growth promotion of seedlings. These fungi were found to show high phosphate solubilizing abilities with 14-50 mg orthophosphates from 250 mg of insoluble phosphates. The acid phosphatase activity of the cell free broths ranged from 2-7 µg nitrophenol/ ml/ 10 minutes whereas the cell-bound acid phosphatase activity ranged from 20-40 µg nitrophenol/ ml/ 10 minutes for different fungi studied. The *in vivo* assays showed an increment in biomass of inoculated seedlings from 20-50% over control. Ectomycorrhizal bioinoculants are thus suitable candidates for sustainable management of tree nutrition in forests and agroforests.

Keywords: *Terminalia arjuna*; Tasar host plants; Ectomycorrhiza; Sustainable nutrient management; agroforests; *Phlebopus*

MSD-17 (Poster)

Assessment of Degradation Potential of Fungal Isolate for Biofertilizer Production from Different Agriculture Waste

Kirti[1], Namita Singh[1] and **Renu Singh[2*]**
*renucollege09@gmail.com

[1]Department of Biotechnology, Guru Jambheshwar University of Science and Technology (GJUST), Hisar, Inida; [2]PhD, Plant Research International, Wageningen University and Research, Netherlands

Abstract: With the increasing population and diminishing agricultural land, developing biofertilizers from agricultural waste, which contains lignocellulosic biomass, using fungal consortia provides a sustainable solution. This approach enhances soil fertility and crop yields, addressing both food scarcity and efficient land use. The study aimed to produce biofertilizers from rice husk, mixed plant leaves, and peels to improve soil fertility and support sustainable crop yields. Rice husk peels, and plant leaves were inoculated with fungi and allowed to degrade for 30 days. Post-degradation measurements were taken to assess cellulose, hemicellulose, lignin degradation, and NPK content increase. This study also investigates the functional groups, surface morphology, and elemental composition of a sample using various analytical techniques. Fourier Transform Infrared Spectroscopy (FTIR) was employed to identify and characterize the functional groups present in the sample. Scanning Electron Microscopy (SEM) was utilized to examine the surface morphology, providing insights into the texture and structure of the sample. Energy-Dispersive X-ray Spectroscopy (EDX) was used for elemental mapping, revealing the presence and distribution of various elements within the sample. The combination of these techniques offers a comprehensive understanding of the sample's chemical and physical properties. In conclusion, the study successfully demonstrated the potential of fungal consortia to transform

agricultural waste into valuable biofertilizers. This approach not only enhances soil fertility and crop yields but also offers a sustainable solution to the challenges of food scarcity and diminishing agricultural land. The findings underscore the viability of using agricultural waste as a resource for eco-friendly agricultural practices, contributing significantly to sustainable farming and efficient land use.

Keywords: Agriculture waste, Lignocellulosic Biomass, Biofertilizer, Microbial Consortium.

MSD-18 (Poster)

Transforming Forestry Waste into Bioethanol and Antifungal Agents: A Sustainable Approach

Pooja Sharma*
*gunjanpu333@gmail.com

Department of Biological and Chemical Sciences, Baba Farid College, Bathinda, Punjab (151002), India

Abstract: The increasing need for sustainable bio-fuels has prompted investigations into the holistic utilization of forestry waste. This study focuses on converting leaves, stems and wood into bioethanol while synthesizing lignin-derived zinc oxide nanoparticles (ZnO-NPs) to combat phyto-pathogenic fungi. The fermentation process for bioethanol production was optimized using Response Surface Methodology (RSM) software, analyzing key parameters such as temperature, pH and substrate concentration. The resultant bio-ethanol exhibited promising yield and efficiency. Concurrently, lignin was extracted and converted into ZnO-NPs, which demonstrated significant antifungal activity against 3 common phyto-pathogens (*Fusarium oxysporm, F. proliferatum* and *Stemphylium vesicarium*). The study not only highlights the potential of forestry waste as a resource for renewable energy but also emphasizes dual benefit of producing eco-friendly antifungal agents. This holistic approach contributes to environmental sustainability by reducing waste and promoting the use of bio-based materials in agriculture. Future work will focus on scaling up production processes and further evaluating the efficacy of ZnO-NPs in field applications.

Keywords: Bioethanol; Lignin; Zinc xide nanoparticles; Forestry waste; Antifungal agents

MSD-19 (Poster)

Effect of Herbicides on Plant Growth Promoting Activities of *Nostoc* sp.

Anand Arunrao Atnoorkar*
*anand_atnoorkar@rediffmail.com

Department of Microbiology,
Vai. Dhunda Maharaj Degloorkar College, Degloor. District Nanded, Maharashtra, India

Abstract: The plant growth promoting cyanobacteria produces variety of plant growth promoting compounds. Glyphosate, metsulfuron methyl and oxyfluorfen are the common herbicides used in paddy fields. The present study was conducted to assess the effect of selected herbicides on plant growth promoting activities of *Nostoc* sp. The plant growth promoting activities viz. IAA production, phosphate solubilization and ammonia excretion was lowered at increased concentrations of herbicides. Oxyfluorfen significantly reduced the plant growth promoting activities of *Nostoc* sp.

Key words: *Nostoc,* Herbicides, Plant growth Promoting activities

MSD-20 (Poster)

Metabolic Engineering in *Azospirillum brasilense* for Heterologous Production of (+)-valencene

Dattesh Bala Saranga[1], Poonam Chahar[2], Kiran NR[1], Aafreen zehra[2], Rudra Prakash Mohanty[1], Pranav Murali Sharma[1], VS Pragadheesh[1] and Mukti N Mishra[1*]
datteshbs@gmail.com

[1]*CSIR-Central Institute of Medicinal and Aromatic Plants Research Centre, Bangalore, India*
[2]*CSIR-Central Institute of Medicinal and Aromatic Plants, Lucknow, India*

Abstract: (+)-valencene, a sesquiterpene, imparts a woody citrus characteristic and is economically important because it gives a juicy impression in citrus flavourings and fragrances. Currently, the market volume for (+)-valencene is about 10,000 kg per year, and another 5,000 kg of (+)-valencene is used per year for the production of nootkatone, which is used to provide a grapefruit-like flavour to soft drinks. (+)-valencene is produced in different plants. However, their presence in very low quantity makes the isolation difficult. Furthermore, their chemical synthesis is economically not viable. These facts have shifted the interest towards heterologous production of (+)-valencene in suitable microbial hosts by metabolic engineering. Although several microbes have been engineered for (+)-valencene production, the industrial scale yield is difficult to achieve in most them. The major issues are: (i) lack of efficient enzymes or their efficient/optimized expression to convert FPP into (+)-valencene; (ii) lack of sufficient starting substrate (FPP) for (+)-valencene production; and (iii) intracellular accumulation of the non-native (+)-valencene to the toxic level due to their insufficient extracellular transport. This study attempts to address the last two issues by engineering *Azospirillum brasilense*, a plant growth promoting bacterium, for heterologous (+)-valencene production, and investigating the effect of improvement in FPP pool and extracellular transport on the (+)-valencene yield. Expression of only CnVS of *Callitropsis nootkatensis* (an active (+)-valencene synthase) in an improved carotenoid producing strain (Car-3) of *A. brasilense* produces 1.9mg/L (+)-valencene. However, simultaneous expression of FPP synthase (IspA), DXS and Idi (the rate-limiting enzymes of the DXP pathway), which supposed to improve the flux toward FPP, using *CnVS-ispA-dxs-idi* operon improve the yield by 12-fold. Furthermore, over-expression of selected endogenous efflux-pumps in the above strain further improve the (+)-valencene yield by almost 2-fold (overall 25 fold). These results indicate the potential of this bacterium as a sesquiterpenoid producing host, and suggests the importance of extracellular transport engineering by identification and expression of (+)-valencene -specific efflux pumps to improve the (+)-valencene yield.

Keywords: Metabolic Engineering, Synthetic biology, Bacteria, *Azospirillum brasilense*, Heterologous expression, (+)-valencene.

MSD-21 (Poster)

A Study of Isolation and Identification of Antibiotic Resistant Bacteria from Waste Water of East Kolkata Wetlands from the Viewpoint of Sustainable Development

Purav Mondal[1] and Sarita Sarkar[1#]
puravmondal1993@gmail.com, sarita_sarkar@yahoo.in

[1]*Department of Biotechnology, The Neotia University, 24 PGS (South), West Bengal (743368), Inida*

Abstract: Antibiotic resistance is an emerging global threat to the environment and human health. One of the major causes of antibiotic resistance may be the aquatic ecosystem of wetlands that have emerged to be the most potential reservoir of antibiotic resistance gene as it is the disposal site of urban wastewater and sewage of human or animal origin loaded with clinical antibiotics. Wastewater from clinical, agricultural, industrial and livestock farms are often released without treatment into these wetlands that change the physiochemical niche of the microbes and expose them to different antibiotics or antibiotic resistance gene that alters their genetic constituents to transform them into potential pathogenic biofilm forming microbes and the contribution of the biofilm to act as a hotspot for bacterial antibiotic resistome in aquatic environment. Many people who are engaged in these wetlands for their livelihood are unknowingly being exposed to such deadly pathogens ignorant of the consequences. It is important to raise concern for the sustainability of water use for the welfare

of human health. Sustainable Development Goal 6 is concerned with the accessibility of clean water and sanitation. It is of crucial importance for innovative sustainable solution other than conventional wastewater treatment methods to combat the global challenges of antibiotics resistance that will help to mitigate the effect of antibiotics as a pollutant. East Kolkata Wetland, one of the most important RAMSAR site in Kolkata is acting as a dumping ground for antibiotics from various source. From the point of SDG 6, this presentation will focus in isolation and identification of coliform and non-coliform bacteria and their antibiotic resistance developed over time and their potential ability of biofilm formation, which may be directly related with the various health hazards of the people engaged in EKW.

Keywords: Antibiotic resistance, Wastewater, Biofilm, RAMSAR site, Sustainable Development Goal, EKW

MSD-22 (Poster)

Phenol Degradation by Orthocleavage Pathway of *Pseudomonas stutzeri* Strain Naun-1B

Utkarsh Singh[1]* and Shikha Sharma[1]
utkarshbiotech@yahoo.com

*[1]*Department of Microbiology, RCP (PG) College of Allied Sciences, Roorkee, Uttarakhand, India*

Abstract: A number of species of bacteria hold the ability to catabolize phenol and other phenolic compounds through the formation of the respective catechols and their cleavage either by an ortho-cleaving enzyme, catechol-1,2-dioxygenase, or by a meta-cleavage enzyme, catechol 2,3-dioxygenase, the product of the ring cleavage being the cis-cis-muconic acid and 2-hydroxymuconic semialdehyde respectively. Generally, bacterial species degrade phenol through the meta-pathway. The majority of *Pseudomonas* species degrade phenol through meta-pathway. However most yeast species reported to degrade phenol utilize the ortho-pathway. There are only a few reports of bacteria utilizing the ortho-pathway for the degradation of phenol. The effluent samples and soil samples were collected from dumping site of coke oven in Haridwar (U.K.) following the standard methods mentioned in American Public Health Association (APHA). Effluent and soil samples were plated on nutrient agar plates containing phenol and cyanide which incubated at 28°C for 24 hours. The cell debris were removed by centrifugation for 20 min at 15000 rpm. The supernatant fluid was used for the enzyme assay. The protein content of the cell free extract was estimated by Lowry's method. Phenol hydroxylase activity was checked by formation of catechol from phenol degradation. Catechol was identified by using thin layer chromatography technique (TLC). Catechol 1,2-di oxygenase was assayed according to Nakajawa and Nakajawa (1970). Catechol 2,3-di oxygenase was determined by method of Nozaki (1970). Out of 15, 02 isolates NAUN-1B and NAUN-16 displayed maximum survivability in presence of phenol and cyanide. NAUN-1B and NAUN-16 showed phenol tolerance upto 1800 mg/l whereas cyanide tolerance was upto 300mg/l and 340 mg/l respectively. Usually *Pseudomonas* degrade phenol through meta-pathway, but *Pseudomonas stutzeri* strain NAUN-1B isolated by coke oven effluent degraded phenol through the ortho-pathway. The strain tolerated phenol up to 1700 mg/l. Cell-free extracts of the strain had catechol 1,2-dioxygenase (C1,2-D) showing ortho-cleavage activity but no meta-cleavage as catechol 2,3-dioxygenase activity was not found significant. The study can be implemented for bioremediation process in phenolic waste water contaminated sites.

Keywords: Pseudomonas stutzeri, American Public Health Association (APHA), NAUN-1B and NAUN-16

MSD-23 (Poster)

Ammonium Excreting *Microbacterium bengalensis sp.* nov. GB16_1_BI from Rice Rhizosphere

Papri Nag[1,2*], Nibendu Mondal[2], Jagannath Sarkar[2] and Sampa Das[2]
paprinag2003@yahoo.com

[1]ICAR-IIRR, Rajendranagar, Telangana, India
[2]Bose Institute, Kolkata, West Bengal, India

Abstract: A novel gram positive, high GC content bacterial strain, GB16_1_BI, was isolated from rice roots cultivated in the Madhyamgram field station of Bose Institute, West Bengal, India. GB16_1_BI is a, non-motile,

nitrate reducing, ammonium releasing bacterium. Whole cell fatty acid analyses showed C16:0 iso, C17:0 anteiso and C15:0 anteisowere the predominant fatty acids. 16S rRNA phylogeny showed 99.28% similarity with *M. proteolyticum*^{T} CECT 8356 and 98.68 % similarity with *Microbacterium hominis*^{T}DSM 12509. The Average Nucleotide Identity-analysis of GB16_1_BI showed highest identitywith *M. proteolyticum*^{T} CECT 8356 (ANIb: 81.71 %; ANIm: 86.30 %). Comparison of DnaB and RecA sequence of GB16_1_BI with genomes sequences available publicly also showed that GB16_1_BI is a novel species. Based on our studies, we designate that GB16_1_BI (= MTCC 13245) as *Microbacteriumbengalensis* sp. nov GB16_1_BI.

Keywords: *Microbacterium bengalensis sp*., GB16_1_BI, ammonium releasing bacterium, *M. proteolyticum*^{T}

MSD-24 (Poster)

Screening and Biochemical Characterization of Halotolerant Bacteria Isolated from *Chenopodium album* L. Rhizosphere

Tanisha Gangrade[a], Monika Kayasth[a*], Jagdish Parshad[a] and Sunaina Kumari[a]
tanishagangrade@gmail.com

[a]*Department of Microbiology, College of Basic Sciences & Humanities, Chaudhary Charan Singh Haryana Agricultural University, Hisar (125004), Haryana, India*

Abstract: The rhizosphere, the soil region surrounding plant roots, is a dynamic environment rich in microbial diversity. Among these microorganisms, halotolerant bacteria play a crucial role in supporting plant growth under saline conditions. *Chenopodium album* L., a common plant species known for its resilience in various soil types, particularly in saline soils, provides a unique habitat for these bacteria. Isolation, screening, and biochemically characterizing halotolerant bacteria from the rhizosphere of *C. album* is essential for understanding their potential applications in agriculture. These bacteria can enhance plant tolerance to salinity, promote growth, and improve soil health, making them valuable candidates for sustainable farming practices in saline environments.

This study focused on isolating and characterizing these bacteria to explore their potential applications in various research fields. Soil samples from the rhizosphere were collected and subjected to serial dilution and plating techniques on selective media supplemented with varying concentration of salt to isolate halotolerant bacterial strains. The isolates were screened for their tolerance to various salt concentrations and identified based on morphological and biochemical characteristics. On the basis of various biochemical and morphological characteristics the isolated were tentatively identified as *Bacillus* and *Pseudomonas*. The findings suggest that the halotolerant bacteria isolated from *Chenopodium album* L. rhizosphere may have practical applications in developing bioinoculants for improving crop productivity in saline-affected areas.

Keywords: Halotolerants, Rhizosphere, *Chenopodium*, Bacteria

MSD-25 (Poster)

Holistic Approach on Bio-Enzyme Production and Pretreatment of Sweet Sorghum Bagasse for Enhancement of Biogas Yield

Yashika Aggarwal[a] and Urmila Gupta Phutela[a&b]
aggaryashika3107@gmail.com

[a]*Department of Microbiology, Punjab Agricultural University, Ludhiana (141004), Punjab, India*
[b]*Department of Renewable Energy Engineering, Punjab Agricultural University, Ludhiana (141004), Punjab, India*

Abstract: Generating biogas from the lignocellulose-rich residue through the anaerobic digestion process by the diverse microbial communities proved an effective solution in managing the agricultural leftovers after crop cultivation. Sweet sorghum, primarily a fodder crop, is widely recognized as an ideal substrate for biofuel (ethanol) production due to its balanced composition of soluble and insoluble carbohydrates. However, high

lignin content and highly polymerized and crystallized cellulose in sweet sorghum results in low digestibility, necessitating the pretreatment process to enhance the cellulose availability for improved microbial or enzymatic attack. This study focuses on enhancing biogas production by biologically pre-treating the sweet sorghum bagasse with bio-enzymes. Bio-enzyme is a fermented solution produced by the anaerobic fermentation of organic substances with jaggery and water in the ratio of 3:1:10 with the help of diverse indigenous microflora. Here, the present studies were conducted on the production of bio-enzymes from the mosambi peels and analyzed for their physical, biochemical, and enzymatic properties. The sweet sorghum bagasse pretreated with 10% bio-enzyme for 4 days showed a reduction of around 56.97% in total solids, 4.31% in volatile solids, and 16.16% in hemicellulose and 25.43% in cellulose respectively while the lignin was decreased at 7.02% as compared to untreated sets. Biogas production studies at lab scale plants showed improved biogas yield of about (>85%) as compared to untreated sweet sorghum bagasse. Thus mosambi-based bio-enzyme is found to be a cost-effective environment-friendly solution for enhancing biogas production from various organic wastes.

Keywords: Sweet-sorghum, Biogas, Pre-treatment, Bio-enzymes, Fermented, Mosambi

MSD-26 (Poster)

Combined Effect of Zinc Oxide Nanoparticles and *Mesorhizobium* on Nodulation and Growth of Chickpea Crop

Raksha Jain, Ajay Kumar*, Meena Sindhu, Ankush Dhanda, Raj bala and Prema Siva Naga Teja Alapati
rakshajain98@hau.ac.in

Department of Microbiology
CCS Haryana Agricultural University, Hisar (125 004), India

Abstract: Chickpea (*Cicer arietinum* L.) is a crucial legume which is highly nutritious, offering proteins, carbohydrates, dietary fiber, unsaturated fatty acids, and potassium. Despite these benefits and its superior protein quality, chickpea yields have remained stagnant over the past decade, largely due to seed deterioration from adverse environmental conditions. Chickpeas respond poorly to nitrogen, phosphorus, and potassium (NPK) fertilizers but benefit from micronutrients, with zinc being vital for enzyme functions and growth. Chickpeas are more sensitive to zinc compared to cereals, necessiting the need for effective zinc management. This study explores the interaction of *Mesorhizobium* and zinc oxide nanoparticles followed by combined effects of zinc oxide (ZnO) nanoparticles and *Mesorhizobium* on chickpea crop. Interaction result showed that nanoparticles did not adversely affect either *Mesorhizobium* or chickpea up to 1000 ppm under laboratory conditions. Subsequent pot house studies evaluated the combined effect of ZnO nanoparticles at concentrations of 300, 400, 500, and 1000 ppm with *Mesorhizobium*, focusing on physiological parameters such as chlorophyll content, nutrient uptake (phosphorus, nitrogen, and zinc), yield, and nodulation efficiency. The study found that the combined application of ZnO nanoparticles and *Mesorhizobium* enhanced the plant growth and production as compared to individual application. The findings suggest that ZnO nanoparticles, when used in conjunction with *Mesorhizobium*, can significantly enhance chickpea yield in both quality and quantity.

Keywords: *Mesorhizobium*, Nanoparticles, Chickpea, Nodulation

MSD-27 (Poster)

Effect of Bio-stimulants on Fibre Quality Traits of Contrast Cotton Genotypes

Siddharth Saroha[1*], Vinod Kumar[1], Karmal Singh[1], Anil Kumar Dhaka[1]and Swati[2]
Sidsaroha1997@gmail.com

[1]*Department of Agronomy, CCS Haryana Agricultural University, Hisar (125 004), India*
[2]*Department of Botany and Plant Physiology, CCS Haryana Agricultural University, Hisar (125 004), India*

Abstract: A field experiment was conducted during the *Kharif* 2021 at the Cotton Research Area, CCS Haryana Agricultural University, Hisar, Haryana, to investigate the influence of bio-stimulants on fibre quality

characteristics of contrasting cotton genotypes. The factorial randomized block design (FRBD) included two main plots: *Bt* cotton varieties RCH 776 and non-*Bt* cotton H 1098i, each subjected to four sub-plot treatments: B1 (bio-stimulant at 30, 45 and 60 days after sowing [DAS]), B2 (bio-stimulant at 45, 60, and 75 DAS), B3 (DMSO spray at 30, 45, 60 and 75 DAS), and B4 (control water spray at 30, 45, 60 and 75 DAS), replicated thrice. The longest span length (27.40 mm) was numerically recorded in treatment B1, followed by B3, with genotype RCH 776 exhibiting the longest span length (27.10 mm). Treatment B1 also resulted in the highest ginning out turn (30.55%), followed by B2, while genotype RCH 776 showed a significantly higher ginning out turn (29.74%) compared to H 1098i. Micronaire value analysis indicated that treatment B1 recorded the highest value (4.50 µg inch-1), followed by B2 and B4, with no significant genotype effect observed. However, RCH 776 consistently displayed higher micronaire values (4.41 µg inch^{-1}) than H 1098i (4.28 µg inch^{-1}). These findings highlight the potential of bio-stimulants to positively influence fibre quality parameters in cotton, specifically span length, ginning out turn, and micronaire value. The results underscore the importance of optimizing bio-stimulant application strategies to enhance cotton fibre quality, thereby contributing to sustainable cotton production practices.

Keywords: Bio-stimulants, Cotton genotypes, Fibre quality, Span length, Ginning out turn, Micronaire value

MSD-28 (Poster)

Biodigested Straw Based Microbial Cellulase Production and Pretreatment of Paddy Straw for Improved Biogas Yield

Karvembu Palanisamy[a] and Urmila Gupta Phutela[ab]
vembubiomicro@gmail.com

[a]*Department of Microbiology*
[b]*Department of Renewable Energy Engineering*
Punjab Agricultural University, Ludhiana (141004), Punjab, India

Abstract: Paddy straw, the major lignocellulosic residue generated from the paddy cultivation mainly consists of holocellulose (Hemicellulose and Cellulose) core fraction surrounded by the polymerized structures of silica-lignin. Despite the conventional usage, the production of biogas from the organic rich paddy straw sought to be a sustainable waste valorisation technology. The installation of large number of these paddy straw-based biogas plants creates another problem in the management of anaerobically digested straw materials. The commonly practiced process utilization as a soil amendment such as organic fertilizer, and conditioner doesn't meet the desired accountability. So, in the present study the experiment for the production of Cellulolytic enzymes (Endoglucanase, β-glucosidase and total cellulase) was conducted by utilizing the digested spent waste as a growth substrate and then ultimately utilizing these hydrolytic enzymes for biologically pre-treating the paddy straw for biogas generation. The digested straw was characterized for the chemical and elemental analysis and culturing the cellulolytic microbes (*Phanerochaete chrysosporium* MTCC787, *Pleurotus ostreatus* MTCC142 and *Trichoderma reesei* MTCC164) in solid state fermentation. It was observed that the *Trichoderma reesei* MTCC164 produced high cellulolytic enzyme activities as compared to other two cultures. The maximised yield of endoglucanase (21.58 IU/gds); β-glucosidase (13.11 IU/gds) and total cellulase (8.46 FPU/gds) was observed at the optimized growth conditions of 30°C, 60% (v/w) moisture content and 5.5 pH after 4 days of incubation. The biogas production studies on 2L lab model plant showed that the paddy straw pretreated with crude cellulase enzyme showed (>33%) improved biogas yield as compared to untreated paddy straw.

Keywords: Paddy straw, Biodigested straw, Microbes, Cellulase, Pretreatment, Biogas.

MSD-29 (Poster)

Potato Waste Valorization for Gluconic Acid Production Using Microbial Consortium: A Step towards Waste to Wealth

D. Vijaysri[1], Livleen Shukla[1*], S. T. M. Aravindharajan[1], S. H. Manoj[1] and Sandeep Kumar Singh[1]
lshukla65@gmail.com

[1]*Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi (110012), India*

Abstract: Gluconic acid, one of the organic acids is the product of glucose oxidation. It is the naturally existed poly hydroxyl carboxylic acid occurring naturally in various substances *viz.*, plants, vegetables, fruits, and other foodstuffs such as rice, dairy products, meat, honey, wine and vinegar. The demand for gluconic acid is increasing in recent years because of its wider applications in various fields such as chemical, food, beverage, pharmaceutical, textile and other industries. Therefore, an attempt was made for the enhanced production of gluconic acid with potato waste using microbial consortium. 15 bacteria and 20 fungi were isolated from potato waste and screened qualitatively for the gluconic acid production. Thin layer chromatography and quantitative screening had confirmed that 3 fungal isolates were efficient compared to all other isolates with the yield ranging from 59.79±0.6 to 79.67±1.70 g/L. The isolates were further used for the development of consortium and it was observed that the consortium prepared using all the three fungal isolates were able to produce highest gluconic acid (85.76 ± 0.45 g/L) when compared to other combinations. Therefore, further with the process optimization, the microbial consortium can be used for enhanced production of gluconic acid using potato waste.

Keywords: Potato waste, Valorization, Gluconic acid, Consortium, Thin Layer Chromatography (TLC)

MSD-30 (Poster)

Isolation and Screening of Lignocellulolytic Enzyme Producing Bacteria from Hydrilla Compost

Sunaina Kumari[a], Monika Kayasth[a*] and Jagdish Parshad[a]
*monakayasth@gmail.com

[a] *Department of Microbiology, College of Basic Sciences & Humanities, Chaudhary Charan Singh Haryana Agricultural University, Hisar (125004), Haryana, India*

Abstract: The quest for sustainable and eco-friendly solutions has led researchers to explore the potential of lignocellulolytic enzymes in breaking down complex plant materials. These enzymes, produced by certain bacteria, can degrade lignocellulose, a major component of plant biomass, into simpler sugars. This process is crucial for applications in biofuel production, waste management, and sustainable agriculture. In this study, the compost was prepared by mixing shredded hydrilla, paddy straw, and cattle dung, and subjected to aerobic composting under controlled conditions. Isolation and screening of bacteria from hydrilla compost that produce lignolytic enzymes. Microbial populations were isolated by serial dilution and plating on selective media enriched with lignocellulosic substrates after different intervals of time. Colonies showing distinct growth patterns were screened for lignocellulolytic activity by assessing their ability to degrade cellulose and lignin. Cellulase activity was evaluated using carboxymethyl cellulose as substrate while Laccase activity was assessed by taking guaiacol as a substrate in quantitative assay. In the study, we found that the isolate SK20 is capable of producing both cellulase and laccase in an effective quantity suggesting it's potential role in enhancing composting processes and bioconversion applications.

Keywords: Hydrilla, Lignocellulolytic enzymes, Compost

MSD-31 (Poster)

Harnessing Phragmites Biomass: A Sustainable Strategy for Chilika Wetland Ecosystem Management and Conservation

Deepsikha Panigrahi[1] and Vishakha Raina[1*]
*vraina@kiitbiotech.ac.in

[1]*Environmental Biotechnology Lab, School of Biotechnology, KIIT University, Campus-11, Bhubaneswar, Odisha (751024), India*

Abstract: Chilika Lake, the largest brackish water coastal biodiversity hotspot on the east coast of India is currently facing effects of climate change resulting in ecological degradation, primarily due to several cyclones, increased sedimentation and the proliferation of invasive plant species like *Phragmites karka*. This invasive reed, owing to its rapid growth and large biomass is encroaching on large areas of the lake thereby decreasing water column and affecting lake biodiversity. We aim to investigate the potential of *P. karka* as a bioresource for biomass valorization and provide it as a strategy for its effective management and conservation of biodiversity. *P. karka* biomass obtained from Northern sector of Chilika Lake was processed and subjected to alkali treatment, bleaching, and acid hydrolysis for extraction of cellulose. The elimination of non-cellulosic component and enhancement of crystallinity of cellulose increased following acid hydrolysis. The samples were analysed by FTIR and XRD. The extracted cellulose was found to be suitable for papermaking (by Kraft pulping process) and production of different composite materials (polymer based particleboard) through processes like mechanical size reduction, drying, adhesive application, pressing, and curing. The particle boards were tested for tensile and flexural strength to show suitability to be utilised as an alternative material for formation of corrugated boards, furniture, tiles etc. Handmade paper prototypes were analysed on a microscopic level to check quality of fibre and packing.
The invasive plant in the lake although a menance, can be harnessed as a renewable resource to produce valuable products thereby reducing reliance on traditional wood sources, offering sustainable livelihood to the local population, countering the effects of deforestation, and addressing the challenges posed by its rapid spread.

Keywords: Chilika lake, Phragmites karka, Biomass valorization, Cellulose extraction, Composite materials, Sustainable livelihood

MSD-32 (Poster)

Unravelling Methanogens Evolution: A Comparative Study of Phylogenetic Methods

Rashmi Dhanwar[1], Ujjwala Wagmare[1], Dimple Davray[2] and Om Prakash[1]
rashmidhanwar@gmail.com

[1]*Symbiosis Centre for Climate Change and Sustainability, Symbiosis International (Deemed University), Lavale, Pune (412115), Maharashtra, India*
[2]*Dr. D. Y. Patil Biotechnology and Bioinformatics Institute, Tathawade, Pune (411033), Maharashtra, India*

Abstract: Methanogens are a group of archaea capable of methanogenesis and, hence, have a significant role in biogas production. Based on their metabolism, methanogens are grouped into different categories: methylotrophic, hydrogenotrophic, acetoclastic and alkylotrophic methanogens. Amongst these, hydrogenotrophic methanogens have been of interest in biogas upgradation technologies due to their metabolism to produce methane (CH_4) from carbon dioxide (CO_2), sequestering carbon and tackling climate change.
Phylogenetic characterization of these methanogens is mostly based on 16S rRNA gene sequence and a unique functional marker of methanogens, i.e., the *mcrA* gene sequence, which encodes the alpha subunit of methyl-coenzyme M reductase that catalyzes the last step of methanogenesis. To identify which method of phylogenetic characterization offers a more accurate phylogenetic resolution, we have compared the phylogenetic trees constructed based on 16S rRNA gene sequence, *mcrA* gene sequence and the complete genome sequence of 87 methanogens, which were selected based on the availability of the complete genome sequences on the NCBI database. The trees were constructed using the Genome Taxonomy Database and MEGA 11 software. It was found that the proper grouping as per genus and known classification of these methanogens was found only using the complete genome sequence.

Keywords: Phylogenetic Methods, Methanogenesis, *mcrA* gene sequence, MEGA 11 software

MSD-33 (Poster)

Exploration of Pigmented Endophytic Fungi from Medicinal Plants for Sustainable Production of Bioactive Red Chromes and Testing of their Potential as Cosmetic Colourants

Mehak Kaur[1,2] and Dr Mayurika Goel[1*]
mayurika.goel@teri.res.in

[1]*Sustainable Agriculture, the Energy and Resources Institute, TERI-Gual Pahari, Gurugram, Haryana (122001), India*
[2]*Department of Botany, University of Delhi, Delhi (110007), India*

Abstract: Colours have been used since ancient times to enhance the beauty and aesthetic of many commodities. Synthetic colorants that are currently being employed heavily in cosmetic, food and textile industries are known to be recalcitrant, toxic, mutagenic, and carcinogenic. Their effluents in water bodies decrease sunlight penetration, photosynthesis and plant proliferation. Thus, in the search of sustainable and natural sources of pigments, medicinal plant *Avicennia marina* from the mangrove Alibaug forest of Maharashtra, India was explored for bioactive pigment producing endophytic fungi. Amongst the many, *Talaromyces* sp. CPEF04 was identified as elite pigmented strain with profuse extracellular dark red pigment. Optimum culturing media and extraction solvent were identified to sustainably upscale the pigment for enhanced yield and maximum red colour (reported as milligram equivalent of Carmine). Its methanolic pigment was found to possess antibacterial activity against human anthropogenic bacteria *Staphylococcus aureus, Salmonella typhimurium,* methicillin-resistant *S. aureus* (MRSA) and *Vibrio cholerae*, antifungal activity against phytopathogenic fungi *Alternaria solani, Colletotrichum capsici, Fusarium oxysporum* and *Rhizoctonia solani,*and antioxidant activity against free radicals, 2,2-diphenyl-1-picrylhydrazyl, 2,2'-azino-bis(3-ethylbenzothiazoline-6-sulfonic acid), DNA nicking assay and reactive oxygen species. The pigmented extract had no cytotoxicity against human embryonic kidney HEK 293T and murine macrophage RAW264.7 cell lines and exhibited prolific anti-inflammatory activity through lipopolysaccharide induced nitric oxide inhibition in RAW264.7 cell line. Its pigment was characterized via ultra-high-performance liquid chromatography-photodiode array detector-mass spectrometry (UPLC-DAD-MS). To assess the market viability of the pigment, pigmented lip tints/salves were formulated, assessed using colorimeter's CIE l*a*b* values for optimal red hue and texture analyzer for enhanced softening effect. The selected tints were stable for six months at different temperatures with a sun protective factor of 30. A sensory assessment involving 25 participants indicated significant consumer approval. Bioprospecting medicinal plants for bioactive pigment producing endophytes has the potential to foster an eco-friendly lifestyle.

Keywords: Microbial pigments, Bioactives, Antimicrobial, Anti-Inflammatory, Sustainable cosmetics, Sensory evaluation

MSD-34 (Poster)

Physiological Characterization of Fish Scale Degrading Bacteria from the Marine Environment

Pragati Shetty, Manjusha L, Amjad K. Balange, B.B.Nayak and Sanath Kumar H*
sanathkumar@cife.edu.in

Fish Processing Technology- FRHPHM Division, ICAR-Central Institute of Fisheries Education, Mumbai, Maharashtra (400061), India

Abstract: Several bacteria produce collagenase enzymes that can degrade fish collagen, producing collagen peptides and amino acids. The marine bacteria are good sources of collagenolytic enzymes, and these have higher catalytic activities against fish bone, scale, and skin collagen. Fish scales, which typically weigh between 1-2% of the body weight of fish, are an important component of fish waste generated post-processing. Due to their slow degradation and negative environmental impact, fish scales offer a formidable challenge for their disposal. The biological method of degrading the scales is an effective and environment-friendly method of remediating fish waste. Thus, this study aimed to identify and characterize fish scale degrading bacteria from the

marine environment and employ them to hydrolyze fish scales on a laboratory scale. Fifteen isolates used in this study were identified by sequencing of partial 16S rRNA gene. Preliminary experiments using Rohu and mixed carp scales revealed that all 15 isolates could degrade the scales at varying levels in Luria Bertani (LB) broth and simple nutrient broth containing peptone or tryptone and salt. Following this, the degradation experiments were carried out for 5, 10, 15, and 20 days using different media prepared in seawater. Of all the bacterial isolates tested in this study, *Priestia flexa (*A9) showed the highest scale degradation efficiency of 68% in LB broth prepared in seawater after five days of incubation. Other isolates also exhibited scale degrading abilities in the 40-60% range over varying incubation periods. Some isolates, such as *Macrococcus caseolyticus*, *Staphylococcus epidermidis*, and *Bacillus stratosphericus*, *Bacillus subtilisStenotrophomonas maltophilia*, *Virgibacillus salaries* and *Lysinibacillus fusiformis* exhibited efficient scale degrading abilities in all the media tested in this study. This study shows that bacteria of marine origin can be valuable for remediating fish scales and reducing environmental impact. Further, the degradation of scales and collagenase production can be achieved using peptone derived from fish waste. This would make the process economical and ensure a circular bio-economy that utilizes all forms of fish waste generated in fish processing industries.

Keywords: Scale, Bio-degradation, Waste management, Bio-economy, Collagenase

MSD-35 (Poster)

Optimisation of the Production Parameters of a Novel Heteropolysaccharide Obtained from *Periconia* sp., RA1 an Endophyte of Native Rice Variety

Hiran Kanti Santra[1] and Debdulal Banerjee[1,2]
db@mail.vidyasagar.ac.in

[1]*Microbiology and Microbial Biotechnology Laboratory, Department of Botany and Forestry, Vidyasagar University, Midnapore (721102), West Bengal, India.*
[2]*Centre for Life Sciences, Vidyasagar University, Midnapore (721102), India*

Abstract: Exopolysaccharides from microbes hold a variety of potential in both agriculture and pharmaceuticals. The major bottleneck for their mass application is the low quantity of production. Here, we have performed a three-phase optimisation to maximise the production of a potent antioxidative heteropolysaccharide of endophytic fungal origin. Initially, the One Factor At a Time technique (OFAT) was adopted to fix the media composition and culture requirements to enhance the outcome, and 16 g L^{-1} of dextrose, 4 g L^{-1} of yeast extract, 1.5 g L^{-1} of NaCl, and 0.5 g L^{-1} of $(NH_4)_2SO_4$, a media pH of 7.5, agitation of 120 rpm, and 6 days of dark incubation at 28±2°C with a basal potato dextrose broth at a 1.5 L bioreactor with 0.3 L headspace and 100 mL/min O_2 availability had been detected to cause a 2-fold increase in EPS yield (6.15±1.01 g L^{-1} to 13.69±2.47 g L^{-1}). The second level of enhancement was recorded upon adopting Response Surface Methodology (RSM) and Box Behnken Design (BBD), where the four most interactive factors were statistically validated for their highest impact on EPS generation using a second-order polynomial equation and a 0.5-fold (19.13±2.98 g L^{-1}) surge was noted. Finally, the epigenetic modulator, i.e., the histone methyl transferase-specific probe of BRD4770, was supplemented (100 nm) to the culture broth, and 23.67±3.01 g L^{-1} of EPS was produced. For its biotechnological utility, a higher production of endophytic heteropolysaccharide is required, given its promising antioxidative action and potential for on-field application.

Keywords: Exogenous antioxidants, Bio-active endophytes, Extra-cellular polymers, Biological macro-molecules, Process optimisation.

MSD-36 (Poster)

Acid-Tetrahydrofuran-Organosolv Sequential Two-step Microwave-Assisted Pretreatment for Lignocellulosic Biomass Fractionation to Valuable Platform Chemicals: A Circular and Sustainable Approach

Lakshana G Nair and Pradeep Verma*
lakshanagnair@gmail.com, pradeepverma@curaj.ac.in

Bioprocess and Bioenergy Laboratory, Department of Microbiology,
School of Life Sciences, Central University of Rajasthan,
Bandarsindri, Kishangarh, Ajmer, Rajasthan (305817), India

Abstract: Lignocellulosic biomass (LCB) is undeniably a sustainable and efficient feedstock that can be exploited to produce various value-added products like biofuels, fuel precursors, and other platform chemicals. To overcome the recalcitrance of the LCB, the present system employs a pretreatment method involving a microwave-assisted organosolv pretreatment, using Tetrahydrofuran (THF), a high lignin dissolution solvent. Initially, the system was monitored using 50% THF with a solvent-biomass ratio of 20:1, with LCB sources like rice straw, wheat straw, coconut husk, and sugarcane bagasse. Pretreatment results revealed that the system at 100°C and 40 min with rice straw, under microwave heating was found to be most efficient, with a sugar yield of 65.21% (72 h). Pretreatment performed in a conventional heating apparatus with similar conditions to the microwave reported sugar yields of 23.99% (72 h). Further, a two-step acid-based organosolv pretreatment involving an initial step of 10 min pretreatment using 0.5% H_2SO_4 and 30 min of 50% THF-based organosolv pretreatment in the next step, both using microwave-assisted heating at 100°C led to a final sugar yield of 96.77% (72 h), which was higher as compared to the conventionally heated sample (78.97%). Moreover, the FTIR and XRD analysis confirm changes in the structure and crystallinity of the pretreated samples compared to untreated LCB. LC-HRMS analysis also confirms the presence of ~12 platform chemicals in the hydrolysates of the microwave-assisted samples. The screened platform chemicals are known to have great importance as starting materials in various industries. This confirms the use of microwave-assisted-organosolv pretreatment system as an efficient to convert LCB into valuable platform chemicals.

Keywords: *LCB, THF, Pretreatment, Organosolv, Microwave, Platform chemicals*

MSD-37 (Poster)

Enrichment-Based Isolation and Identification of 4-Chlorophenol Degrading Bacteria from Industrial Polluted Soil

Ritu Rani and Dharmender Kumar*
dkbiology@gmail.com

Department of Biotechnology, Deenbandhu Chhotu Ram University of Science & Technology,
Murthal Sonipat-(131039), India

Abstract: The remediation of industrially polluted soil presents considerable challenges for the environment, particularly with pollutants such as 4-chlorophenol (4-CP), a hazardous and persistent organic molecule. Due to rapid development, population growth and socioeconomic advancement have significantly increased human impact on ecosystems, which is the primary cause of pollution in the environment. The purpose of this study was to isolate and characterize bacterial strains capable of degrading 4-CP from contaminated soil utilizing an enrichment technique. Soil samples were taken from a polluted industrial area and enriched in a minimal salt medium (MSM) with 4-CP as the only carbon source. After several enrichment cycles, bacterial strains were successfully identified and purified. Here, out of interest, we reported two 4-CP degrading isolates. Morphological, biochemical, and molecular characterizations were used to identify the bacteria, and 16S rRNA gene sequencing confirmed their taxonomic status. The degradation potential of these strains was assessed in liquid MSM cultures, with conc. 600mg/L of 4-CP degradation quantified with 4- aminoantipyridine (APA) test. Furthermore, results of (APA) showed degradation efficiency of *Pseudomonas sp*. NCP 1 strain (PQ215898) is 90% andfor *Bacillus subtilis* BCP4strain (PQ215895) is 95%. The strains efficiently degraded 4-CP,

highlighting their potential for bioremediation applications. The findings reveal that these isolated bacterial strains could be used effectively in bioremediation procedures to reduce 4-CP contamination in industrial soils.

Keywords: 4-Chlorophenol Degrading Bacteria, Minimal salt medium (MSM), rRNA gene sequencing, *Bacillus subtilis* BCP4strain

MSD-38 (Poster)

Ammonia Oxidation by Ammonia-Oxidizing Bacteria (AOB), *Staphylococcus* Sp.

Arti Chamoli and Santosh Kumar Karn*
chamoliarti90@gmail.com, santoshkarn.sbsu@gmail.com

Department of Biochemistry and Biotechnology, Sardar Bhagwan Singh University, Balawala, Dehradun (248008),, Uttarakhand, India.

Abstract: Current research focuses on screening efficient AOB strain which can utilize ammonia as a sole energy source and is proficient in transforming ammonia into less harmful forms. A bacterial strain named Am (RS) was isolated from plant roots of green gram. The isolated strain was grown in a liquid medium with different concentrations of ammonia ranging from 100 to 1000 mg/l for 10 days. Growth and transformation were measured spectrophotometrically. Bacterial growth was found less in lower concentrations (100 mg/l). Maximum transformation of ammonia was observed at 400 mg/l with 86% into nitrate and less into nitrite. Gaseous nitrogen was also observed during the transformation by the strain. The experimental observation states that the strain is highly efficient for the transformation of the nitrogen compounds. Further, the strain was identified molecularly using 16S rRNA sequencing as *Staphylococcus* sp. Next, this strain is now being prepared for an *In-situ* remediation experiment.

Keywords: Ammonia-oxidizing bacteria (AOB); Ammonia; Nitrite; Bioremediation; Sequencing.

MSD-39 (Poster)

Bacterial Pigment: Sustainable alternative to Synthetic Dyes

Shruti. B. Mhaske* and Rohini.P. Kulkarni
*mhaskeshruti21@gmail.com

**Department of Microbiology, Government Institute of Science, Aurangabad (431004), India*
Department of Microbiology, Government College of Arts and Science, Aurangabad (431004), India

Abstract: In the recent years use of synthetic dyes has been issue of concern due to its adverse effect on various factors like health risk, environmental pollution, depletion in the use of resources etc and exposure of its large dose can be toxic so the focus has been shifted towards the use of natural pigments. As natural pigment can be obtained from plants, animals and microorganisms as they are safer than the synthetic dyes.
In present studies, Natural pigments were obtained from different Bacterial cultures isolated from various sources from different regions of Maharashtra. The samples were primarily enriched and screened on Nutrient agar to obtain pigment producing bacterial isolates. Further standard procedure for their morphological, biochemical test were followed and 03 isolates were selected on the basis of their intense pigment producing ability and then samples were send to NCMR, Pune for the identification and further physicochemical optimizations were carried out depending on different parameters like pH, Temperature, Biomass and Salt concentration for maximun pigment production.

Keyword: Natural Pigment, Synthetic dyes

MSD-40 (Poster)

Optimization of Cultivation Conditions and Upstream Bioprocess Development for Higher Production of Recombinant Clostridial Cellulolytic Chimeric Enzyme (*Ct*GH1-*Ct*GH5-F194A)

Vishwanath Yadav* and Arun Goyal
*vishwanath.yada@iitg.ac.in

Department of Biosciences and Bioengineering,
Indian Institute of Technology Guwahati, Assam, India.

Abstract: The conversion process of cellulosic biomass to glucose involves synergistic action of three cellulolytic enzymes: endoglucanase, cellobiohydrolase and β-glucosidase. To make this process cost effective, Nath et al., 2019 constructed a recombinant plasmid containing gene encoding chimeric enzyme (*Ct*GH1-L1-*Ct*GH5-F194A) using pET-28a(+) vector and expressed it in *E. coli* BL21 (DE3) cells. The chimera demonstrated bifunctional activity, combining the capabilities of β-glucosidase (*Ct*GH1) and endoglucanase (*Ct*GH5-F194A). Both enzymes were derived from the thermophilic bacterium *Clostridium thermocellum*. Current study focusses on developing a bioprocess to enhance the cell density of *E. coli* cells as well as chimeric enzyme production. After screening several media, M9 minimal salt medium was found to be best which gave higher chimera (*Ct*GH1-L1-*Ct*GH5-F194A) production. Two different carbon sources; glycerol and glucose were screened for achieving higher cell OD. Glycerol gave a higher cell OD of 5.0 and acetic acid accumulation of 3.0 g/L towards the end of log phase, while glucose gave reduced cell OD, 4.0 and acetic acid accumulation of 3.0 g/L towards the mid-log phase. Upon screening with different inoculum size in M9 medium with glycerol, 5% v/v inoculum gave highest cell OD of 6.0 in a shake flask culture of 100 mL working volume. Under previously optimized conditions (glycerol and 5% inoculum size) the culture with pH 7.0 gave a maximum cell OD of 7.0, when screened with different pH conditions. Cultivation performed using the M9 medium supplemented with 30 g/L glycerol in 1.0 L Shake flask with a working volume of 500 mL gave 4.5 cell OD at 600 nm (3.0 g_{DCW}/L). Upon purification of chimera from 500 mL culture total 6.6 mg/g_{DCW} protein yield was achieved. Batch cultivation in a bioreactor with 1.5L working volume using 5L bioreactor equipped with standard measuring and control units was performed under the conditions (C-source, inoculum size and culture pH) optimized earlier that gave highest cell OD_{600nm} of ~20 (12 g_{DCW}/L) after 12 h. Upon purification of chimera from the bioreactor harvested cells (500 mL), total protein yield of 11.1 mg/g_{DCW} was obtained with 1.7-fold higher protein yield than shake flask.

Keywords: Upstream bioprocess, β-glucosidase, Chimeric enzyme production, (*Ct*GH1-L1-*Ct*GH5-F194A), Bioreactor harvested cells

MSD-41 (Poster)

Molecular Characterization and Bioremediation Potential of Isolated Cadmium-Resistant *Pseudomonas* Strains from Industrial Sludge

Sachin Malik and Dharmender Kumar*
dkbiology@gmail.com

Department of Biotechnology, Deenbandhu Chhotu Ram University of Science & Technology,
Murthal Sonipat-(131039), India

Abstract: Heavy metals' continuing occurrence in soil and water is a key contributor to environmental contamination globally due to high impact of anthropogenic conducts. These metals are extremely reactive at minimal concentrations and can accumulate in food chain networks, thus, posing serious risks to public health. Cadmium is extremely poisonous and non-essential and it can be harmful to living things even at very low concentrations (0.001-0.1 mg/L). Detoxification and ecological entity restoring for these metals have been made possible through the economical and environmentally beneficial use of bioremediation of highly contaminated locations. Therefore, in this study cadmium contaminated industrial soil samples were utilized for isolation of cadmium resistant bacteria for that matter. Seven different isolates were purified and screened. Biochemical tests and microscopic examination were performed to prove their validity. Here, out of interest, we reported two

cadmium-resistant isolates named *Pseudomonas knackmussii* strain CS3 (PP514684) and *Pseudomonas* sp. strain CS4 (PP514689) identified by 16S rRNA based gene sequencing and their phylogenetic analysis. These isolates were screened for their maximum tolerance concentration (MTC) for Cd^{2+}. These two isolates tolerated upto 250 and 200 ppm $CdCl_2$ respectively. Furthermore, results of Atomic Absorption Spectroscopy (AAS) showed removal efficiency of these isolates between 30-50%. The present study demonstrates the isolates CS3 and CS4 to be potential strains to be implemented against cadmium contaminated area in future for biodegradation applications.

Keywords: Bioremediation potential, *Pseudomonas knackmussii* strain, Atomic Absorption Spectroscopy (AAS), Cadmium contamination

MSD-42 (Poster)

Adaptive Laboratory Evolution to Enhance Tolerance of *Saccharomyces cerevisiae* against Furfural

Sukhwinder Singh[1] Sukesh Chander Sharma[1*] and Tanzeer Kaur[2]
sukeshcs@pu.ac.in

1 Department of Biochemistry, Panjab University, Chandigarh (160014), India
2 Department of Biophysics, Panjab University, Chandigarh (160014), India

Abstract: Bioethanol production using lignocellulosic biomass as a feedstock is one of the promising alternatives to the fossil fuels owing to its abundance and renewability. However, it is still struggling with many obstacles including presence of inhibitory compounds released during the pretreatment process. These inhibitors such as furfural, vanillin, acetic acid negatively affect the fermentative capabilities of the microbial strains, thereby reducing bioethanol production. Thus, increasing the tolerance of strains is of great significance for the industrial bioethanol production. To overcome the obstacle of inhibitors various strategies have been explored. Adaptive laboratory evolution (ALE) among other strategies including genetic engineering, genome shuffling, offers distinct approach. ALE is an approach for directed evolution applying artificial selection pressure by mimicking natural environment under laboratory conditions. This method has advantage of facile strain transformation to select for evolved strain with desired traits. In the present study, ALE was employed to improve the tolerance of *S. cerevisiae* against 2-furaldehyde (furfural). ALE resulted in adapted *S. cerevisiae* strain with increased 2-furaldehyde tolerance as compared to the parental strain. Spot dilution assay on YPDA solid plates containing 20mM furfural displayed enhanced tolerance by the adapted *S. cerevisiae* as compared to the parental strain. To validate the results of spot dilution assay, liquid cultivation under conditions of 20mM furfural in YPD media were performed. The lag phase of 68hours was observed in parental strain, however, adapted *S. cerevisiae* showed a significant reduction of 40 hours, displaying lag phase of 20 hours. The adapted *S. cerevisiae* can be screened for beneficial mutations by analytical tools such as genomics, transcriptomic and proteomics to resolve the molecular mechanisms of adaptive evolution.

Keywords: Adaptive laboratory evolution, Furfural, Bioethanol, *S. cerevisiae,*

MSD-43 (Poster)

Process Development for Converting Rice Straw into Biofertilizer Formulation for Sustainable Agricultural Practices

Jyoti Yadav[1], Sanjiv Kumar Soni[1], Raman Soni[2] and Deepak Kumar Rahi[1]
jyotikakrala15051998@gmail.com

[1] *Department of Microbiology, Panjab University, Chandigarh, India*
[2]*Department of Biotechnology, D.A.V College, Chandigar, India*

Abstract: Effective management of agricultural waste and developing sustainable practices are critical challenges in modern agriculture. This study focuses on transforming rice straw, a significant agro-residue in India, into biofertilizer formulations to promote sustainability. Rice straw, often burned, contributes to air

pollution and greenhouse gas emissions and is rich in cellulose, hemicellulose, and lignin, making it an excellent substrate for biofertilizer production. We utilized plant growth-promoting rhizobacteria (PGPR) strains, including Klebsiella pneumoniae KMB-407, Micrococcus luteus AS-17, and Brevundimonas naejangsanensis A-407, isolated from rhizospheric soil. These strains exhibit significant traits such as nitrogen fixation, potassium and phosphate solubilization, HCN production, siderophore production, ammoniacal nitrogen production, and IAA production.

The enzymatic hydrolysis of rice straw using cellulolytic and hemicellulolytic enzymes produced by Aspergillus niger achieved maximum concentrations of 0.404 g/100 mL of reducing sugars and 0.136 g/100 mL of glucose over 20 days. These compounds served as substrates for microbial growth, leading to biofertilizer formulations.

Seed germination assays demonstrated significant improvements in germination rates and seed vigor index across all crops treated with the consortium of PGPRs, particularly in turnip (100% germination, seed vigor index of 1400) and okra and radish (50% germination). The consortium proved most effective, highlighting the synergistic benefits of multiple PGPRs.

This research provides a sustainable alternative to chemical fertilizers, reducing environmental impacts associated with rice straw burning and fertilizer runoff. Future studies will focus on scaling up production and validating efficacy through field trials.

Keywords: Rice Straw, Biofertilizer, Sustainable agriculture, Enzymatic hydrolysis, Plant growth-promoting bacteria, Environmental sustainability.

MSD-44 (Poster)

Extraction of Renewable Biochemicals from Enzolv Pretreated Cotton Stalk Using Column Chromatography

Santhoshkumar Subramaniam[1], Kumutha Karunanandham[2] and Sivakumar Uthandi[1]*
santhoshkumar1180@gmail.com , usiva@tnau.ac.in

[1]*Biocatalysts Laboratory, Department of Agricultural Microbiology, Tamil Nadu Agricultural University, Coimbatore (641003), India.*
[2]*Department of Agricultural Microbiology, Agricultural College and Research Institute, Madurai (625104), India*

Abstract: EnZolv is one of the green pretreatment methods that are currently valued highly owing to its environmentally friendly process. Initially, the EnZolv process parameters were optimized in cotton stalk for a maximum lignin reduction of 68.68% at 0% moisture, 50U laccase, incubated at 50 ^{0}C for 5 h at 150 rpm. EnZolv pretreated cotton stalk hydrolysate (CSH) was acid precipitated (16% H_2SO_4) to obtain a lignin yield of 0.12 g g^{-1} of biomass. Lignin depolymerisation using enzyme cocktail 0.05U of LiP: 0.005U of MnP: 3U of LccH in CSPT-Lignin showed depolymerisation efficiency of 35.82% at 16 h of incubation. A sequential column fractionation using solvents of varied polarity partially separates the lignin derived aromatics (LDA). The results showed that in CSH the proportion of lignin-derived aromatics was higher in chloroform fraction (85.49%) followed by ethyl acetate (55.28%). The LDAs predominant in the chloroform fraction of CSH are N,N'-di-benzoyloxy-Cyclobutane-1,1-dicarboxamide (24.47%), benzoic acid (19.77%), N,N'-di-benzoyloxy-Heptanediamide (10.068%), and benzaldehyde (6.10%). In ethyl acetate fraction of CSH, benzoic acid (22.15%), and 4 [(chloroamino)sulfonyl]-Benzoic acid (9.7%) were reported with the maximum area. When the optimized enzyme cocktail treated CSPT-Lignin was fractionated, the maximum LDAs were noted in fractions of petroleum ether (73.67%), and methanol (63.69%). Benzoic acid (65.45%) was the predominant LDA found in petroleum ether fraction whereas 1,3-Benzenedicarboxylic acid (62.46%) was found maximum in methanol fraction. This study paves way for the production of renewable biochemicals from lignocellulosic feedstocks using green technology thereby supporting sustainable development goals.

Keywords: Column chromatography, Cotton stalk, EnZolv, Lignin derived aromatics, Solvents.

MSD-45 (Poster)

Bioinformatics Analysis Reveals Pathways Involved in Ethanol Tolerance in *Saccharomyces cerevisiae* during Ethanol Fermentation

Amandeep kaur[1] Sukesh Chander Sharma[1*] and Sonia Bhonchal Bhardwaj[2]
sukeshcs@pu.ac.in

[1]*Department of Biochemistry, Panjab University, Chandigarh (160014), India*
[2]*Department of Microbiology, Dr. Harvansh Singh Judge Institute of Dental Sciences & Hospital, Panjab University, Chandigarh (160014), India.*

Abstract: The push for sustainable energy has brought bioethanol into focus as a promising alternative to fossil fuels, offering reduced emissions and compatibility with existing engines. However, industrial bioethanol production faces challenges, mainly due to ethanol's toxicity to yeast during fermentation. This toxicity disrupts yeast growth, viability, and can cause cell death, lowering fermentation efficiency. Developing strategies to enhance ethanol tolerance in yeast is crucial for improving the cost-effectiveness of bioethanol production. Studies on the identification of the genes that are up- or down-regulated under ethanol stress provide an ideal opportunity to identify and comprehending the regulatory events that contribute to cellular protection. In the present study, a systems-based network approach was employed to identify targets associated with ethanol tolerance. Three Gene Expression Omnibus (GEO) datasets were merged, and significantly common differentially expressed genes (DEGs) were identified to analyse with bioinformatics analysis. Gene ontology (GO) and enrichment analyses were performed via Shiny GO 0.80 and protein–protein interaction (PPI) networks of the DEGs were constructed using cytoHubba software. Results showed that 304 genes were differentially expressed, and GO analysis revealed that ethanol stress affect various biological process, cellular components and molecular functions. Moreover, enrichment analysis of top DEGs indicated that biosynthesis of pyrimidine ribonucleotide, amino acids biosynthetic pathway, cholesterol biosynthesis and histidine, purine and pyrimidine super pathway are significantly enriched during ethanol stress to increase energy requirement during stress conditions. Overall, this work provides a novel and comprehensive understanding of potential regulatory networks involved in response to ethanol stress. The identified response can indicate future directions for the genetic engineering of yeast strains, which could improve many fermentation processes, such as those used for bioethanol production and beverages.

Keywords: Ethanol stress, DEGs, Gene ontology analysis, Target identification.

MSD-46 (Poster)

Assessment of Phosphate Solubilization and Plant Growth Promoting Activities of Hilly Area Isolates of *Trichoderma* and their Influence on Soil Health and Biomass of Chickpea (*Cicer arietinum*) Under Net House Conditions

Divya Pant, Seema Bisht, Varsha Mishra and Lakshmi Tewari
Divyapant231999@gmail.com, seemabisht262@gmail.com, varshamishra1807@gmail.com, Lakshmimtewari@gmail.com

Department of Microbiology, G.B.P.UA&T, Pantnagar, Uttarakhand, India

Abstract: Considering the Phyto stimulating mechanism of *Trichoderma*, forty-eight strains were isolated from the rhizosphere of rice plants growing in Almora district of Uttarakhand, and assessed in vitro for their phosphate solubilizing potential using different inorganic fixed phosphorus (P) sources, viz. TCP, $Zn_3(PO_4)_2$, FePO4. During qualitative analysis by plate assay, only 11 isolates showing vigorous growth on TCP amended MSM medium were selected and quantified for phosphate solubilization. The concentration of phosphate mobilized from TCP in culture filtrates ranged from 30.19 to 448.52 µg/mL followed by 26.0 to 324.07 µg/mL and 46.11 to 217.13 µg/mL from $Zn_3(PO_4)_2$and FePO4 respectively in 96 h. Out of 11 strains, four potential strains (RAF4, RAF5, RAF6, RAF8) were selected and investigated for their other plant growth promoting activities. The isolate RAF8 showing maximum phosphate release from all the three fixed P sources was found superior followed by the isolate RAF4. Further the consortia using the potential P solubilizing isolates were developed and the consortium comprising of RAF4+RAF8 showing synergistic action was

selected and assessed for impact on P availability in soil, soil enzyme activities, viz. phenol oxidase , urease, phosphatase as an indicator of soil health and on plant growth parameters and biomass yield of chickpea under net house conditions. The study reveals a green strategy, using a potential bioagent *Trichoderma* equipped withboth biocontrol and plant growth promoting activities as an alternative to chemical fertilizer, for enhancing chickpea plant growth of chickpea and soil health management.

Keywords: Biofertilizers, Chickpea, *Trichoderma*, Phosphate solubilization

MSD-47 (Poster)

Bioconversion of Food Waste into Stable Enzyme Formulation for Sustainable Waste Management

Bishakha Thakur[1], S.K. Soni[1], Raman Soni[2] and D.K. Rahi[1]
bishakhathakur1998@gmail.com

[1]*Department of Microbiology, Panjab University, Chandigarh (160014), India*
[2]*Department of Biotechnology, D.A.V. College, Chandigarh0 (1600)1, India*

Abstract: This study investigates the bioconversion of food waste residues into enzyme formulations, offering a sustainable approach to waste management. Quantitative analysis revealed high carbohydrate content, particularly cellulose and starch, in the residues. Various food waste residues were evaluated for their ability to support the growth of *Aspergillus niger* S-30 and induce the production of 21 industrial enzymes. Stable liquid and solid enzyme formulations were developed from the *Aspergillus niger* S-30 culture on food waste biomass. These formulations, comprising cellulase, hemicellulase, amylase, pectinase, inulinase, protease, lipase, and alginate lyase, demonstrated consistent enzyme activities. These enzyme preparations were concentrated to enhance their activity levels. The liquid enzyme preparation exhibited activity levels of 150-250 IU/ml of CMCase, 30-40 IU/ml of FPase, 25-35 IU/ml of Avicelase, 30-40 IU/ml of β-glucosidase, 160-175 IU/ml of salicinase, 800-900 IU/ml of xylanase, 260-275 IU/ml of mannanase, 12500-15000 U/ml of α-amylase, 400-500 IU/ml of glucoamylase, 2100-2300 U/ml of protease, and 190-210 U/ml of lipase and alginate lyase. Supplemented with 0.01% formaldehyde and stored at 4°C, the enzyme activities showed an insignificant loss over two years. The solid enzyme preparation exhibited activity levels of 100-108 IU/ml of CMCase, 80-90 IU/ml of FPase, 200-300 IU/ml of Avicelase, 70-80 IU/ml of β-glucosidase, 80-90 IU/ml of salicinase, 500-600 IU/ml of xylanase, 100-200 IU/ml of mannanase, 1000-1500 U/ml of α-amylase, and 400-500 IU/ml of glucoamylase. The enzyme activity remained nearly constant during storage at room temperature for six months. This research introduces an innovative approach to address food waste by producing valuable enzyme formulations, promoting sustainable and eco-friendly solutions.

Keywords: Bioconversion, Food waste, *Aspergillus niger*, Enzyme formulations, Sustainable waste management, Industrial enzymes

MSD-48 (Poster)

Characterization of the *Saccharomyces cerevisiae SPR3* Gene Homologue in The Riboflavin over Producer *Ashbya gossypii*

Y. Vishal, D. Simadri and S. Vijayalakshmi*
vijayaiitm@gmail.com

Department of Biotechnology, VELS University, Velan Nagar, Pallavaram (600117), India

Abstract: The riboflavin over producer *Ashbya gossypii* is a filamentous hemiascomycete closely related to the yeast *Saccharomyces cerevisiae*. In factthe genome of *S.cerevisiae* is supposed to have arisen by duplication of the *A.gossypii* genome. On account of this many fundamental processes in these two organisms are similar. Therefore, research in this organism is important both from the point of view of addressing fundamental questions in cell biology of fungi as well as with regard to riboflavin oversynthesis by this fungus. In this context an important question to be addressed is how does septation correlate with riboflavin secretion into the

external medium. The septum wall prevents vacuoles which store the riboflavin, important enzymes etc from being transported. The *A.gossypii SPR*3 gene is involved in septum formation. In the present study we present a preliminary characterization of the *AgSPR*3 gene and show that it has a conserved P – loop region relating it to septin proteins, it also has Leucine Zipper motifs and may play a regulatory role in *A.gossypii* at the transcriptional level.

Keywords: *Saccharomyces cerevisiae, SPR3* gene, *A.gossypii,* Riboflavin secretion

MSD-49 (Poster)

N-Acetylcysteine as Potent Antioxidant in COVID-19 Patients: The Clinical Trial and Future Prospective

Neha Jaiswal[1], Lilly Ganju[2], Prem Nyati[3] and Sudhir Maurya[4]
jaisneha411@gmail.com

[1]*Scientific Officer IMCHRC, Malwanchal University, Indore, India*
[2] *Director Research, Malwanchal University, Indore, India*
[3]*Prof and Head, Dept. of Pharmacology, IMCHRC, Malwanchal University, Indore, India*
[4]*Prof and Head, Dept of Medicine, IMCHRC, Malwanchal University, Indore, India*

Abstract: COVID 19 has emerged as one of the worst pandemics distressing the globe. Being highly infectious in mild and moderate cases, it likely to caused fever, headache, myalgia, throat irritation and dry cough whereas delayed or insufficient immune reaction leads to a pulmonary phase which manifests as viral pneumonia with hypoxia and in worsens condition typically labelled as 'cytokine storm' with excess level of pro-inflammatory cytokine protein. N-acetyl L cysteine (NAC) has antioxidant, anti-inflammatory, and immunomodulating properties and may prove beneficial in modulating the excessive inflammatory activation during Coronavirus disease. Furthermore, NAC has been extensively used as a mucolytic agent to improve airway clearance in chronic respiratory diseases. To investigate the impact of NAC administration on COVID-19 patients for short-term and long-term outcomes the study was designed. Time of hospitalization, ICU admissions and mortality rates of the patients were recorded under short-term consequences whereas alterations in CT score, carbon-monoxide transfer capacity by lungs and dyspnoea score after 6 months were considered as long-term consequences. Patients were divided into two groups' placebo control and NAC treated (600 mg BD) and received the experimental drug along with the conventional treatment of COVID (as per Govt. guidelines). The results indicated no major differences in ICU admission, mortality rates and CT scores. However significant difference in time of hospitalization was observed in NAC treated patients as compared to the placebo groups. Oral N-acetylcysteine administered at 600 mg thrice daily has been shown to reduce mortality in hospitalised SARS-CoV-2 patients. The clinical course of our patient suggested that high-dose N-acetylcysteine antioxidant therapy was able to control the cytokine storm of SARS-CoV-2 infection. Intravenous NAC at doses 100mg/kg to 150 mg/kg is suggestive for patients with ARDS.

Key words: COVID-19, N-acetyl cysteine, Glutathione, Nutraceutical, Antioxidant, Cytokine storm.

MSD-50 (Poster)

Extraction and Characterization of Polyhydroxyalkanoates (PHA) from Locally Isolated Microalgae Species

Mayuri Gupta, Harsha Wakudkar and Sandip Gangil
mayuri281210@gmail.com, harsha.wakudkar@gmail.com, gangilsandip@yahoo.co.in

ICAR- Central Institute of Agricultural Engineering

Abstract: Polyhydroxyalkanoates (PHAs) are biopolymers produced by various microorganisms and are viewed as alternatives to petroleum-based plastics. They possess mechanical properties akin to those of synthetic polymers, can be processed using similar methods, and are completely biodegradable. Several studies indicate that microalgae are microorganisms that can produce PHAs more cost-effectively due to their low nutrient

requirements for growth and their phototrophic nature, meaning they utilize light and CO_2 as their primary energy sources. In the present study focus was to extract and characterize the PHA from microalgae isolated from local environment. Algal strains were cultivated in BG-11 medium, and an initial bioprospecting study was performed to assess the growth profiles of all algal strains based on their dry cell weight. The maximum cell growth of 2.46 g/L was achieved on dry cell weight basis. In addition, the efficacy of methods used to extract PHA from *Chlorella sp*. and to examine the influence of these methods on the purity, properties and composition of the polymers. PHA was characterized by Fourier transform infrared spectroscopy (FTIR) and Thermogravimetric analysis (TGA). The efficacy of the extraction method varied with the PHA accumulation between 4.3 to 24.08%. This work contributes to the understanding that the extraction methods interferes with the accumulation and purity of PHA and the locally isolated *Chlorella sp*. can be a promising species to produce bio-resources in commercial systems.

Keywords: Polyhydroxyalkanoates, *Chlorella sp*., Biopolymer, Extraction.

MSD-51 (Poster)

Cost Effective Media Optimization for PHB Production by Bacteria Isolated from Soil

Sonika[ab], Anil Kumar[b], Monika Kayasth[a*] and Jagdish Parshad[a]
monakayasth@gmail.com

[a] *Department of Microbiology, College of Basic Sciences & Humanities, Chaudhary Charan Singh Haryana Agricultural University, Hisar-125004, Haryana, India*
[b] *Department of Biotechnology, Guru Jambheshwar University of Science and Technology, Hisar (125004), Haryana, India*

Abstract: Polyhydroxybutyrate (PHB) is a biocompatible and biodegradable polymer produced by various microorganisms under stress conditions, serving as an energy reserve in the form of inclusion bodies. PHB possesses material characteristics similar to those of petroleum-derived plastics and presents a viable solution to the environmental issues caused by non-biodegradable plastics. This study aims to optimize the culture conditions for PHB production by bacteria isolated from soil. The bacterial isolate was screened using biochemical tests. Five different agricultural wastes—molasses, bagasse, wheat husk, oat seeds, and potato peels—were evaluated as sole carbon sources, while cotton cake and orange peel were used as nitrogen sources to assess their impact on PHB production. Among these, molasses proved to be the most effective carbon source, yielding 21.2 mg/ml of PHB, while cotton cake was the best nitrogen source, yielding 29.4 mg/ml of PHB. The effect of cultural parameters on PHB production was further studied using a Box–Behnken design. Response Surface Methodology (RSM) was employed to enhance PHB yield, resulting in a maximum of 65.50 mg/ml at an initial pH of 6, with 10% molasses as the carbon source and 1% cotton cake as the nitrogen source, closely matching the predicted yield of 63.66 mg/ml. FTIR analysis of the extracted PHB confirmed the presence of functional groups CH3, CH2, C=O, C-O, CH, and OH, verifying the successful extraction of PHB from the selected bacterial isolate.

Keywords: Polyhydroxybutyrate, Biodegradable, Biocompatible, Optimization

MSD-52 (Poster)

Harnessing Microbial technology for Sustainable Economic growth

Shweta Laura[*1], Rohit Nain[2]
Shwetalaura2@gmail.com

[1]*Msc, Department of Agricultural Economics, Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana (125 004), India*
[2]*Msc, Department of Soil Science, Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana (125 004), India*

Abstract: Microbial technology is increasingly recognized as a key player in driving sustainable economic growth by providing innovative solutions across a range of sectors, including agriculture, healthcare, energy and

environmental management. This technology taps into the unique abilities of microorganisms, enabling the development of eco-friendly and cost-effective alternatives to traditional practices. In agriculture, microbial applications are improving soil fertility, boosting plant growth and reducing dependency on chemical inputs. In the energy sector, biofuels produced from microbes present cleaner energy options, while bioremediation technologies are being used to detoxify polluted environments. Furthermore, microbial fermentation and synthetic biology are paving the way for the production of high-value goods like pharmaceuticals, bio-based materials and industrial enzymes. Despite facing challenges such as regulatory hurdles, intellectual property issues and the requirement for significant capital investments, microbial technology offers a sustainable route to economic development. By encouraging innovation, minimizing environmental impacts and enhancing industrial efficiency, microbial technology holds great promise for supporting long-term economic resilience and improving societal well-being.

Keywords: Microbial technology, Sustainable economic growth, Agriculture, Biofuel bioremediation, Synthetic biology, Industrial enzymes, Environmental management

MSD-53 (Poster)

Phytochemical Analysis of*Catharanthus roseus* Leaves and its Antimicrobial Activity

Shikha Sharma[1]* and Utkarsh Singh[1]
shikhasharma90169@gmail.com

[1]*Department of Microbiology, RCP (PG) College of Allied Sciences, Roorkee, Uttarakhand, India*

Abstract: Plants derived compounds have played a vital role in the development of several chemotherapeutic agents. *Catharanthus roseus* is well known plant of Ayurveda. *Catharantus roseus* have a strong potential for many different types of pharmacological properties such as antimicrobial, antidiabetic, anticancer, antiulcer, antioxidant etc. The plants leaves contain more than 70 types of chemical constituents such as indole types of alkaloids, ajmalicine, serpentine and reserpine. Many different ailments, including hypertension, cancer, skin conditions, diabetes, menstrual irregularities, indigestion, have been treated with *C. roseus*. The plant has a wide range of pharmacological effects and rich in bioactive chemicals *roseus* plants leaves are used for cancer treatment. The current study's objective is to examine the phytochemical analysis and antimicrobial activity of *Catharanthus roseus* aqueous, ethanol, methanol and acetone extracts. Alkaloids, phenol, saponins, tannins, flavonoids, steroids, quinines and protein are all found in photochemical screening results after qualitative analysis and antimicrobial activity of different solvent extract of *C. roseus* was conducted using agar well diffusion method. Acetone and aqueous extract of *C. roseus* shows highest antimicrobial activity and methanol, ethanol extracts shows least antimicrobial activity. Thin layer chromatography (TLC), the industry-standard method for isolating organic compounds, was used to find additional phytochemical presences. The aqueous extract of *C. roseus* leaves contain rich phytochemical constituents which in turn resulted in the identification of different compounds by TLC. According to the finding, leaf extract has the strongest antimicrobial activity and photochemical activity. The plant studied here can be seen as source of useful drug and it also justifies the folklore medicinal uses and claims about the therapeutic value of this plant as curative agent. It has multiple applications in foods, cosmetics and pharmaceuticals industries. These types of plants antioxidant mainly apply to prevent lipid peroxidation in the food industries.

Keywords: *Catharanthus roseus*, Phytochemical analysis, Antimicrobial activity, Thin Layer Chromatography (TLC)

MSD-54 (Poster)

Valorization of Whey Using Potential Lactic Acid Bacterial Isolate Pediococcus Damnosus 107: Production of Lactic Acid and its Purification

Stuti Sharma, Nivedita Sharma[1] and Neha Gautum[2]
stutisharma2024@gmail.com

Microbiology Research Laboratory, [1]Department of Basic Sciences
[2]Department of Food Science and Technology
Dr Y S Parmar University of Horticulture and Forestry, Nauni, Solan (173230), Himachal Pradesh, India

Abstract: Disposal of whey has become a conundrum for dairy industry. Production of lactic acid from whey can greatly boost economy of dairy sector and can reduce environmental concerns. In this study the low cost production of lactic acid was done using whey. The approach employed producing lactic acid from whey which accomplished two goals: it produces lactic acid, which helps to address the problem of environmental pollution caused by the dairy industry. The aim of this work was to investigate lactic acid synthesis from whey using probiotic lactic acid bacteria Pediococcus damnosus 107. Maximum lactic acid production was showed by whey with supplementation of yeast extract i.e. 3.31 g/L. Purification of lactic acid was done by salt saturation method. A significant achievement in percent recovery was obtained i.e. 262 % and purification fold was 2.0.

Keywords: Lactic acid, Fermentation, Whey, Purification, Pediococcus damnosus 107.

MSD-55 (Poster)

Diffusion Permeability of Enriched Microcapsules: A Novel Analysis

Shaik Tabasum[1*], Umang[1] and Leela Wati[2]
[*]tabasumshaik28@gmail.com

[1]Ph.D. student, Department of Microbiology, College of Basic sciences & Humanities
[2] Principal Scientist, Department of Microbiology, College of Basic sciences & Humanities
Chaudhary Charan Singh Haryana Agricultural University, Hisar (125004), Haryana, India

Abstract: Sustained release of microcapsules depends upon the diffusion of active or core materials to an intended site. The microcapsules are naturally semipermeable to the metabolites produced which are primarily responsible for microbial sustenance and plant growth. Survivability of the bacteria embedded inside the microcapsule relies on the ability to perform key cell functions such as nutrient transport, pH maintenance, osmotic regulation and water penetration is maintained by a characteristic called 'Diffusion permeation'. In the current study, microcapsules of *Pseudomonas* strain P-36 and *Azotobacter chroococcum* Mac 27 were taken into consideration. To evaluate the diffusion permeation ability, the microcapsules were enriched with D, L-tryptophan acting as a marker molecule for the production and diffusion of indole acetic acid (IAA). These enriched bacterial cultures were formed into microcapsules by using sodium alginate-humic acid by external gelation and inoculated in tryptic soy broth and incubated. The interactive effect of variables *viz.*, weight of microcapsules and pH of tryptic soy broth were analyzed from 3rd to 5th day of incubation and ranged from 0 to 1.5 g and 4-11 respectively. The beads in tryptic soy broth showed increased IAA diffusion from 4th day and reached maximum IAA concentration of 84.18 µg/ml on 5th day of incubation. It was also observed during this period the increased in weight of beads from 0.5-1.0 g and pH from 5-7.5 which leads to the optimal diffusion of IAA and further increases in these variables have decreased the diffusion of IAA. It is concluded from the above results that D, L-tryptophan posed as a suitable maker material for metabolite diffusion to evaluate microcapsules permeability.

Keywords: Diffusion permeation, Microcapsules, Indole acetic acid diffusion, Semipermeable

MSD-56 (Poster)

Identification and Analysis of Plant Growth-Promoting Rhizobacteria from Sorghum Plants

Prema Siva Naga Teja Alapati[1], Baljeet Singh Saharan [1*], Ankush Dhanda[2], Pummy Kumari[3], Tejashree Musini[1] and Raksha Jain[1]
Baljeetsaharan@hau.ac.in

[1]*Department of Microbiology,*
[2]*Department of Soil Science,*
[3]*Department of Genetics and plant breeding*
Chaudhary Charan Singh Haryana Agricultural University, Hisar (125 004), India

Abstract: Plant development depends on soil, which offers necessary nutrients and a home for helpful bacteria. Its fertility is mostly determined by organic content. Despite the widespread use of chemical fertilizers, their overuse can result in soil degradation. In contrast, plant growth-promoting rhizobacteria (PGPR) offer a sustainable alternative by enhancing nutrient uptake in plants. For this study bacteria were isolated and evaluated for their PGPR traits from the rhizospheric soil of *Sorghum bicolor*. Various plant growth-promoting traits, including the solubilization of phosphorus (P), potassium (K), and zinc (Zn), ammonia excretion, IAA production, biosurfactant production, and siderophore production were analyzed. Out of 60 isolates, four were selected for further analysis. Germination tests were conducted for all four isolates using the CSV53F variety of sorghum, followed by pot experiments in both sterile and non-sterile soils. The impact of the isolates on the plant growth was evaluated after one month in both soil and plants. Various morphological, physiological, and biochemical parameters were measured, including stem diameter, leaf area, HCN content, and nutrient content (N, P, K, Zn, Fe, Mn). Of all the treatments, the one with a consortium of all four isolates recorded significantly highest Fe, Zn, N, and K concentrations 752 ppm, 82 ppm, 27,750 ppm, and 20,750 ppm respectively in the plant tissues grown in the sterile soil and P recorded 6000 ppm in the non-sterile soil. The consortium not only had the highest fresh and dry weights (4.8g and 1.75g, respectively) but also the largest stem diameter (4.27cm) and leaf area (87.4cm^2). This study concludes that the use of PGPR significantly enhances both the quality and quantity of forage sorghum, highlighting its potential as a sustainable agricultural practice.

Keyword: Plant growth-promoting rhizobacteria (PGPR), Biosurfactant production, Siderophore production, CSV53F

MSD-57 (Poster)

Isolation, Screening and Morphological and Biochemical test of Cypermethrin Degrading Bacteria from Contaminated soil

Renu Sheokand*and Anil Kumar
renusheokand844@gmail.com

Department of Biotechnology, GJUST, Hisar, Haryana, India

Abstract: Continuous use of pesticides in agriculture is a major environmental issue. Synthetic pyrethroid is a class of pesticide used in agriculture to control pests. Cypermethrin is an insecticide commonly used to control insect disease in agriculture, forestry, residential areas, and hospitals. However, their use in agriculture leads to harmful effects on the environment, population, and food chain and also disrupts the biological cycles. To overcome these problems, several methods like landfills, chemical treatment, incineration, etc are used, but these methods involve many disadvantages like pollution, so the use of microbes present in the soil and water is the natural method for the biodegradation of cypermethrin. In the current investigation, 75 bacterial isolates were isolated from 47 soil samples from various regions of Haryana in primary screening over MSM media. Out of these 75 isolates, 12 isolates were selected for further biochemical testing and named RS1-RS12. Then secondary screening was done by UV –VIS Spectrophotometer and only 4 bacterial isolates were screened out as potent degraders of cypermethrin pesticide. It was found that RS12 isolates have the highest capacity to degrade cypermethrin. Further, isolate RS12 was selected for protein estimation using Lowery method and the results indicated that RS12 have the highest protein content of 6.2.

Keywords: Soil samples, Primary screening, Secondary screening, Cypermethrin, Biodegradation.

MSD-58 (Poster)

Diversity Analysis of Phosphate Solubilizing Fungi in Rhizospheric Soil from Arid and Semi-Arid Zones of Haryana

Raj Bala, Ajay Kumar*, Meena Sindhu, Raksha Jain, Mansi Phogat and Ritika
akjiari@gmail.com

Department of Microbiology
CCS Haryana Agricultural University, Hisar (125 004), India

Abstract: Phosphorus (P) is a crucial nutrient for plant growth, but its availability in soil is limited due to its transformation into insoluble forms. Despite the global addition of P fertilizers, only about 0.1% becomes available for plant uptake, with approximately 70% of applied P precipitating in the soil and becoming unavailable. The depletion of global phosphorus reserves is a concern, with projections indicating they may be exhausted by 2050. Phosphate-solubilizing fungi (PSF) play a vital role in enhancing P availability by dissolving inorganic phosphates through the secretion of organic acids and other compounds. In the present investigation, soil samples were collected from different locations of Haryana namely Hisar, Bhiwani, Sirsa, Fatehabad, Kaithal, Panipat, Rewari (Bawal) and Jhajjar. A total of 144 fungal isolates were obtained, further screened under qualitative and quantitative analysis. After that selected phosphate solubilizing fungal isolates with high solubilization efficiency were characterized by staining techniques. Selected fungi were identified as *Aspergillus*, *Penicillium, Trichoderma* and *Verticillium*. Selected phosphate-solubilizing fungal isolates were evaluated for plant growth promoting traits like ammonium excretion, indole acetic acid (IAA) production, siderophore production and solubilization of potassium and zinc. The PGP tests revealed BF9 as the most efficient isolate for ammonium excretion (4.871±0.011 mg) and JF4 for indole acetic acid production (240.74±1.161 mg). While no isolates showed significant zinc or potassium solubilization, BF1 and PF1 demonstrated high siderophore production. The most promising fungal isolates identified in this study are BF9, PF1, JF4, SF2 and BF1. These phosphate solubilizing fungi can be used for management of phosphate deficient soil and sustainable agriculture production.

Keywords: Solubilization, Screening, Fertilizer, Plant growth promoting traits

MSD-59 (Poster)

Isolation and Characterization of Novel Phage ST BD and EC BD for the Biological Control of *Salmonella* and *Escherichia coli* in Dairy Food Matrices

Madhvi Chahar[1] and Namita Singh[1]
madhvi23rana@gmail.com&namitasingh71@gmail.com

Lab No. 202, Microbial Biotechnology, Department of Biotechnology,
Guru Jambheshwar University of Science & Technology, Hisar, Haryana (125001), India

Abstract: Bacteriophages are intended as a new approach for the control of foodborne pathogens in food matrices. In the present study, two novel phages (ST BD and EC BD) specific for *Salmonella* and *E. coli* were isolated from buffalo dung samples. The efficiency of plating and scanning electron microscopy analysis revealed the high lytic activity of phage ST BD and EC BD against *S. Typhimurium* and *E. coli* with a huge burst size and a short latent period. Potential phage ST BD and EC BD showed high stability at 4°C with only 10% and 26% reductions in phage activity during 26 weeks of storage. Transmission electron microscopy micrographs revealed that both novel phages belong to the Myoviridae family. The whole genome sequencing data revealed that both phages were inclined towards completely lytic and showed a lack of toxins, antibiotic resistance, and virulence genes. Comparative genome analysis suggested that phage ST BD and EC BD constitute novel members of the genus *Duplodnaviria* and family Myoviridae. The efficiency of phage ST BD and EC BD were determined in dairy food matrices such as milk, cheese, and paneer samples artificially contaminated with *S. Typhimurium* andenterotoxigenic *E. coli*, resulted in *a* a significant ($p \leq 0.05$) reduction of 7.0, 6.9, and 5.6 log CFU/mL of *Salmonella* growth and 4.8, 4.9, and 4 log CFU/mL reduction of *E. coli* growth in milk, cheese, and paneer, respectively, after 6 days of phage treatment at 4°C.This study suggested that phages ST BD and EC BD might have potential as a biocontrol approach against *Salmonella* and *E.*

coli foodborne infections. The identified novel phages provide a basis for the future development of potential biocontrol candidates against *Salmonella* and *E. coli* in a wide variety of food matrices.

Key words: Bacteriophage, *Escherichia coli*, *Salmonella*, Antimicrobial, Food safety, Whole genome

MSD-60 (Poster)

Inducing Bioactive Secondary Metabolites in Microbes via Co-cultivation

Poonam Choudhary[a,b], Mohd Murtaza[a,b] and Sundeep Jaglan[a,b,*]
sundeepjaglan@iiim.res.in

[a]*Fermentation & Microbial Biotechnology Division, CSIR-Indian Institute of Integrative Medicine, Jammu (180001), India*
[b]*Academy of Scientific and Innovative Research (AcSIR), Ghaziabad (201002), India*

Abstract: Microbes are promising sources for the production of novel bioactive compounds. One of the major challenges faced by the natural product industry is the frequent re-discovery of known compounds as most of the Biosynthetic Gene Clusters (BGCs) are either expressed at a very low concentration or are transcriptionally silent under standard laboratory conditions. Co-culture is one of the efficient ways to explore the microbial metabolic potential of developing new antibiotics and other therapeutic agents.Different industrially significant microbial strains were co-cultivated, and the combinations were evaluated based on their interaction patterns and bioactive potential. Among the various combinations, the co-cultivation extract of***Beauveria nivea* (557) and *Bacillus coagulans* (3543)** showed MIC values of 128 µg/ml, 64 µg/ml, 64 µg/ml, 32 µg/ml, 32 µg/ml against *B. subtilis*, *S. aureus*, *E. coli*, *C. albicans*, and *Aspergillus niger,* respectively. Similarly, the extract of ***Beauveria nivea* (557) and *Flexibacter* sp. (1312)** showed MIC values of 128 µg/ml, 64 µg/ml, 64 µg/ml, 32 µg/ml, 32 µg/ml against *B. subtilis*, *S. aureus*, *E. coli*, *C. albicans*, and *Aspergillus niger*, respectively. These investigations suggest that co-cultivation-based extracts have the potential to obtain novel bioactive compounds of pharmaceutical and industrial importance.

Keywords: Co-cultivation, Bioactive metabolites, Biosynthetic gene clusters (BGCs)

MSD-61 (Poster)

Ecosystem Services of PGPR in Sustainable Production of Fenugreek (*Trigonella foenum -graecum* L.).

Ravinder and Mohd Kashif Kidwai
Kashif357313@yahoo.co.in

Department of Energy and Environmental Sciences, Chaudhary Devi Lal University, Sirsa, Haryana (125055), India

Abstract: Fenugreek (*Trigonella foenum-graecum* L.) is an important spice, leafy vegetable and medicinal plant originated in South-Eastern Europe belonging to the family Fabaceae. PGPR (Plant Growth Promoting Rhizobacteria) are unique rhizospheric microorganisms including endophytes providing valuable ecosystem services to plants. PGPR enable plants to adapt and survive under different environmental conditions and enhances the tolerance of various plant species against biotic and abiotic stresses. PGPR contribute significantly in boosting key morphological and physiological processes and helps in promoting the growth and development of plants and are reported to stimulate the production of various secondary metabolites viz. siderophores, phenols, phytohormones etc. and provide various ecosystem services such as Photosynthesis, Nitrogen fixation, carbon fixation, solubilization of phosphate etc. PGPR also induces resistance in wide variety of plants against diverse pathogens thereby helps in achieving sustainable agriculture with the reduction in use of hazardous agrochemicals. PGPR aids the plants in nutrient uptake in the soil and complement in regulating osmotic balance along with ion homeostasis. PGPR also support the plants in enhancing water use efficiency which address the issue of sustainable use of water in agriculture and microbe assisted phytoremediation of heavy metals, pesticides etc. In case of Fenugreek (*Trigonella foenum-graecum* L.) PGPR such as *Pseudomonas*

species, *Sinorhizobium* species etc.are reported to play an important role in induction of bioactive compounds and phytohormones. The production of specific biochemical such as Trigonelline and Nicotinic Acid are influenced by PGPR. The ecosystem services by PGPR complementthe growth and yieldof fenugreek along with the environmental sustainability.

Keywords: PGPR, Ecosystem services, Phytoremediation, Secondary metabolites.

MSD-62 (Poster)

Evaluation of Microbially Induced Calcium Carbonate Precipitation (MICP) ability of bacteria

Pratika Kakad[1]and Prafulla Shede[1]*
pns.agc@mespune.in

[1]*Department of Microbiology, Maharashtra Education Society's Abasaheb Garware College (Autonomous), Karve Road, Pune (411004), Maharashtra, India*

Abstract: Concrete is one of the most significantly used raw materials in construction industry. Although, it offers a wide range of advantages, it has a tendency to undergo crack formation as a result of different physical, chemical and biological parameters. These factors reduce the life of concrete which upsurges the cost of the repair and maintenance. Existing remedies offer weak resistance to weather, moisture sensitivity and low sustainability. Hence, there is a need to explore alternative sustainable treatment technologies. One such emerging technology is the use of bioconcrete, formed by the process of Microbially Induced Calcium Carbonate Precipitation (MICP). Bioconcrete is a mixture of concrete along with bacteria possessing the ability to precipitate calcium carbonate that seals the cracks that appear in it. This study was aimed to isolate and screen bacteria capable of precipitating calcium carbonate for their potential use in production of bioconcrete. Samples were collected from different sites in Satara and Nashik districts of Maharashtra. Screening revealed 26 isolates to precipitate calcium carbonate. 16S rRNA sequencing of 8 shortlisted isolates showed bacteria to belong to the three genera – *Bacillus*, *Sporosarcina* and *Paenibacillus*. Characterization of calcium carbonate crystals by Scanning Electron Microscopy and Energy Dispersive X- Ray analysis showed crystals with hexagonal and rhombohedral symmetry with the presence of Carbon, Oxygen and Calcium elements in them. X-ray Diffraction micro-analysis and Fourier Transform Infrared Spectroscopy confirmed the peaks associated with carbonate crystals. These promising results suggest the application of these bacteria in bioconcrete.

Keywords: Concrete, Crack, MICP, Bioconcrete, Calcium carbonate precipitation, Sustainability

MSD-63 (Poster)

Optimization of Growth Conditions for Chlorpyrifos–Degrading Microbes in Contaminated Field Soils of Parbhani, Maharashtra

Suaad Khadeeja[1*] Brijesh Kumar Mishra[1], Livleen Shukla[1*],
Sandeep Kumar Singh[1] and Dolamani Amat
khadeejasuaad@gmail.com; bkmmicro@gmail.com

[1]*Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi (110012), India*

Abstract: Chlorpyrifos (O,O-diethyl O-3,5,6-trichloro-2-pyridyl phosphorothioate), an organophosphate pesticide, is widely used in agriculture but posses significant environmental and health risks to its persistence in soil. The study aimed to isolate microbes with chlorpyrifos degrading potential and optimizing their growth conditions, including temperature, pH and chlorpyrifos concentration. In the study soil sample collected from the fields of Parbhani, Maharashtra from 06 different locations where chlorpyrifos was applied as treatment. The enrichment culture technique were used, with minimal salt medium (MSM) supplemented with commercial grade chlorpyrifos IFFCO. After enrichment fungi and bacterial were isolated by serial dilution and plating on RMM medium supplemented with 50mg / kg. Total 20 bacterial and 08 fungal species were isolated from

chlorpyrifos contaminated soil using enrichment culture technique. The viable count method on selective media from enriched culture resulted in bacterial population 1.6×10 6 cfu/ml and fungal count was observed as 2.0×10 5 cfu/ml. Each bacterial isolate exhibiting unique morphological characteristics, with colony colours ranging from yellow, pink, white to cream. Gram staining the bacterial isolates showed 14 bacterial strains as gram positive i.e cocci, rods shape and 6 were gram negative in rod shape. The results indicate a substantial growth of cultures in chlorpyrifos concentration, confirming the potential of microbial inoculants as a sustainable and eco-friendly solution for detoxifying contaminated agricultural soils.

Keywords: Remediation, Chlorpyrifos, Pesticide, Degradation process, Contaminated soil

MSD-64 (Poster)

Optimization of Cellulase Production Using Response Surface Methodology from *Bacillus pumilus* Strain FZM Isolated from Fecal Sample of Spotted Deer (*Axis axis*)

Shaikh Mohammedfaizan, Maaz Ahmed and **Krishan Kumar** *
*krishan.kumar20140@paruluniversity.ac.in

Department of Life sciences, Parul Institute of Applied Science, Parul University, Waghodia, Vadodara, Gujarat (391760), India

Abstract: The rapid utilization of fossil fuel-based energy sources increased demand for alternate sustainable energy sources. One of best alternate energy source can be lignocellulosic biomass. The major constitute of lignocellulosic biomass is cellulose that can be converted into simple sugar using cellulase enzyme followed by fermentation for ethanol production. Although cellulolytic bacteria have already been isolated from variety of different sources but still fecal sample of spotted deer (*Axis axis*) is unexplored. Potential mesophilic cellulolytic bacteria M4 was isolated and screened from fecal sample of Spotted Deer (*Axis axis)* based on high zone of hydrolysis on CMC agar plates. The morphological, biochemical, and molecular characterization identified M4 as *Bacillus pumilus* strain FZM (PP264922). The cell free supernatant of *Bacillus pumilus* strain FZM showed maximum CMCase activity at pH 6.0 and 37°C. The enzyme hydrolysed product of CMC showed oligosaccharides on TLC plate which indicated the endo-β-1,4-glucanase activity of enzyme. The maximum enzyme production from *Bacillus pumilus* was also optimized by Response Surface Methodology techniques. This investigation showed that this mesophilic bacterium possessedthe potential for current mainstream biomass conversion into fuel and agricultural, brewing and detergent sectors can be benefited from this bacterial isolate.

Keywords: Lignocellulosic biomass, Cellulase, Carboxymethyl cellulose (CMC), Mesophilic enzyme, β-glucosidase

MSD-65 (Participation Only)

Valorising Agro-Waste into High-Value Nutraceuticals: A Pathway to Sustainable Nutrition

Babli Yadav[1], Pardeep Kumar[1], Prince Chawla[2], Ajay Kamboj[1] and **Joginder Singh Duhan[1]*** duhanjs68@gmail.com

[1]*Department of Biotechnology, Chaudhary Devi Lal University, Sirsa, Haryana, India*
[2] *Department of Food Technology and Nutrition, Lovely Professional University, Phagwara, Punjab, India*

Abstract: Waste-to-wealth has gained significant attention for creating value from waste materials while effectively managing problematic agro-waste. Worldwide, agro-waste industries produce vast amounts of pre- and post-processing waste daily, with much of the untreated waste causing serious environmental issues. It is estimated that approximately 1.3 billion tons of waste are generated globally each year. From agro-industrial raw materials results in 40% of the waste of everything that is processing or less through out in the production chain including field during processing, logistics, retail and post-consumption. Agro-waste obtained from fruit extracts, plant fiber, nutshells as well as forest residues are always reactive to carbon. This waste can be

designed to be valorized in a sustainable way with cutting-edge technologies not only to generate value-added products but also to offer jobs. Valorization of agro-waste into alternative and renewable energy generation is a popular practice in several industries to meet the in-house energy requirement as well as for returns to offset the economic constrain of the ongoing process. The application of wastes from pineapple, sugarcane, açai, coconut, peanut, grape, wheat and rice were explored. This review described various methods used for the transformation of agro waste to different value-added compounds such as Biofuels (Biogas, bioethanol), Enzymes (Cellulase, protease, Xylanase, Tannse, CMCase), Antibiotic (Lovastatin, Tetracycline), Organic Acid, Levulinic Acid and also produce proanthocyanidins to release more bioavailable flavan-3-ols, abscisic acid and polyphenols and other products (Pulp, Panel board, dyes) etc.

Keywords: Agro-waste, Bioactive compounds; Enzymes, Valorisation.

PMI-1 (Oral)

Effect of *Priestia flexa* IIRRPSB14 Phosphate Solubilizer on the Growth and Development of ISM rice cultivar

Bandeppa S*[1], P.C. Latha[1], Amol S Phule[2], V. Manasa[1], R. Gobinath[1], K. Surekha[1], G. Rajani[1] , M.B. Kalyani[1], M.B.B Prasad Babu[1] and R. M. Sundaram[1]
bgsonth@gmail.com

[1]*Indian Institute of Rice Research, Hyderabad (110 012), India*
[2]*Dr. D.Y.Patil Biotechnology and Bioinformatics Institute, Dr. D.Y.Patil Vidyapeeth, Pune, India*

Abstract: Phospharous is an indispensable nutrient, playing a crucial role in metabolic processes and serving structural, energetic, and regulatory functions for plant development and growth. The amount readily accessible to plants is often a small portion of total phosphorus because of its fixation, which binds to soil particles or transforms into insoluble compounds. In comparison with other nutrients like nitrogen (N) or potassium (K), phosphorus is less mobile in soil. Phosphorus is second only to nitrogen among mineral nutrients, most commonly limiting crop growth. Typically, soil contains approximately 0.05% (w/w) of phosphorus, but plants only utilize 0.1% of this amount. Soil microbes play a vital role in the development of healthy soil structures and play a key role in providing soil nutrients to crops. Rice fields represent unique aquaterrestrial ecosystems that harbour a diverse group of microorganisms and beneficial soil microbes, such as phosphate solubilizer, pottasium solubilizer, and free-living nitrogen fixing bacteria. Besides nitrogen fixation, phosphate solubilizer microbes have made significant contributions to plant growth promotion, which enhances nutrient uptake in rice. In the present investigation, soil samples were collected from the farmer fields in Nalgonda districts of Telangana and the IIRR research farm to study the change in microbial population dynamics through enumeration in different rice establishment methods. A total of 21 potential phosphorus solubilizing agents were isolated, and an isolate of IIRRPSB14 was identified as Priestia flexa IIRRPSB14. Priestia flexa IIRRPSB14 inoculated rice seeds significantly improved seed germination and germination index compared to the inoculated control. Whole-genome sequencing of Priestia flexa IIRRPSB14 was performed to identify the phosphate-metabolism and plant growth-promoting genes that helps in the plant bacterial interaction and found that its genome possesses phosphate-metabolizing genes along with plant growth hormone (indole-3-acetic acid) synthesis genes, nitrogen fixation, anti-microbial activity, quorum sensing, genes for abiotic stress tolerance, and underlying mechanisms that control the bacterial ability to provide fitness advantages to the plant.

Keywords: *Priestia flexa* IIRRPSB14, Phospharous, Nitrogen fixation

PMI-2 (Oral)

Synergistic Interactions and Metabolic Activities of Bacterial Isolates in Rhizoremediation of Heavy Metals

Jagdish Parshad[1], Monika Kayasth[1], and Baljeet Singh Saharan[1]
jagdishhau@hau.ac.in

[1]*Department of Microbiology, CCS Haryana Agricultural University, Hisar (125004), India*

Abstract: Heavy metal contamination in soil poses significant environmental and health challenges, necessitating effective remediation strategies. The research focuses on the interaction or synergistic effect among Cobalt and Chromium resistant eight bacteria isolates in mixed culture conditions. Under mixed culture conditions, these isolates demonstrated successful co-culture growth without antagonistic effects. Similar growth patterns were observed in colony morphology or colour when bacteria were grown together compared to when grown individually. The highest metal-chelating activity was observed in HCr2 and HCo2, which produce the most potent chelating agents among the tested isolates. Siderophore production was also observed for metal-chelating enzyme activity. The least active isolates, HCr1 and HCr4, yield the least potent chelating agents. The chromium-degrading bacterial strains showed evidence of positive biofilm formation. This indicates that biofilm formation and chromium resistance may be related, which could improve the bacteria's ability to survive and break down heavy metals. Conversely, the strains HCo1 to HCo3, associated with cobalt degradation, did not exhibit biofilm formation, except for HCo4. This variability in biofilm formation among cobalt-degrading strains could indicate differences in their adaptive mechanisms or effectiveness in heavy metal degradation. The controls, not exposed to heavy metals, showed no biofilm formation, highlighting the potential role of heavy metal exposure in inducing biofilm development in these bacterial cultures. The findings provide valuable insights into microbial interactions in rhizoremediation.

Keywords: Rhizoremediation, Heavy Metals, Cobalt, Chromium, Siderophore production, Synergy, Metabolic activity

PMI-3 (Oral)

Shift in Tree Species Leads to Dramatic Changes in the Belowground Fungal Communities in Boreal Forests

Sunil Mundra*
*sunilmundra@uaeu.ac.ae; sunilmundra@hotmail.com

Department of Biology, College of Science, United Arab Emirates University, Al-Ain, Abu-Dhabi, United Arab Emirates

Abstract: Trees and understory vegetation are tightly connected with belowground microbiota andthese interactions are susceptible to change in tree species. Replacements of native birch with exotic Norway spruce has been initiated in Norway to increase long-term carbon storage, with limited knowledge on belowground impacts. We examined the impact of the tree species shift (birch to spruce) on the belowground microbial communities, fungal biomass, and their relationship with vegetation biomass and soil organic C (SOC) along a soil depth gradient (up-to 30cm). Replacement of birch with spruce negatively influenced the bacterial and fungal richness and strongly altered compositional patterns in the forest floor layer, most strikingly for fungi. Tree species-mediated variation in soil properties was a major driver for bacterial communities. For fungi, both soil chemistry and understory vegetation were important structuring factors, even more pronounced for ectomycorrhizal (ECM) fungi compared to saprotrophs. The relative abundance of ECM and ECM:saprotrophic fungi ratio, were higher in spruce compared to birch stands, particularly in the deeper mineral soil layers, and vice versa for saprotrophs. The positive relationship between ergosterol and SOC stock in forest floor layer suggests higher C sequestration potential in this layer of spruce forests, which further affects ecosystem functioning.

Keywords: Boreal forest; Carbon and nitrogen stock; Downy birch (*Betula pubescens*); Ectomycorrhiza; Fungal guild; Norway spruce (*Picea abies*); Tree species effects

PMI-4 (Oral)

Optimizing *Bacopa monnieri* Micropropagation: the Role of Plant Growth Regulators as Catalysts for Enhanced Development

Avni Dahiya[1*], Namita Singh[2], Subhash Kajla[3], Madhu Choudhary[1] and Adhisha[2]
avnidahiya.icar@gmail.com

[1] *ICAR-Central Soil Salinity Research Institute, Karnal (132001), Haryan, India*
[2] *Dept. of Biotechnology, GJUS&T, Hisar (125001), Haryana, India*
[3] *Dept. of Botany, CCSHAU, Hisar (125001), Haryana, India*

Abstract: *Bacopa monnieri* (L.), commonly known as "Brahmi", is a medicinal herb from the Scrophulariaceae family, valued for treating nervous disorders and mental health issues. This study investigates the effects of various plant growth regulators on the*in-vitro* micropropagation and survival of Brahmi plants. *In-vitro* propagation allows for the mass production of high-quality, disease-free plants under controlled conditions, enhancing genetic uniformity and meeting the rising demand for Brahmi in medicinal applications. For micropropagation, plant shoot cultures were grown on Murashige and Skoog (MS) medium supplemented with different plant growth regulators, including Benzylaminopurine (BAP), Kinetin (KIN), Indole-3-acetic acid (IAA), and Naphthaleneacetic acid (NAA), either individually or in various combinations. When used alone, the highest number of adventitious shoots observed was 6.7±0.69 on MS + 0.5mg l^{-1} BAP, as measured on the 28th day. Increasing the concentration of these plant growth regulators, when used alone, did not result in any further increase in the number of shoots per explant. Among the combinations tested, media supplemented with BAP (0.50mg l^{-1}) + KIN (0.75mg l^{-1}) + IAA (1.50mg l^{-1}) produced the highest number of shoots averaging 8.1±0.29. This was closely followed by the treatment combination BAP (0.50mg l^{-1}) + KIN (0.75mg l^{-1}) + IAA (0.50mg l^{-1}), which yielded 7.2±0.11 shoots. Rooting efficiency was evaluated using half-strength basal medium, which facilitated superior root development. The well-rooted plantlets were then transplanted into pots with different soil mixtures. The transplanted plants demonstrated nearly cent percent survival in several soil mixtures, including sand:soil:FYM (1:1:1), sand:soil:vermicompost (1:1:1), and coco peat:vermicompost:perlite (3:1:1) under greenhouse conditions. This study lays the groundwork for enhancing the efficiency of Brahmi propagation and offers avenues for future exploration in both controlled environments and field settings.

Keywords: *Bacopa monnieri*, *in-vitro* micropropagation, plant growth regulators, shoot multiplication, soil mixtures, rooting efficiency

PMI-5 (Oral)

Role of Rhizosphere Methylotrophic Bacteria in Rice Plant Growth Promotion and Improvement of Soil Health

Kavya T*[1], Geeta Singh[1] and Venkadasamy Govindasamy[1]
*kavyayadav6231@gmail.com

[1]*Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi (110 012), India*

Abstract: The rhizosphere is a hotspot for many beneficial organisms, including a ubiquitous group of microorganisms known as methylotrophs, which utilize one-carbon compounds like methanol and methane as their sole carbon and energy sources. In this study, we isolated methylotrophic bacteria from the rice rhizosphere and characterized them morphologically using different media. These isolates were then qualitatively and quantitatively screened for their plant growth-promoting (PGP) traits under in vitro conditions, including Nitrogen fixation, Phosphate solubilization, Potassium solubilization, Zinc sulfate ($ZnSO_4$) and Zinc carbonate ($ZnCO_3$) solubilization, Ammonia production and Indole-3-acetic acid (IAA) production. Pigments were extracted using 0.1N NaOH and analyzed using Fourier-transform infrared spectroscopy (FTIR) to detect the presence of recalcitrant carbon-like compounds, which serve as precursors to soil humic substances. Parameters related to humification, such as E_2/E_3, E_4/E_6, specific UV absorbance (SUVA), Bacterial necromass carbon, and Aromaticity, were assessed to determine the similarity of these compounds to soil humic substances. Further based on their carbon use efficiency and PGPR traits six isolates were selected. These 6 isolates were tested in two different *in planta* experiments like petri dishes and pot experiments. The results demonstrated

improvements in both plant growth parameters and soil health. Overall, this research highlights the promising role of methylotrophic bacteria in enhancing rice growth and development while also contributing to soil carbon sequestration.

Keywords: Plant growth-promoting (PGP), Zinc sulfate ($ZnSO_4$), Zinc carbonate ($ZnCO_3$)

PMI-6 (Oral)

Biotechnological Potential of Bifunctional *Pantoea* sp. for Developing Sustainable Agriculture System in Arunachal Pradesh

Bhagyashree Bora[1], Takam Akash[1,] Refad Ahmed[1, 2] and Natarajan Velmurugan[1,2,*]
*natarajan@neist.res.in

[1]*CSIR-North East Institute of Science and Technology (CSIR-NEIST), Branch Laboratory-Itanagar, Naharlagun (791 110), Arunachal Pradesh, India*
[2]*Academy of Scientific and Innovative Research (AcSIR), Ghaziabad (201 002), India*
Dr. Natarajan Velmurugan – CSIR-North East Institute of Science and Technology (CSIR-NEIST), Branch Laboratory-Itanagar, Naharlagun (791 110), Arunachal Pradesh, India

Abstract: Due to lack of accessibility to endangered medicinal plants of high-altitude Himalayan Mountains, the biotechnological potential of microorganisms associated with these plants has not been largely explored. Here, we demonstrate the beneficial phenotypic and genomic characteristics of culturable bacterial symbionts associated with an endangered medicinal plant *Aconitum heterophyllum* from high-altitude Himalayan Mountain ranges. We have successfully isolated and characterized a bifunctional and metabolically stable *Pantoea* sp. AHE68 from *A. heterophyllum*. *Pantoea* sp. AHE68 was demonstrated to simultaneously convert inorganic phosphate into organic phosphate (29.8% increases in available phosphorus content) and synthesis growth-promoting IAA (45.34±0.82 µg mL^{-1}) thereby enhances photosynthetic microalgal productivity in synthetic co-culture system. AHE68 was found to simultaneously secrete organic acid (10.42 mM mL^{-1}) to convert the inorganic phosphate into organic phosphate as well as produces high level IAA under stress conditions. Interactions of AHE68 and long chain fatty acids (LCFA) producing photosynthetic microalga *Micractinium* sp. GA001 were characterised in different combinations of synthetic co-culture systems. The endophyte AHE68 was found to significantly enhance 22.71% and 79.27% increase in microalgal cell numbers and lipid contents in co-culture systems, respectively. In co-culture studies, AHE68 was found to be metabolically capable to simultaneously synthesise active forms of IAA and organic acids under salt-stress conditions. The findings of the phenotypic and genotypic analysis give us the proof that the bacterial symbionts were metabolically stable for extended period of time (up to 30 days) to improve microalgal productivity. The findings were further complemented with genomics studies of symbiont which was subjected to multiple sequencing approaches to assemble and annotate their genome, resulting in key genes involved in PGP activities, metabolites production and transportation being identified. The bacterial symbiont was fully characterized by the whole genome sequencing with two different sequencing approaches. Hybrid genome of the bacterial symbiont had been obtained with SPAdes using a hybrid method, combining Illumina paired end reads with Nanopore single-end reads. Hybrid genome assembly is a strategy to overcome the limitations of individual sequencing techniques including long-read and short-read techniques. Illumina and PacBio/Nanopore were well-known next generation sequencing (NGS) techniques to produce short and long length reads, respectively. However, several limitations were associated with these techniques such as large genome fragmentations (in Illumina), identification of transposons, mobile genetic elements, unambiguous reads, horizontal gene transfers events, and large scale errors (in PacBio/Nanopore). The approach helped us to assemble and annotate symbiotic bacterial genome yielded highly accurate, fully finished hybrid genome along with plasmids and core genes. This study expands the benefits and bioprocessing potential of bacterial symbiont of Himalayan medicinal plant.

Keywords: Himalayan mountains, Long chain fatty acids, *Micractinium* sp, Microalgal productivity, NGS.

PMI-7 (Oral)

Rhizospheric Soil Micobiome of Landrace and Domesticated Wheat Variety of North-Western India Cultivated Under Phosphate Stress

Garcha S, Garg S, Srivastava P and Mavi GS
sgarcha@pau.edu

Department of Microbiology, Punjab Agricultural University, Ludhiana, India

Abstract: The objective of this study was to evaluate the combined influence of phosphate starvationand genotype on the rhizospheric community structure in tillering stage of wheat. We choosetwo independent variables- wheat varieties and P level of the soil. Wheat varieties- landraceLC306 and cultivar PBW 725 were procured from the Department of Plant Breeding andGenetics, Punjab Agricultural University Ludhiana. Rhizospheric soil sample was collected attillering stage. NCBI database was used for 16s V3-V4 region for bioinformatics analysis of amplicons of DNA. A total of 24 phyla, 48 classes, 99 orders, 191 families, and 370 generawere identified in the rhizospheric soil. The predominant phyla in the soil was Firmicutes (C306- 56.15% and 16679 OTUs; PBW 725- 53.47% and 17173 OTUs); Proteobacteria(C306- 35.38% and 10511 OTUs; PBW 725- 37.99% and 12202 OTUs); Bacteroidetes(C306- 6.74% and 2002 OTUs; PBW 725- 6.59% and 2116 OTUs) and Actinobacteria (C306- 1.4%, 418 OTUs and PBW 725- 1.6%, 525 OTUs). The descending order of theirabundance was Lactobacillaceae (>25%), Staphylococcusceae, Enterobacteriaceae (>15%), Moraxellaceae (>10%), Bacillaceae and Paenibacillaceae (>5%). The other analyses like Heatmap, core microbiome, Dendrogram, Alpha diversity, Beta diversity, PCOA plot, Rarefaction curve built using online resource of www.microbiomeanalyst.ca will be discussed.

Keywords: Moraxellaceae, Bacillaceae, Paenibacillaceae, Dendrogram

PMI-8 (Poster)

Assessment of Drought Tolerant Bacteria for Sustainable Production of Mustard in Alkaline Soils of South- West Haryana.

Tanvi Bhatia[1]*, Abhinav Saini[1], Ankush Sharma[1], Ashwani Sharma[1], Pinki[1] and Simran[1]Alimer[1]
bhatiatanvi54@gmail.com

CCSHAU College of Agriculture, Bawal (123501), India

Abstract: Water is the main limiting factor in agricultural production worldwide. Drought is a key global agricultural production constraint that is projected to worsen much more in future. Coping with drought stress in plants requires a variety of adaptations and mitigation techniques. Plant growth promoting rhizobacteria (PGPR) that has coevolved with plant roots in harsh environments over time could play a significant role in alleviation of drought stress in plants. By producing exopolysaccharides (EPS), phytohormones, 1-aminocyclopropane-1-carboxylate (ACC) deaminase, volatile compounds, causing the accumulation of osmolytes, antioxidants, up- or down-regulating stress-responsive genes, and changing root morphology, these beneficial microorganisms colonise the rhizosphere/ endo-rhizosphere of plants and impart drought tolerance. In our study, after isolation of plant growth promoting bacteria from the rhizosphere of different trees and plants grown in CCSHAU Bawal campus (South- West Haryana), they were assessed for their ability to mitigate drought stress in mustard crop. We investigated the distribution of culturable bacteria and characterised their halophilic behaviour, biofilm formation, phosphate solubilisation, and synthesis of 1-aminocyclopropane-1-carboxylate deaminase (ACCd). It was observed that some selected isolates improved the morphology and yield in mustard crop hence imparting drought stress tolerance in the crop.

Keywords: Drought tolerance, Plant growth promoting Rhizobacteria, Mustard, Mitigation, Adaption, Rhizosphere

PMI-9 (Poster)

Investigating the Biocontrol activity of Marine Actinobacteria against Fungal Pathogen *Fusarium Oxysporum Pallidoroseum* in Saline Conditions

Parth Ahir[1], Hazel Mendes[1], Kushboo Rathod[1] ,Pinakin Dhandhukia[2] and Janki N. Thakker[1].
parthahir167@gmail.com

[1]*Department of Biological Sciences, P. D. Patel Institute of Applied Sciences, CHARUSAT University, Anand, Gujarat (388421), India*
[2]*Department of Microbiology, School of Science and Technology, Vanita Vishram Women's University, Surat, Gujarat, India*

Abstract: Elevated salt levels in soil result from industrial operations, especially in areas close to industrial zones. By 2025, the area projected under salt-affected soils in India is about 13 million ha.Soil Salinity leads to large agricultural production loss and it has been claimed that Gujarat State suffers 4.83 million tons of loss because of soil salinity. Furthermore, current developments in chemical fungicides, fertilizers, and herbicides have raised crop output temporarily. Concerns have been expressed concerning this practice's potential long-term effects on ecosystems, human health, and soil fertility. The solution to this issue is the employment of microorganisms as a substitute to naturally strengthen plants' defenses against pathogens, shielding crops from disease. It helps the plants to grow on land with high salt concentrations. This study investigates the actinobacterial species isolated from marine habitats and their possible uses as biocontrol agent in the presence of salt.Actinobacterial isolates showed promising biocontrol capabilities against common phytopathogenic fungi. Isolate was tested against two common fungal pathogen *Fusarium oxysporum pallidoroseum* (cow pea pathogen). Dual culture plate assay, Broth assay, MDA (Malondialdehyde) Assay, & SEM were carried out in normal and saline conditions, and further results were checked in pot studies. Dual culture assay showed a clear decrease in the growth of the pathogen in the presence of isolate in comparison to control plates. Broth assay showed a reduction in fungal growth. The MDA levels were observed to increase with isolate treatment as compared to without isolate treatment. This indicates that the organism was effective in degrading the fungal cell membrane, which was observed in the SEM too. In Pot studies Cowpea was used as a model plant and significant differences were observed between control plants and treated plants, especially in saline conditions where isolate gave both PGP and biocontrol effect as compared to controls, The findings highlight the role that marine actinobacteria play in plant protection in saline conditions.

Keywords: Marine actinobacteria, Biocontrol, *Fusarium oxysporum pallidoroseum*, Salinity, Cowpea.

PMI-10 (Poster)

Prospecting the Role of Non-Rhizobial Bacterial Endophytes in Enhancing Soybean Growth and Nodulation Efficiency

Kirti Suman, Hirudhaya Ravi, Pushpendra Sharma, Meena Rathore and Rajeev Kaushik
kirtisumanmedicos1@gmail.com

Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi, India

Abstract: Soybean (*Glycine max*), a globally significant commercial crop, faces increasing challenges due to climate change, impacting sustainable production as its cultivation spreads to new regions. Developing innovative nutrient management strategies and managing abiotic and biotic stress are crucial to overcoming these challenges. In addition to symbiotic rhizobia, soybean root nodules are also inhabited by non-rhizobial bacterial endophytes (NREs), whose roles remain unclear. However, recent studies suggest that certain NRE strains or species may positively influence nodulation, presenting potential significance for soybean cultivation. In this study, 334 NREs were isolated from root nodules of seven popular soybean cultivars grown in central India. These endophytes were assessed qualitatively and quantitatively for plant growth-promoting characteristics such as nutrient solubilization (N, P, K, Fe, Zn), ammonia production, exopolysaccharide (EPS) formation, and hormone production (IAA, cytokinin, gibberellic acid, ethylene). Their abiotic stress tolerance was also evaluated through PEG assays and the estimation of proline and glycine betaine levels. From this, 50 NREs exhibiting both plant growth-promoting traits and abiotic stress tolerance were selected for further study.

These promising endophytes underwent morphological analysis and Colony Box PCR, classifying them into different clades. Molecular identification through 16S rRNA gene sequencing revealed that these NREs predominantly belonged to genera including *Bacillus*, *Paenoarthrobacter*, *Stenotrophomonas*, *Microbacterium*, *Agrobacterium*, *Enterobacter*, *Pristia*, and *Oikibacterium*. A seed germination assay demonstrated significant improvements in root and shoot length, germination rate, and seed vigor. In conclusion, non-rhizobial endophytes (NREs) effectively promote soybean growth and enhance nodulation efficiency. The study also identified several bacterial genera previously unreported as soybean NREs, which exhibited strong plant growth-promoting abilities and abiotic stress tolerance. This research highlights the potential of leveraging these beneficial interactions between NREs and rhizobia for biotechnological applications in soybean production.

Keywords: Non-rhizobial endophytes (NREs), Plant-growth promoting traits, Abiotic stress tolerance, *Glycine max*

PMI-11 (Poster)

Enhancing Wheat Resilience: The Role of Halotolerant Exopolysaccharide Producing Bacteria under Salt Stress

Suman Jayakumar Kankanwadi, Sushma N N and Leela Wati
sumankankanwadi678@gmail.com

Department of Microbiology, College of Basic Science & Humanities
Chaudhary Charan Singh Haryana Agricultural University, Hisar (125004), Haryana, India

Abstract: Plants are exposed to a wide range of complex biotic and abiotic challenges as a result of the advent of human civilization and anthropogenic activities brought about by global urbanization and climate change. Salinity has emerged as a substantial concern, negatively affecting crop output. Crop productivity is negatively impacted by salt in the soil in dry and semi-arid regions of the world. Wheat (*Triticum aestivum* L.) is one of the most cultivated cereal crop and salinity being serious constraint to wheat production, resulting in 65 % yield losses. The systematic use of microorganisms concerning agricultural crops is one of the most recent and innovative methods that has gained popularity due to their beneficial effects on crop productivity, health and growth. Halotolerant bacteria are emerging as effective biological agents to alleviate the detrimental impacts of elevated salinity and enhance plant development, while concurrently rehabilitating damaged saline soils. Halotolerant bacteria mitigate salt stress in plants by many pathways that elicit multifaceted physiological, biochemical, and molecular responses. These encompass alterations in the expression of defence-related proteins, synthesis of exopolysaccharides, activation of antioxidant systems, accumulation of osmolytes, regulation of Na^+ kinetics, enhancement of phytohormone levels and nutrient absorption in plants. Effective application of exopolysaccharide (EPS) producing halotolerant bacteria can alleviate the condition of derelict soil, boost crop productivity and restore ecosystem diversity. EPSs can be applied to the soil to encourage bacterial colonization of soil particles and plant roots, in order to increase soil structure and ultimately plant growth. As a high molecular-weight polymer, extracellular polymeric substances (EPS) offer safety in the processes such as surface attachment, microbial accumulation, plant–microbe interaction and bioremediation. Plants are protected from salt stress by root-colonizing bacteria and EPS matrix, which increase water-holding capacity and reduce sodium ion uptake. Hence, halotolerant EPSs-producing bacteria offer defence against a salinity stress.

Keywords: Abiotic stress, Exopolysaccharide, Halotolerant, Plant microbe interaction Salinity, Wheat

PMI-12 (Poster)

Relationship between Electrical Conductivity, pH and Microbial Soil Enzyme Activity in Salt Affected Agricultural Fields of Lentil

Deepak Sharma[1,2*], Madhu Choudhary[1], Rakesh Kumar[2], Vijayata Singh[1] and Awtar Singh[1]
deepakyashrajsharma@gmail.com

[1]*ICAR-CSSRI, Karnal , Haryana (132001), India*
[2]*CCSHAU, Hisar, Haryana (125004), India*

Abstract: Soil salinity is a major abiotic stress factor affecting soil health and crop productivity, particularly in legumes like lentils (*Lens culinaris*). This study aims to investigate the microbial enzyme activities in salt-affected soils under lentil cultivation, with a focus on understanding the relationship between electrical conductivity (EC), pH, and microbial populations.The study was conducted at ICAR-CSSRI, Karnaland samples were analyzed for EC, pH, microbial countsand enzyme activities (dehydrogenase and phosphatase).The EC of soils ranges from 2.5 to 6.8 dS/m, indicating moderate to high salinity.The pH of the soils ranged from 7.2 to 8.9, indicating predominantly neutral to alkaline conditions. Microbial counts were assessed using standard plate count methods that indicate low bacterial counts in soils with higher EC values.Dehydrogenase activity, an indicator of overall microbial activity, value ranges from 114.10 TPF µg g^{-1} day^{-1} for normal soil to 51.74 TPF µg g^{-1} day^{-1} for highly saline soil. Acid Phosphatase activity, involved in phosphorus cycling, value ranges from102.40 µg P-NP g^{-1} $h^{-1}$for normal soil to 71.25 µg P-NP g^{-1} h^{-1} for highly saline soil whereas for alkaline phosphatase value ranges from 179.6 µg P-NP g^{-1} $h^{-1}$for normal soil to 43.57 µg P-NP g^{-1} h^{-1} for highly saline soil. Data shows that Ec Significantly correlated with pH (r=0.83*) and correlation of enzyme activity (r=0.80). Decline in activity was observed with increasing salinity, indicating reduced phosphorus availability in salt-affected soils.The study demonstrates that salinity significantly impacts the microbial ecosystem of lentil-cultivated soils, leading to reduced microbial counts and enzyme activities. These findings underscore the importance of managing soil salinity to maintain soil health and ensure sustainable lentil production.

Keywords: Electrical conductivity, Lentil, pH, Microbial enzyme activity, Salt-affected soils.

PMI-13 (Poster)

Synergistic Impact of Multi-trait *Kosakonia* sp. and *Serratiamarcescens* in Improving Maize (*Zea mays*) Germination and Root Morphology under Drought Stress

Ashish Kumar[1]* and Ajay Veer Singh[1]
*ashishkumar67233@gmail.com

[1]*Department of Microbiology, College of Basic Sciences and Humanities*
G. B. Pant University of Agriculture and Technology, Pantnagar (263145), Uttarakhand, India

Abstract: Drought is a major abiotic stress that severely limits crop growth and reduces agricultural productivity worldwide, particularly affecting maize (*Zea mays*), one of the world's most important staple crops. It is highly vulnerable to abiotic stresses, often leading to significant decreases in yield. Here, the present study investigates the synergistic effects of three multi-functional plant growth-promoting bacteria (PGPB), ***Kosakonia* sp. FMEP1, *Serratiamarcescens* FMRP24** and ***Serratiamarcescens* SRK14** on mitigating drought stress and enhancing maize germination. These bacteria exhibit significant osmotolerance, as evidenced by robust growth in 30% Polyethylene glycol (PEG 6000) containing medium. The qualitative and quantitative analysis showed that the osmotolerant isolates are highly efficient in phosphate, potassium, and zinc solubilization and siderophore production. These isolates were consistently able to produce phytohormones and extracellular polysaccharides under stressed and non-stressed conditions, demonstrating their adaptability and effectiveness in plant growth promotion under diverse environments. Based on molecular characterization, the isolates FMEP1 and FMRP24 were identified as *Kosakonia* sp. and *Serratiamarcescens*,respectively. Additionally, germination assay was performed using maize seeds to evaluate the effectiveness of the selected bacterial isolates and their consortium. The findings of the experiment demonstrate the significant improvement in length, weight, vigor index, and germination percentage of the seedlings. Root morphology was studied using RhizoScanner, which revealed significant changes in root structure following consortium treatment. Scanning

Electron Microscopy (SEM) analysis revealed the presence and attachment of bacterial isolates on the root surfaces. Present research indicates that the interaction between maize seeds and bacterial isolates shows great potential for establishing a strong plant-bacteria symbiosis, especially under drought conditions.

Keywords: Crop resilience, PGPB, Drought stress, Germination, Nutrient solubilization, Maize

PMI-14 (Poster)

Salicylic Acid Pretreatment Elevates the Endogenous Concentration of Salicylic Acid to Protect against *Fusarium oxysporum*-Led Biotic Stress in *Vigna Mungo*: Transcriptomics and Molecular Insights of Defense Pathways

Lucky Duhan[1*], Ritu Pasrija[1], Deepak Kumar[2] and Raman Manoharlal[3]
luckyduhan84@gmail.com

[1]*Department of Biochemistry, Maharshi Dayanand University, Rohtak (124001), India*
[2]*Department of Botany, Institute of Science, Banaras Hindu University, Varanasi, Uttar Pradesh, India*
[3]*ITC Limited, ITC Life Science and Technology Centre (LSTC), Peenya Industrial Area, 1st Phase, Bengaluru, Karnataka, India.*

Abstract: *Fusarium oxysporum*, a soil-borne pathogen, poses a significant threat to crops globally, with limited control strategies available. This study explores the protective efficacy of seed pretreatment with salicylic acid (SA) in mitigating F. oxysporum-induced stress in Vigna mungo, a key legume crop. SA-treated (100 µM) and *F. oxysporum*-exposed plants were analyzed for various physiological, biochemical, antioxidant, and metabolic profiles. Fungal infection resulted in diminished growth, chlorophyll, protein, phenolic, and flavonoid contents, while stress markers and antioxidant levels were elevated. SA pretreatment alleviated these detrimental effects by enhancing antioxidant responses, increasing endogenous SA levels, and upregulating phenylalanine ammonia-lyase (PAL) activity. This triggered a more robust antioxidant response to quench reactive oxygen species (ROS). Furthermore, SA modulated metabolic processes, leading to elevated phytoalexin and antioxidant levels in infected plants. The transcriptomic analysis confirmed the activation of SA-mediated defense pathways, revealing an upregulation of genes in SA-treated plants compared to untreated controls. These findings further validate the proposed mechanism of SA action in enhancing plant defense

Keywords: *F. oxysporum*, Stress, Salicylic acid, *V. mungo*, Endogenous SA, Antioxidant, Metabolic profile

PMI-15 (Poster)

Identification and Characterization of Cyanobacterial Isolates from the Himalayan Region for Plant Growth Promotion

Srishti Yaduvanshi[1]*, Shobit Thapa[2] and Smriti Mall[3]
srishtigkp2013@gmail.com

[1]*Department of Microbiology, Faculty of Allied Health Sciences, Mahayogi Gorakhnath University, Gorakhpur (273007), Uttar Pradesh, India*
[2]*Microbial Technology Unit II, ICAR-National Bureau of Agriculturally Important Microorganisms (NBAIM), Mau (275103), Uttar Pradesh, India*
[3]*Department of Botany, DDU Gorakhpur University Gorakhpur (273007), Uttar Pradesh, India*

Abstract: Cyanobacteria are ancient photosynthetic prokaryotes that are responsible foroxygenic photosynthesis similar to plants. They are ecologically versatile microorganisms, occupying diverse habitats, from hot deserts to deep oceans and from saline lakes to thermalsprings. The Himalayan region is still unexplored in terms of cyanobacterial diversity beingfree from anthropogenic interventions. The current study was carried out to investigate theplant growth-promoting (PGP) attributes of the different types of cyanobacterial culturesobtained from various regions of Himachal Pradesh and Uttarakhand. The Twelvecyanobacterial obtains were studied based on their pigments and PGP traits. The chlorophylla content ranged from 0.707–11.57 µg mL-1 whereas

the carotenoid content was from 0.098–3.914 µg mL-1. Phycobiliprotein content varied from 0.005–0.234, 0.024–0.266, and 0.010–0.130 µg mL-1 for phycocyanin, allophycocyanin, and phycoerythrin respectively. RegardingPGP attributes, siderophore production ranged from 2.1– 25 percent siderophore units,phosphate solubilisation varied from 0.29–17.9 µg mL-1, and ammonia production from 6.5–47 ppm for different isolates. The Indole acetic acid production data showed by 6 isolateswithout tryptophan whereas all the isolates were able to produce the hormone after addingtryptophan. Isolates were also able to enhance the germination rate in the seed germinationassay. Some isolates were also able to show an increase in root and shoot length, fresh anddry weight, and number of roots over control. The best five isolates were also characterized according to their morphological as well as molecular characteristics using cyanobacterial-specific primers. Isolates characterized were; two isolates were Leptolyngbya and one eachfrom Scytonema, Neowestiellopsis, and Aphanothece. These cultures can be further tested forsecondary metabolites production as well as for field application.

Keywords: Phycobiliproteins; Himalayan; siderophores, Seed germination, AmmoniaProduction

PMI-16 (Poster)

Exploring Biocontrol and Plant Growth Promoting Potential of Multifaceted PGPR against the Causal Agent of Alternaria Blight for Agricultural Sustainability

Sheetal Alchoni[1]* and Ajay Veer Singh[1]
sheetal.alchoni@gmail.com

[1]*Department of Microbiology, College of Basic Sciences and Humanities.*
G. B. Pant University of Agriculture and Technology, Pantnagar (263145), Uttarakhand, India

Abstract: Plant diseases pose a serious threat to global food security. Although chemical pesticides are widely used to control pathogens, their overuse raises serious environmental concerns. Biological control agents (BCAs), particularly plant growth-promoting rhizobacteria (PGPR), offer an eco-friendly alternative to manage plant diseases, improve growth, and enhance yields, supporting sustainable agriculture. In this context, the present study explores the potential of PGPR as biocontrol agents against *Alternaria alternata*, the causative agent of Alternaria blight in pea plants (*Pisum sativum* L.). Two rhizobacterial strains, *Bacillus altitudinis* PWR15 and *Bacillus paramycoids* MWR1, demonstrated significant inhibition of *A. alternata* growth under *in vitro* dual culture assays. These strains were further evaluated for their production of hydrolytic enzymes (chitinase, amylase, protease, xylanase, and pectinase) and their plant growth-promoting abilities (siderophore, HCN, ammonia, and IAA production, nitrogen fixation, zinc, and phosphate solubilization). Additionally, one consortium was also developed based on biocompatibility test among the selected bacterial antogonist PWR15 and preisolated and characterized PGPR. Further the consortium was evaluated for its plant growth promotion and hydrolytic enzyme production capabilities. Consortium displayed significant effectiveness in reducing *A. alternata* mycelial weight by 83.33%. Furthermore, the outcomes of the pot experiment confirmed the efficacy of the bacterial strains and consortium in significantly reducing Alternaria blight in peas. Both the bacterial strains PWR15, MWR1, and the consortium significantly reduced disease incidence (38.89%, 44.44%, and 27.78%) compared to the negative control group (83.33%) proving that the strains were notably more effective at inhibiting the disease and enhanced various growth parameters of pea plants. GC-MS analysis of PWR15 and MWR1 revealed the presence of diverse potent antifungal compounds known for their antifungal abilities. Their ability to significantly inhibit *Alternaria alternata*, demonstrates their efficacy in plant disease management. Hence, these findings suggest that the selected bacterial strains hold promise as biocontrol and plant growth-promoting agents.

Keywords: Food security, Biological control, PGPR, Biotic stress, Sustainable agriculture, Plant-microbe interaction

PMI-17 (Poster)

Assessing the Drought-Tolerance, Growth-Promoting Potential of Strawberry (*Fragaria* × *Ananassa* Duch.) Rhizobacteria for Consortium Bioformulation

Vinay Kumar Dhiman[a*] and Neerja Rana[a]
vinaykrdhiman4@gmail.com

[a] *Department of Basic Sciences, Dr. Yashwant Singh Parmar University of Horticulture and Forestry, Nauni, Solan (173230), India*

Abstract: In the present study, rhizobacteria from strawberry plants were screened for stress tolerance under osmotic stress in TSB-mediated PEG 6000 (-0.73 MPa) and tested their ability to produce proline, exopolysaccharide, and free amino acids, all of which induce and regulate stress tolerance. The rhizobacteria were also distinguished for the production of 1-aminocyclopropane-1- carboxylate deaminase (ACCd) for the mitigation of drought stress. Among the 111 rhizobacterial isolates, 41 isolates grow above threshold limit in osmotic stress tolerance, 33 of which exhibited stress tolerance. Further characterization screened 27 isolates as capable growth promoters. Among the experimentally screened rhizobacteria, the isolates SBU4 and SDK8 [*Pseudomonas fluorescens* (OP627557) (PGPR1) and *Pseudomonas glycinae* (OP627558) (PGPR2)] exhibited the most promising phyto-beneficial potential. Both the isolates grew exponentially well during the log phase, with increased growth in Log CFU ml-1 under experimentally produced osmotic stress. The drought stress tolerance test results of the SBU4 and SDK8 isolates revealed the presence of proline (1.93 µg/ml, 2.05 µg/ml), exopolysaccharide (2.19 mg/mg protein, 2.58 mg/mg protein), and free amino acid (11.47 µmol/g, 13.32 µmol/g) and positive growth in ACCd-enriched DF media, an ACCd assay (αketobutyrate (0.56 µmol/ml, 0.64 µmol/ml) and ammonia (0.37 µg/ml, 0.53 µg/ml)). The isolates SBU4 and SDK8 performed well in qualitative tests for P solubilization, N fixing ability, siderophore chelation, HCN, and ammonia production, as well as in assays involving P producers (94.57 µg/ml and 92.86 µg/ml), siderophore units (52.14% SU and 63.12% SU), and IAA producers (74.63 µg/ml and 72.64 µg/ml). These rhizobacterial isolates were optimized under various growth factors (pH, temperature, incubation) to achieve a relatively high log CFU ml^{-1}.The growth of cultures on cross-streaked nutrient agar plates was tested for an efficient, effective consortium bioformulation that enhances growth and specific traits (drought stress mitigation) in strawberry plants.

Keywords: PGPR, Stress, Drought, ACCd, Strawberry, Pseudomonas

PMI-18 (Poster)

Comparative Analysis for Plant Growth Promoting and Biocontrol Traits in *Bacillus carbialesii* strains Isolated from Rhizosphere Soil of Chickpea

Prajwal S.K., Sushil K. Sharma* and S.K. Jain
sushil.sharma1@icar.gov.in

School of Crop Health Management Research
ICAR-National Institute of Biotic Stress Management, Raipur, India

Abstract: *Bacillus cabrialesii* was first reported from the Mexicoas a potentialbiocontrol and plant growth promoting agent and thereafter reported from other parts of the globe including India. This study presents comparative analysis of plant growth promoting and biocontrol traits in both the strains IS-10 and BATS-13 of *B. cabrialesii* isolated from rhizosphere soil of chickpea cultivated in Chhattisgarh state. In terms of PGP traits, *B. cabrialesii* IS-10 produced higher amount of IAA (9.86 ± 0.65 µg/ml), soluble zinc (36.8 ± 0.40 µg/ml), and siderophore (68 ± 0.95 %) compared to BATS-13 whereas strain BATS-13 produced more ammonia production (3.58 ± 0.24 µM/ml) as compared to IS-10 (3.003 ± 0.27). In term of biocontrol trait, *B. cabrialesii* IS-10 inhibited *Fusarium oxysporum* f. sp. *ciceris, Sclerotium rolfsii* and *Macrophomina phaseolina* to 61.00, 44.05 and 48.34 %, respectively while and BATS-13 inhibited *F. oxysporum* f. sp. *ciceris, S. rolfsii* and *M. phaseolina* to 58.45, 40.75 and 42.82 %, respectively. Strains IS-10 and BATS-13 did not produce chitinase, DNase, and hydrogen cyanide (HCN), however, produced volatiles which enhanced radial growth of *F. oxysporum* f. sp. *ciceris in vitro*. This is in contrary to the previous finding where most of the volatiles produced by bacteria inhibited the growth of pathogens. Crude extract of strains IS-10 and BATS-13 also demonstrated strong oil

dispersion assay (2.83±0.39), emulsification index (62.26±0.77) and positive Parafilm M test confirmed their biosurfactant activity. Furthermore, both strains displayed crude biosurfactant concentration-dependent inhibition of *F. oxysporum* f. sp. *ciceris*, with superiority being observed in strain IS-10. Analysis of nature of biosurfactants produced by *B. cabrialesii* strains IS-10 and BATS-13 revealed presence of surfactin and fengycin as descendible by TLC and UPLC-MS. Overall, *B. cabrialesii* IS-10 was found as more potent plant growth promoting and biocontrol agent as compared to strainBATS-13.

Keywords: *Bacillus cabrialesii*, Biosurfactant, BATS-13, *F. oxysporum*, Parafilm M test

PMI-19 (Poster)

Examining *Microcella putealis* for its Biotic and Abiotic Defense Mechanisms in Conjunction with the Promotion of Plant Growth

Meetkunwar Dahiya[1], Pinakin Dhandhukia[2]and Janki N. Thakker[1]
meetkunwardahiya63@gmail.com

[1]*Department of Biological sciences, P. D. Patel Institute of Applied Sciences, CHARUSAT University, (388421), Anand, Gujarat, India.*
[2]*Department of Microbiology, School of Science and Technology, Vanita Vishram Women's University, Surat, Gujarat, India.*

Abstract: Diverse tactics are employed to increase agricultural productivity in reaction to the growing food needs resulting from population growth. Among the many approaches, using plant growth-promoting bacteria (PGPB) has proven to be a practical way to apply novel agricultural techniques. Although PGPB derived from rhizospheric soil has been extensively studied, more research on marine microorganisms is required. As marine environment is an extreme environment the marine bacteria is adapted to grow at extreme conditions which enables them to produce various secondary metabolites which can be useful in certain ways. The current study attempts to explore marine microorganisms' capacity to stimulate plant growth. The bacteria isolated form marine environment *Microcella putealis* was found tolerating upto 13% and more of salinity. This bacteria is able to solubilize various essential minerals such as phosphate and potassium and able to produce ammonia from soil nitrogen fixation and IAA (Indole-acetic acid), which makes it a possible plant growth promoter. The study was done on *Pennisetum glaucum* (Pearl Millet) crop at difference salt concentrations (1000mM, 2000mM and 3000mM) NaCl concentrations and pot trials were performed with the control (untreated) and treated (*Microcella putealis* coated seeds) and treated with *Fusarium javanicum*, observation says that the bacteria is able to promote plant growth at the saline condition upto 16% in soil. The stress markers such as SOD, POX, L-Proline and Total-Phenolics were found to increase in treated seeds. As well as increase in plant length and weight was found. These results describe that *Microcella putealis* functions as an plant-growth promoter from marine environments which is also able to survive the salinity and promote the plant growth.

Keywords: Plant growth promoting bacteria, IAA (Indole-acetic acid), marine bacteria, *Pennisetum glaucum* (Pearl Millet)

PMI-20 (Poster)

Plant Growth Promoting Traits of Marine Bacteria with Bio-Control Capability against *Fusarium sp.* in Cowpea Plant

Bhasha Choksi [1], Archita Patel [2], Pinakin Dhandhukia[3] and Janki Thakkar [1]
bhashachoksi2001@gmail.com

[1]*Department of Pharmacy, Ramanbhai Patel College of Pharmacy, Charotar University of Science and Technology, CHARUSAT Campus, Changa , Anand, Gujarat (388421), India*
[2]*Department of Biological Sciences, P.D. Patel Institute of Applied Sciences, Charotar University of Science and Technology, CHARUSAT Campus, Changa, Anand, Gujarat ((388421), India*
[3]*Department of microbiology, school of science and technology, Vanita Vishram Women's University, Surat, Gujarat, India*

Abstract: Microorganisms have characteristics that aid plant growth and raise the level of vital metabolites in plants for better growth including primary and secondary metabolites as well as several developmental enzymes. Marine bacteria must endure harsh environmental circumstances for their survival so it produces several secondary metabolites to protect themselves. Such metabolites might likewise be advantageous for a plant's growth. However, the effectiveness of marine microbes on plant growth remains unexplored. Present study explored Marine microbes, which can contribute to the sustainable agricultural approach, total 40 isolates were isolated from Dhuvaran beach Khambhat, Gujarat (India), All these strains were screened primarily for Plant growth promoting traits like IAA production, ammonia production, phosphate as well as potassium solubilisation, Zinc solubilization and Biocontrol traits includes Amylase, cellulase, Lipase, protease, glucanase and chitinase production. Strain 10MH11 having maximum traits positive for promoting growth and biocontrol activity was further used and characterized. Strain 10MH17 was identified by doing biochemical tests, 16srRNA sequencing which showed 7.32 mg/ml IAA production, along with mineral solubilisation capacity (Phosphate— 312.786mg/ml, Potassium— 202.79 mg/ml). Apart from having plant growth promoting activity, strain showed inhibition of *Fusarium oxysporum pallidoroseum* growth which might be due to production of 62.3889 mg/ml Chitinase and show positive results on production of hydrolytic enzyme such as Amylase with solubilizing index 5.677± 0.1, protease- 4.677± 0.108 , cellulase - 2.211± 0.15, Lipase- 2.721± 0.065 Further it was tested for growth promotion of Cowpea and showed increased growth as compared to control plants further checking its in vitro effect on vegetative parameters in the presence and absence of pathogen. Hence the strain 10MH17 considered as plant growth promoter and biocontrol agent.

Keywords: Plant growth promoter, In-vivo studies, biocontrol, marine bacteria, Hydrolytic enzymes, Secondary metabolite

PMI-21 (Poster)

Rhizobial and Passenger Nodule Endophytic Bacteria in Combination with Acyl Homoserine Lactones Enhances the Groundnut Growth and Yield

Madhan S[1], Yuvasri E A[1], Anandham R, Balachandar D[1], Johnson I[2], Vincent S[3], and SenthilKumar M[1]
anandhamranga@gmail.com

[1]*Department of Agricultural Microbiology, Agricultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore, India*
[2]*Department of Plant Pathology, Agricultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore, India*
[3]*Department of Crop Physiology, Agricultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore, India*

Abstract: *Rhizobium*-legume symbiosis is a well-known model for mutualistic interactions between bacteria and the eukaryotic hosts, where quorum sensing (QS) and quorum quenching (QQ) play vital roles supporting their interaction. QS is a bacterial communication method that uses diffusible chemical signals to synchronize

the behaviors which are crucial for host interactions, including stress tolerance, resistance to pathogens and induced systemic resistance via jasmonic acid and ethylene secretion. On the other hand, QQ disrupts this signalling. This study examines the impact of QS and QQ molecules on rhizobial, and endophytic bacteria in groundnut growth under pot culture. The QS molecules like C7HSL and 3-oxo-C14 HSL were secreted by the bacterial isolates which helps in the restoration of plant growth-promoting traits suppressed by QQ molecule salicylic acid (SA). Seeds treated with *M. populi* TMV7-4, SA, C7HSL, and 3-oxo-C14 HSL was observed with 20.0 cm root length, 82.1g/plant of biomass, and 167 root nodules. *E. cloacae* S23 treatment showed a shoot length of 16.5 cm while seeds primed with *E. cloacae* S23 + SA + C7HSL + 3-oxo-C14 HSL showed 14 pods/plant, 23.3 kg/ha soil P content, and 59.5 mg/g plant nitrogen. Therefore, this study suggested that bioformulation involving *E. cloacae* S23 + SA + C7HSL + 3-oxo-C14 HSL and *M. populi* TMV7-4 + SA + C7HSL + 3-oxo-C14 HSL could enhance groundnut growth.

Keywords: Quorum sensing, Quorum quenching, AHL, Salicylic acid, Plant growth promoting traits

PMI-22 (Poster)

Exploring the Root Microbiome of Wheat and Barley in Hot and Cold Desert Ecosystems of India: Potential for Enhancing Drought Tolerance

Udita Pushpad, Pushpendra Sharma, Riwika Das[1], Minakshi Grover and Rajeev Kaushik
pushpad1995@gmail.com

Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi
Division of Bioinformatics, ICAR-Indian Agricultural Statistics Research Institute, New Delhi

Abstract: Plant growth and survival in arid and moisture-deficient agroecological regions are severely impacted by extreme temperatures, high solar radiation, soil salinity, and nutrient deficiencies. Among these, osmotic stress due to drought is a major factor contributing to global crop yield losses. The root-associated microbiomes of desert plants offer a promising source of novel microbes that are well-adapted to these extreme conditions, providing a valuable reservoir of metabolites that can promote crop growth and improve tolerance to abiotic stresses. This study investigated the spatial variation in the structure and functions of bacterial root microbiomes in wheat and barley, two dominant monocots cultivated in the arid ecosystems of India. The hypothesis was that the root microbiomes of these plants harbour beneficial bacteria capable of mitigating the harmful effects of moisture-associated osmotic stress. The core and transient root microbiomes of wheat and barley grown in the hot and cold deserts of India were analyzed through 16S rDNA sequencing. Root and bulk soil samples were collected from Leh (cold desert) and Bikaner (hot desert), and bacterial populations were isolated using six different growth media. A total of 196 isolates were obtained, with 64.8% from Leh and 35.2% from Bikaner. The isolates were cultured, and their 16S rDNA was sequenced for phylogenetic analysis. Proteobacteria was the dominant phylum, followed by Firmicutes, Actinobacteria, and Bacteroidota, with *Pseudomonas, Bacillus*, and *Stutzerimonas* as the predominant genera. Comparative analysis of bacterial diversity between rhizospheric and bulk soil samples revealed significant diversity in core bacterial genera across both regions and crop types. Pseudomonas emerged as the most prevalent core genus, underscoring its potential role in promoting plant growth and mitigating stress. Five promising bacterial isolates, identified for their PGPR and moisture-adaptive traits, significantly enhanced root, shoot, and physiological parameters in wheat crops when inoculated, compared to wet and dry controls, under 75% field capacity conditions.

Keywords: Arid Ecosystems, Root Microbiome, Wheat, Barley, Drought Tolerance, Pseudomonas, Phylogenetic Analysis, Abiotic Stress, India

PMI-23 (Poster)

Root Iron Plaques as Potential Inducers of Plant-Microbe Interaction and Fe-Biogeochemistry in Paddy Soil

Subhra Satahrada, Ritesh Pattnaik*
satahrada@gmail.com
rpattnaik@kiitbiotech.ac.in

Applied Research Laboratory,
School of Biotechnology, KIIT-DU Bhubaneswar, Odisha (751024), India

Abstract: The redoximorphic feature of paddy fields are corelated to both seasonal flooding and drainage patterns. Paddy management triggers redox potential oscillations, which control the structure and activity of microbial populations involved in biogeochemical processes. Trace gases including N_2O, N_2, H_2S, CH_4, are released post flooding, and induce microbial reduction activities utilizing NO_3^-, Mn^{4+}, Fe^{3+}, and SO_4^{2-} as electron acceptors. Additionally, the nutrient reduction processes influencing shift in pH suggest the presence of an operational electron shuttle and interconnected nutrient cycles in a paddy system. The mineralizing FeRB (Fe-reducing bacteria) use Fe (III) as an electron acceptor, and the redox potential produced by the coupled Fe (III)/Fe (II) processes may sustain a sizable fraction of the microbial biomass. In both oxic and anoxic environments, Fe-oxidizing bacteria, or FeOB, are crucial to the iron redox cycle. Amongst several mechanisms offered by the plants, iron plaque mechanism in rice roots has come into focus as a result of growing understanding of the intricate interactions between plant microbes in the rhizospheric zone and the concentration of Fe in a paddy system. Through co-precipitation or adsorption, iron hydroxides have a significant propensity to sequester ions in the rhizosphere. Therefore, for the effective circulation of metal and mineral species, contaminants must be retained on the surface of plant roots. Since most aquatic plants' metal-rich root rinds are produced by comparable methods, aerobic soils like those in wetlands and rice paddies may exhibit this sequestration process. A crucial part of the transit of important biogeochemical components is the balance between the stability and reactivity of iron in the iron plaque matrix. The amount of carbon that dynamic iron plaque absorbs or releases in the rhizosphere is influenced by the Fe redox balance.In considering the essential part that iron plaque plays in carbon sequestration and metal bioremediation, our goal is to investigate the active mechanisms of iron plaque in paddy systems, the microbiome that is engaged, and how these factors contribute to soil iron biogeochemistry.

Keywords: Iron plaque, Fe -biogeochemistry, FeOB, Paddy system, Carbon sequestration

PMI-24 (Poster)

Nano Bioremediation of Arsenic in Rice: Combining Arsenic-Resistant Bacteria and Zinc Oxide Nanoparticles for Rice Improvement under Arsenic Stress

Rahul Beniwal [1]**,** and Ramakrishna Wusirika*
beniwal127@gmail.com

Department of Biochemistry, Central University of Punjab, Ghudda, Punjab (151401), India

Abstract: Arsenic poses a significant threat to both plant and human health. The toxicity of arsenic is particularly pronounced in rice due to the reducing environment of flooded rice fields, which enhances arsenic mobility. In this study, we isolated native arsenic-resistant bacteria from soil in the Goniana paddy fields of Punjab and synthesized zinc oxide (ZnO) nanoparticles using zinc acetate and sodium hydroxide.
The bacteria were tested for resistance to various metals, as well as for their ability to withstand drought and salt stress. Additionally, their potential for promoting plant growth was evaluated. Bacteria were tested for antibiotic resistance using antibiotics of different classes and haemolytic activity was evaluated on blood agar plates. Bacteria were characterized using 16s rRNA sequencing. ZnO nanoparticles were initially characterized using UV-visible spectrometry, and their particle size was determined by Dynamic Light Scattering (DLS). Bacterial complexicity after ZnO treatment was determined using Flow Cytometry.
Rice pot trials were conducted at the Central University of Punjab, Ghudda Bathinda, using PB1121 and PR126 rice varieties. Parameters such as plant height, fresh weight, root length, and root fresh weight were measured

for the rice varieties. Additionally, biochemical analyses including measurements of alkaline phosphatase activity, soil dehydrogenase activity, superoxide dismutase activity, malondialdehyde (MDA) content, and reduced and oxidized glutathione content, were performed on soil, rice roots, and shoots to assess the effects of ZnO, bacteria, and ZnO-coated bacteria on rice growth under arsenic stress.

Keywords: Zinc oxide nanoparticles, Rice, Arsenic, Plant growth, Stress, Bacteria

PMI-25 (Poster)

Impact of Rice Cultivation Systems on Bacterial Abundance, Microbial Metabolic Activity and Growth of Succeeding Chickpea Crop: A Comparative Study under Transplanted and Direct-Seeded Rice

Koj Haniya[1], VijayPooniya[3] and Karivaradharajan Swarnalakshmi[1]
swarnalakshmi.ars@gmail.com

[1]*DivisionofMicrobiology,ICAR-IARI, New Delh, Indiai*
[2]*DivisionofBiochemistry, ICAR-IARI, NewDelhi, India*
[3]*Division of Agronomy, ICAR-IARI, New Delhi, India*

Abstract: An experiment was conducted to evaluate the bacterial abundance, microbial function, and nodulation capacity of chickpea grown in soil collected from transplanted (TP) and direct-seeded rice (DSR) as well inoculation response. Six treatments were compared: T1-uninoculated control (UI), T2-recommended dose of fertilizer (RDF) with 100 kg di-ammonium phosphate ha^{-1}, T3-*Mesorhizobium ciceri* (Mr), T4-Mr + RDF, T5-Mr + P-solubilizer ***Lactococcus lactis*** **(PSB),** and T6-Mr + PSB + RDF under both soil types. Nodulation was more robust in TP soil, with average nodule numbers four times higher than in DSR soil. Nodule dry weight in TP soil was 4.6 times greater than in DSR soil. Overall, in T5, the mean total root length increased by 7.23%. Dehydrogenase activity was higher in TP soil, whereas DSR soil demonstrated superior acid and alkaline phosphatase activities. DSR soil, the treatments with microbial inoculation recorded higher metabolic potential measured by community level physiological profiling (CLPP) than the control which is in contrast to that in TP soil. Shannon's diversity of DSR soil was recorded higher than the TP soil which could be due to the aerobic conditions. The 16S rDNA copy number was 12% higher in DSR soil. The T6 treatment yielded the highest *nif*H copy number (162.65%) and *nif*H/16S rDNA ratio (67.13%). TP soil produced greater plant biomass and seed yield than DSR soil, with T6 leading to the highest average seed yield (173.5%). While TP soil was found to be a superior growing medium, the application of Mr + PSB + RDF treatment exhibited the most pronounced synergy in promoting chickpea growth and yield under TP soil.

Keywords: T3-*Mesorhizobium ciceri* (Mr), ***Lactococcus lactis*** **(PSB),** *nif*H

PMI-26 (Poster)

Endophytic Fungal Community of *Rosa damascena* Mill. as a Promising Source of Indigenous Biostimulants: Elucidating its Spatial Distribution, Chemical Diversity and Ecological Functions

Abid Bashir[a,b], Farha Bhatii[a,b], Maryam Banoo[a,b], Syed Riyaz-Ul-Hassan[a,b]
abid3329@gmail.com

[a]*Fermentation and Microbial Biotechnology Division, CSIR-Indian Institute of Integrative Medicine, Sanat Nagar, Srinagar (190005), India.*
[b]*Academy of Scientific and Innovative Research (AcSIR), Ghaziabad (201002), India.*

Abstract: The role of endophytes in maintaining healthy plant ecosystems and holding promise for agriculture and food security is deeply appreciated. In the current study, we determine the community structure, spatial distribution, chemical diversity, and ecological functions of fungal endophytes of *Rosa damascena* growing in the North Western Himalayas. Culture-dependent methods revealed that *R. damascena* supported a rich

endophyte diversity comprising 32 genera and 68 OTUs. The diversity was governed by climate, altitude, and tissue type. Species of *Aspergillus, Cladosporium, Penicillium,* and *Diaporthe* were the core endophytes of the host plant consisting of 48.8% of the endophytes collectively. The predominant pathogen of the host was *Alternaria* spp., especially *A. alternata*. GC-MS analyses affirmed the production of diverse arrays of volatile organic compounds (VOC) by individual endophytes. Among the primary rose oil components, *Diaporthe melonis* RDE257, and *Periconia verrucosa* RDE85 produced phenyl ethyl alcohol (PEA) and benzyl alcohol (BA). The endophytes displayed varied levels of plant growth-promoting, colonization, and anti-pathogenic traits. Between the selected endophytes, *P. verrucosa* and *D. melonis* significantly potentiated plant growth and the flavonoids and chlorophyll content in the host. The potential of these two endophytes and their metabolites PEA and BA was confirmed on *Nicotiana tabacum*. The treatments of the metabolites and individual endophytes enhanced the growth parameters in the model plant significantly. The results imply that *P. verrucosa* and *D. melonis* are potential plant growth enhancers and their activity may be partially due to the production of PEA and BA. Thus, *R. damascena* harbors diverse endophytes with potential applications in disease suppression and host growth promotion. Further investigations at the molecular level are warranted to develop green endophytic agents for sustainable cultivation of *R. damascena* and biocontrol of leaf spot disease.

Keywords: Rose; Himalayas; Phenyl ethyl alcohol; Benzyl alcohol; *Periconia verrucosa*; *Diaporthe melonis*; Biocontrol

PMI-27 (Poster)

Mesorhizobial Inoculation and Fertilizer Application Influence Microbial Community Structure and Function in Chickpea Rhizosphere

N.S. Nysanth[1], Koj Haniya[1], M. Senthilkumar[2], Vijay Pooniya[3], C. Viswanathan[4], and K. Swarnalakshhmi[1*]
nysanthns@gmail.com

[1] *Division ofMicrobiology, ICAR-Indian Agricultural Research Institute (IARI), New Delhi (110 012), India*
[2]*Division ofBasic Sciences, ICAR-Indian Institute of Pulses Research (IIPR), Kanpur, India*
[3] *Division ofAgronomy, ICAR-Indian Agricultural Research Institute (IARI), New Delhi (110 012), India*
[4] *Division ofPlant Physiology, ICAR-Indian Agricultural Research Institute (IARI), New Delhi (110 012), India*

Abstract: Microbial communities associated with plants play a crucial role in nutrient cycling, plant health, and maintaining environmental stability. A pot experiment was conducted to evaluate impact of *Mesorhizobium* inoculation and the application of recommended doses of fertilizer (RDF) on microbial community structure and functional diversity and growth and yield of chickpea plants. Amplicon sequencing (V3 -V4) and Community Level Physiological Profiling (CLPP) revealed significant changes in microbial diversity, community structure, and metabolic functions. An increase in native bacterial community diversity from nodules to roots, rhizosphere soil, and bulk soil, with distinct changes in response to *Mesorhizobium* inoculation was observed. Firmicutes made up 46.1% of soil communities, with *Streptococcus* accounting for 35.4%, while in plant tissues, Proteobacteria (33.3%) and *Streptococcus* (18.9%) were more prevalent. Additionally, different treatments also led to significant shifts in microbial communities. Proteobacteria were more dominant in absolute control and mesorhizobial inoculation, while Firmicutes decreased. Genus-level changes included a consistent presence of *Streptococcus* across treatments, but with reduced abundance under mesorhizobial inoculation. Functional profiling revealed that *Mesorhizobium* inoculation results in highest levels of microbial activity across all carbon source categories, with a particular increase in carbohydrate, amino acid, and polymer metabolism. The preference for carbon substrates followed the order of carbohydrates > amino acids > polymers > carboxylic acids > amines > phenolic compounds over the 10-day incubation period. Both *Mesorhizobium* and RDF increased biomass and seed yield, with RDF raised them by 32.3% and 5.8%, respectively, and *Mesorhizobium* alone by 17.5% and 16.9% over the uninoculated control. These findings suggest that, in addition to *Mesorhizobium*, legume roots and nodules host non-rhizobial bacterial communities that have yet to be fully characterized.

Keywords: Chickpea root nodule, Legume-Rhizobium interactions, *Mesorhizobium,* Microbiome, Microbial community, Microbial diversity,

PMI-28 (Poster)

Exploring the Role of *Nepenthes Khasiana* Endophytes in Organic Phosphate Mineralization and Plant Growth Promotion

Kiran Dhiman[1, 3], Shiv Shanker Pandey[2,3], and Jeremy Dkhar[1,3]
dhimankiran75@gmail.com

[1]*Agrotechnology Division, CSIR-Institute of Himalayan Bioresource Technology, Palampur, Himachal Pradesh (176061), India*
[2]*Biotechnology Division, CSIR-Institute of Himalayan Bioresource Technology, Palampur, Himachal Pradesh (176061), India*
[3]*Academy of Scientific and Innovative Research, Ghaziabad (201002), Uttar Pradesh, India*

Abstract: One of the mechanisms by which endophytes promote plant growth is solubilizing and mineralizing inorganic (Pi) and organic (Po) phosphate sources present in the soil. We hypothesize that endophytes present in the digestive zone of the pitchers of the insectivorous plant *Nepenthes khasiana* may aid the plant in phosphate mineralization. To confirm this, we isolated 119 bacterial and fungal endophytes from various parts/zones of the *N. khasiana* leaf viz. leaf base, tendril, digestive zone, waxy zone, peristome, and lid, peristome, including roots and seeds. These endophytes were evaluated for their ability to mineralize Po by estimating acid phosphatase (ACP) activity of the lecithin-containing bacterial and fungal broths, using p-nitrophenyl phosphate as the substrate. The top ACP-producing bacterium and fungus were subjected to genome sequencing, resulting in the identification of 1 bacterial and 4 fungal acid phosphatases (ACPs), along with 4 fungal purple acid phosphatases (PAPs). Using ESI-nano LC-MS/MS, we found that one fungal ACP and one PAP are secretory. Additionally, in the bacterium, a secretory protein from the histidine phosphatase family—of which acid phosphatases are a subclass - was identified. The microbes were further tested for their potential to enhance the growth of *Arabidopsis thaliana* in the presence of DNA, a Po source. The results showed significant growth promotion, highlighting these microbes as promising sustainable biofertilizers.

Keywords: *Nepenthes khasiana*, *Arabidopsis thaliana*, Endophytes, Acid phosphatase, Phosphate mineralization, Sustainable biofertilizers

PMI-29 (Poster)

Ecosystem Services of PGPR in sustainable production of Fenugreek (*Trigonella foenum -graecum* L.)

Ravinder and **Mohd Kashif Kidwai**
Kashif357313@yahoo.co.in

Ravinder Kumar, Research Scholar, Department of Energy and Environmental Sciences, Chaudhary Devi Lal University, Sirsa, Haryana (125055), India
Professor Mohmad Kashif Kidwai, Department of Energy and Environmental Sciences, Chaudhary Devi Lal University, Sirsa, Haryana (125055), India

Abstract: Fenugreek (*Trigonella foenum-graecum* L.) is an important spice, leafy vegetable and medicinal plant originated in South-Eastern Europe belonging to the family Fabaceae. PGPR (Plant Growth Promoting Rhizobacteria) are unique rhizospheric microorganisms including endophytes providing valuable ecosystem services to plants. PGPR enable plants to adapt and survive under different environmental conditions and enhances the tolerance of various plant species against biotic and abiotic stresses. PGPR contribute significantly in boosting key morphological and physiological processes and helps in promoting the growth and development of plants and are reported to stimulate the production of various secondary metabolites viz. siderophores, phenols, phytohormones etc. and provide various ecosystem services such as Photosynthesis, Nitrogen fixation, carbon fixation, solubilization of phosphate etc. PGPR also induces resistance in wide variety of plants against diverse pathogens thereby helps in achieving sustainable agriculture with the reduction in use of hazardous agrochemicals. PGPR aids the plants in nutrient uptake in the soil and complement in regulating osmotic balance along with ion homeostasis. PGPR also support the plants in enhancing water use efficiency which address the issue of sustainable use of water in agriculture and microbe assisted phytoremediation of heavy

metals, pesticides etc. In case of Fenugreek (*Trigonella foenum-graecum* L.) PGPR such as *Pseudomonas* species, *Sinorhizobium* species etc.are reported to play an important role in induction of bioactive compounds and phytohormones. The production of specific biochemical such as Trigonelline and Nicotinic Acid are influenced by PGPR. The ecosystem services by PGPR complementthe growth and yieldof fenugreek along with the environmental sustainability.

Keywords: PGPR, Ecosystem services, Phytoremediation, Scondary metabolites.

PMI-30 (Poster)

Unveiling the Plant Growth Promoting Traits of exopolysaccharide Producing Bacteria

Indu Dhiman[1]*, Ravina Yadav[1], Priya Tanwar[1] and Leela Wati[2]
dhimanindu84@gmail.com

[1]Ph.D. student, Department of Microbiology, College of Basic sciences & Humanities, Hisar, India
[2]Principal Scientist, Department of Microbiology, College of Basic sciences & Humanitie, Hisar, India s Chaudhary Charan Singh Haryana Agricultural University, Hisar (125004), Haryana, India

Abstract: Exopolysaccharide (EPS) producing bacteria are a unique group of plant growth promotingbacteria (PGPB) that synthesize complex polysaccharides, playing a vital role in plant-microbeinteractions. These bacteria exhibit a range of plant growth promoting traits, including theformation of biofilms and colonization of the rhizosphere, enhancement of drought toleranceand water retention, facilitation of nutrient solubilization and uptake. The rhizosphere dwellingplant growth promoting rhizobacteria (PGPR) form symbiotic relationship with plant roots,driving growth and development. Through the production and release of various plant growthpromoting compounds, PGPR exert direct and indirect influences on plant health, fostering asupportive environment. In this study, the in vitro plant growth promoting traits of exopolysaccharide-producing bacterial isolates (EPB-1, EPB-2, EPB-3, EPB-4, EPB-5, EPB-6 and EPB-7) retrieved from rhizospheric soil of chickpea were investigated. The bacterial isolates demonstrated the ability to produce indole acetic acid (IAA) and excrete ammonia.Additionally, gibberellic acid (GA) production was observed in five isolates, with concentration ranging from 0.32 to 1.97 mg L−1. The isolate EPB-5 exhibited the highest level of IAA (188 µg/mL), GA (1.97 mg L−1) and ammonia excretion (14.31 µg mL−1). In contrast,the isolates EPB-1 and EPB-7 did not produce GA in the culture solution. Furthermore, thephosphate solubilization capabilities of the isolates were evaluated, revealing a solubilizingrange of 1.85 to 8.68 µg mL−1after 7 days of incubation.

Keywords: Ammonia, Exopolysaccharide, Indole acetic acid, PGPR, Phosphate solubilization

PMI-31 (Poster)

Isolation, Screening and Characterization of Indigenous Bacteria Against Rice Blast Diseases *(Magnaporthae oryzae)*

Ravina, Indu, Rahul Choudhary, and Rakesh Kumar
ravina.khatodia@gmail.com

Department of Microbiology
Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana, India

Abstract: Due to worlds growing population, demand of rice production increasing and expected to reach around 10 billion by 2050. Phytopathogenic fungi cause diseases in rice that adversely affects rice yield and some of the fungal products have the potential to be hazardous when consumed. Therefore, there is a need to improve rice productivity which is adversely affected by biotic factors. Rice blast is considered as one of the most serious infections in the rice caused by *Magnaporthae oryzae*. Various methods are used to control plant diseases including chemical and bicontrol methods. Now a days, biocontrol agents which are environment friendly and high effectiveness are gaining interest as important source of the management of the rice blast diseases. In present investigation, a total of 300 bacterial isolates were isolated from the rhizospheric soil of rice on Luria-Bertani (LB) and nutrient agar (NA) media and were screened for antifungal activities. Twelve isolates

namely were selected which were showing high antifungal activities. These selected antagonistic bacterial isolate(s) were characterized for their plant growth promoting traits. It was observed that bacterial isolate(s) RY13, RY25, RYK11 and RY 68 showed highest antifungal activity 76mm, 68mm, 28mm, 33mm and 28mm respectively. RY68 showed highest ammonium excretion (3.794µg/ml), Hydrogen cyanide and potassium solubilization. The selected potential antifungal bacterial isolate will be used for the further studies.

Keywords: Biocontrol, Diseases, Infection, *Magnaporthae oryzae*, Rice, Rice blast

PMI-32 (Poster)

Investigating Marine Bacteria for Plant Growth Promoting and Disease Control Activity in *Vigna unguiculata*

Aastha Singh[1], Pinakin Dhandhukia[2] and Janki N Thakker[1]
aastha0821@gmail.com

[1]*Department of Biological Sciences, P.D. Patel Institute of Applied Sciences, Charotar University of Science and Technology, CHARUSAT Campus, Changa, Anand, Gujarat(388421), India*
[2]*Department of Microbiology, School of Science and Technology, Vanita Vishram Women's University, Surat, Gujarat, India.*

Abstract: The escalating global environmental degradation and population growth have sparked concerns about the sustainability of food production in meeting the needs of a burgeoning population. The rising awareness of the detrimental effects of excessive use agrochemicals like chemical fertilizers and pesticide on the environment and human health has led to a heightened demand for more sustainable and eco-friendly agricultural practices. Plant growth-promoting bacteria (PGPB) play a crucial role in enhancing plant growth by improving nutrient uptake, increasing tolerance to environmental stresses, synthesizing phytohormones, and offering protection against plant diseases. In this study, a marine isolate was investigated as a potential PGPB and bio-control agent against plant pathogenic strains of *Fusarium oxysporum*. The marine isolate displayed favorable results in plant growth promoting traits such as indole-3-acetic acid (IAA) production, ammonia production, phosphate, potassium, and zinc solubilization. It also exhibited the capacity to produce lytic enzymes including amylase, cellulase, and chitinase. Furthermore, it demonstrated biocontrol activity against several strains of *Fusarium oxysporum*, potentially attributable to its ability to produce lytic enzymes capable of degrading fungal cell walls. The in vivo assessment confirmed that the marine isolate has the ability to enhance plant growth and demonstrate biocontrol activity against *Fusarium oxysporum pallidoroseum* (FOP) in *Vigna unguiculata* (cowpea). Seeds treated with the marine isolate showed improved root and shoot development compared to untreated seeds, indicating its potential to promote growth. Furthermore, when seeds were treated with both the fungus and marine bacteria, the isolate promoted plant growth while preventing FOP infection. These findings highlight the promising potential of marine bacteria as a source of plant growth-promoting bacteria (PGPB) and biocontrol agents, which could be valuable for the development of effective biofertilizers and biopesticides.

Keywords: PGPB, Marine Bacteria, IAA, *Fusarium oxysporum*, Lytic enzymes, Phytohormones

PMI-33 (Poster)

Antioxidant, Antifungal and Growth-Promoting Activity of Halotolerant Endophytic Fungi *Diaporthe tectonendophytica*

[1,2]**Nandita Jana** and [1,2]Debdulal Banerjee*
db@mail.vidyasagar.ac.in

[1]*Microbiology and Microbial Biotechnology Laboratory, Department of Botany and Forestry*
[2]*Centre for Life Sciences, Vidyasagar University, Midnapore (721102), India*

Abstract: Diaporthe tectonendophytica, *an endophytic fungal isolate of* Ipomoea pes-caprae, *can tolerate up to* 2M NaCl stress and exhibits significant antioxidant activity. The ethyl extract of the cell-free culture extract showed potent free radical scavenging ability, with an IC_{50} value of 21.59 ± 0.45 µg mL^{-1} in the DPPH assay, 15 ± 1.55 µg mL^{-1} in the ABTS assay, and 18 ± 2.01 µg mL^{-1} in the Ferric Reducing Antioxidant Power (FRAP) assay. This fungus displayed strong antifungal activity against plant pathogenic fungi *Botrytis* sp., *Colletotrichum* sp., and *Fusarium* sp. Total phenolic and flavonoid content in the extract were 276 ± 1.98 µg mg^{-1} and 130 ± 2.03 µg mg^{-1}, respectively. Along with its antifungal and antioxidant properties, *D. tectonendophytica* promotes plant growth-promoting activity, particularly by producing indole acetic acid (IAA) under 1M NaCl stress. It exhibited plant growth-promoting activities i.e., nitrogen assimilation, hydrogen peroxide degradation, and phosphate solubilization, highlighting its potential as a potent isolate under saline stress. The contributing secondary metabolites extracted from ethyl acetate were identified using the GC-MS technique.

Keywords: Halo tolerant endophytic fungi, Anti-fungal, Antioxidative, PGP-activities.

PMI-34 (Poster)

Plant Growth Promoting Potentialities of Endophytic Actinomycetes Isolated from Medicinally Valuable Plants of Jungle Mahal, West Bengal

[1,2,] **Usha Rani Murmu** and [1,2]Debdulal Banerjee*
ushamurmu19@gmail.com

[1]*Microbiology and Microbial Biotechnology Laboratory, Department of Botany and Forestry*
[2]*Department of Botany and Forestry, Vidyasagar University, Midnapore (721102), India*

Abstract: Plant Growth Promoting Bacteria (PGPB) hold significant promise as biological agents for enhancing plant growth and improving agricultural practices. This study focused on the isolation and characterization of Actinomycetes as Potential PGPB from diverse plant sources. Twenty-one endophytic actinomycetes were isolated from different parts of five medicinally valuable plants collected from adjacent areas of Jungle-Mahal, West Bengal, India. Isolation was performed in both International Streptomyces Project-5 (ISP5) and Tryptone yeast Glucose (TYG) media with a standard incubation period of 10-40 days, incubated at 28±3˚C. Isolates were screened for various plant growth promoting activities *in vitro*. 66% isolates were positive for Indole Acetic Acid (IAA) production in tryptophan (2 mg mL^{-1}) amended International Streptomyces Project-2 (ISP2) broth media, 71% produced ammonia in notable amount in peptone water broth, 52% actinomycetes emitted hydrogen cyanide (HCN) in glycine (0.40%) amended Luria Bertani (LB) media. Thus, these isolates can be further exploited for in planta application related to growth promotion and agricultural productivity. The studied actinomycetes isolates were positive for hydrolysing enzyme production i.e., 66% and 61% isolates synthesised protease and amylase respectively in solid plate assay. These enzyme producing abilities of the isolates confirm their role in plant defense against biotic stress i.e., in combating fungal and bacterial phytopathogens. Isolates were screened for both the phosphate solubilisation and cellulase production and only 4.48% isolate was positive for these assays. Potent isolates were analysed through Gram stating and Scanning electron microscopic study. These findings emphasize the significance of Actinomycetes as valuable contributors to sustainable agriculture and plant growth promotion.

Keywords: Endophytic actinomycetes, PGPB, Sustainable agriculture, *In vitro* plant growth promotion.

PMI-35 (Poster)

Antifungal Activity of Some Selected Endophytic Fungal Isolates of Sunflower Plant against *Fusarium Oxysporum* HALP1, A Potent Sunflower Pathogen

Julekha Bagum[1] and Debdulal Banerjee[1,2,*]
db@mail.vidyasagar.ac.in

[1]*Centre for Life sciences, Vidyasagar University, Midnapore, West Bengal (721102), India*
[2]*Microbiology and Microbial biotechnology laboratory, Department of Botany and Forestry, Vidyasagar University, Midnapore, West Bengal (721102), India*

Abstract: *Fusarium oxysporum* is a highly destructive soil-borne necrotic pathogen that impacts more than 120 plant species globally. It is mainly responsible for root rot and wilt disease in sunflowers, and infection begins at the early stage of plant development through soil. This pathogen leads to a significant reduction in sunflower yields. Biocontrol methods are considered the most effective and safe approach to combatting this issue. Endophytic fungi have emerged as promising biocontrol agents. A total of 25 endophytic fungi were isolated from different parts of sunflower plants and tested for their antifungal activity against *Fusarium oxysporum* HALP1 in vitro. Three endophytic fungi i.e., SERT5, SEL2, SES7.1 gave prominent results against it in dual culture assay, among them SERT5 exhibited 71.18 % of highest inhibition. Ethyl acetate extract of SERT5 also showed antifungal activity against *Fusarium oxysporum* HALP1 in the agar well diffusion assay. This study indicates that this endophytic fungal strain has the potential to be used as a biocontrol agent and can be used in the management of phytopathogens related to Sunflowers.

Keywords: Endophytic fungi, anti-fungal activity, *Fusarium oxysporum*, Sunflower.

PMI-36 (Poster)

A Review on the Potential Use of Plant Growth Promoting Rhizobacteria (PGBR) For the Cultivation of Endangered Medicinal Plants of Nagaland

T Menangrichet Jamir[1]* and Dhritiman Chanda[2]
menagjamir571@gmail.com,

[*1]*T Menangrichet Jamir: Corresponding author and research scholar, Department of Botany, University of Science and Technology, Meghalaya (793101), India.*
[2]*Assistant Professor, Department of Botany, University of Science and Technology, Meghalaya, India*

Abstract: This review focuses on using plant growth-promoting rhizobacteria (PGPR) to conserve and make use of some of the many medicinal plants found in Mokokchung, Nagaland. The Ao Naga tribe has practiced the traditional use of medicinal plants since time immemorial, and it has been passed down through generations. Before civilization, these procedures were the primary source of treatment for a variety of illnesses. However, due to their widespread usage for human well-being, majority of them have been overexploited, and some steps must be implemented to ensure the continued use of these medicinal plants. Additionally, due to the growing population, these wild places are being urbanized, putting these plants at severe risk of extinction.With the help of PGBR, Erythrina arborescens Roxb, Globbaclarkei Baker, Acacia pennata (L.) Willd, and Abelmoschus esculentus (L.) Moench., these medicinal plants can be kept, as the rhizospheric bacteria enable resistance to all environmental challenges related to northeastern India's climate. As a result, preserving them and encouraging their development are crucial elements of the PGBR, which can also help with future research.

Keywords: Ao-Naga, Mokokchung, Nagaland, traditional knowledge, medicinal plants, Plant Growth Promoting Rhizobacteria (PGPR).

PMI-37 (Poster)

Genetic Diversity of Abiotic Stress Tolerant Rhizobia Nodulating Prosopis Species

Ritika, Rajesh Gera, Meena Sindhu, Ajay Kumar, Jagdish Kumar,Rajbala and Bhupender Malik
rajeshgera1967@gmail.com

Department of Microbiology, COBS&H, Chaudhary Charan Singh Haryana AgriculturalUniversity Hisar, Haryana (125004), India

Abstract: Rhizobial strains that are adapted to abiotic stress conditions could serve as effective inoculants for crops cultivated in arid and semi-arid climates. In this study, a total of 14 soil samples were collected from different locations in Haryana (Hisar, Bhiwani, Rewari, and Mahendragarh) to explore the diversity of rhizobia associated with Prosopis species. A total of 27 Prosopis rhizobial isolates were isolated using trap plant method and characterized. All rhizobial isolates were screened for drought, temperature and Salinity tolerance. Genomic DNA was extracted from all rhizobial isolates and assessed for the presence of the nodC gene with the nodCI and nodCF primers. Among the 27 isolates, twenty-four showed amplification of the nif H and nod C genes. The genomic DNA of each isolate was subsequently amplified utilizing 16S rRNA gene primers. The resulting amplified products underwent restriction fragment length polymorphism (RFLP) analysis using the MspI and HaeIII restriction enzymes. This RFLP analysis uncovered diversity among the rhizobial isolates, which were categorized into two primary clusters along with several subgroups. The divergence among the isolates was noted to commence at 89% similarity when analyzed with MspI and HaeIII. The rhizobial isolates were further characterized: HP2 exhibited 95.7% similarity to Allorhizobium undicola ORS 992, BP1B showed 94.8% similarity to Bradyrhizobium yuanmingense DCV2, and MP5Y had a similarity of 97.9% to Rhizobium leguminosarum QW25. These promising rhizobial isolates hold significant potential to enhance soil fertility and boost crop yields in arid and semi-arid challenging environments.

Keywords: Rhizobium, Prosopis, Abiotic stress, RFLP, nodC

PMI-38 (Poster)

Bacillus sp. Present in Soil of Raisen, Madhya Pradesh Enhance the Production of IAA in Wheat Crop

Shephali Rathore*
*shephali098@gmail.com

**Dept of Life Sciences, Ravindranath Tagore University, Bhopal (Madhya Pradesh)*

Abstract: IAA (Indole-3-Acetic acid) is naturally occurring plant hormone responsible for growth and development. Other than these aspects it is also directly or indirectly involved in cell division, tissue differentiation, seed germination, and formation of various plant parts. It also helps to provide resistance to plant from some pathogens and environmental stresses. This hormone is essential for ideal fruiting and flowering of growth and the above mentioned facts have already been explored and studied. Keeping these in mind the current study was designed and microflora of soil from Central India was investigated for their role in optimal production of IAA. Staining revealed their shape to be bacillus. Upon further investigation they were identified as *Pseudomonas putida* and *Pseudomonas cereus*. Further studies analyzed their role and potential and effect on plant growth and net yield in the field which are still in progress.

Keywords: IAA, Raisin, *Bacillus spp.*, *Pseudomonas putida*, *Pseudomonas cereus*

PMI-39 (Poster)

Appraisal of Phosphate Solubilizing Bacteria having multi-PGP Traits Screened From Rhizospheric Soil

Smruti Patel and Archana Gattupalli*
*smrutipatel2312@gmail.com

Department of Microbiology and Biotechnology Centre
The Maharaja Sayajirao University of Baroda, Vadodara (390002), Gujarat, India

Abstract: Plant growth promoting rhizobacteria (PGPR) are beneficial bacteria that play vital role in promoting plant growth and health through various mechanisms, making them a key component of sustainable agriculture. Phosphate solubilizing bacteria (PSB) are PGPR which solubilize and mineralize insoluble soil Phosphorus (P) into a form that plants can absorb. This process relies on various sugars released by plant root exudates, which PSB use to produce organic acids that free P from soil minerals. That is why it is important to study the phosphate solubilization on different carbon sources. In this study, rhizospheric soil of wheat and maize was used to isolate PSB and Pikovskya's agar medium was used for screening of PSB. They were further characterized based on phosphate estimation done via Fiske-Subbarow method, and analysis of PGP traits in-vitro was conducted to determine their potential. Total 21 isolates were selected based on high tricalcium phosphate solubilizing index in the presence of glucose as the sole carbon source, of which 16 isolates were gram negative and 5 were gram positive of which two were actinomycetes. When further tested on Pikovskya's agar medium containing different carbon sources, 6 isolates showed positive results for all the sugars tested and 16 isolates gave phosphate solubilization in the presence of mixture of sugars. Highest pH reduction and phosphate solubilization was observed in presence of trehalose. Only 7 isolates showed positive results for all PGP traits including P solubilization. The results suggest potential of isolates to be successful PSB in field condition.

Keywords: Phosphate solubilization, root exudates, sugars, PGP traits

PMI-40 (Poster)

Bacillus Endophytes Protect Chickpeas from *Xanthomonas* by Defence Priming Mechanism

Apurva Barge[1], Archana Kumari [2]* and Chiranjit Chowdhury, [3*]
bargeapurva123@gmail.com

[1]*CSIR- National Chemical Laboratory, Pune, India*

Abstract: Chickpea (*Cicer arietinum*) is a vital crop in the agrarian landscape of India. It is leguminous crop and a key source of nutrients and proteins. One of the important bacterial diseases of chickpea is the bacterial blight and damping off caused by *Xanthomonas campestris*. Here, *Xanthomonas campestris* pv *campestris* (Pammel) Dowson has been shown to induce Jasmonic Acid (JA) pathway as observed through GUS staining. It also manifests black rot disease symptoms in *Arabidopsis* model system. Outer membrane vesicles were isolated from *Xanthomonas* to understand mode of transmission of the disease. Meantime, endophytes have been shown to confer protection to many plant species against a number of pathogens. In the current study, some endophytic bacteria (KB4, 7A3bI and 7A3bII) were isolated from chickpea leaves. The molecular study confirmed the KB4 as *Neobacillus* spp. Out of the three, only KB4 induces little JA pathway, however, imparts little to induce disease symptoms. It can be presumed that KB4 was capable of potential defense priming to chickpea plants, which could be in turn protect it from other pathogens. To study if KB4 produced antibacterial metabolites against *Xanthomonas*, the antibacterial susceptibility test was performed. This study contributes to understand interplay between micro-organisms and chickpea plants. By unraveling these interaction, the research aims to contribute valuable insights to protect chickpea cultiver, while KB4 would have potential to serve as biocontrolling agent. However, further studies are required to prove this hypothesis.

Keywords: Chickpea, *Xanthomonas campestris,* Bacterial blight, Jasmonic acid, Endophytes, *Neobacillus* spp

PMI-41 (Poster)

Activation of Induced Systemic Resistance in Cotton Plants against *Fusarium* and *Macrophomina* by Microbial Antagonists

Vikram Poria[1], Prakriti Jhilta[1], Sandeep Kumar[1], Anuj Rana[2], Kumar Pranaw[3], and Surender Singh[1*]
surendersingh@cuh.ac.in

[1]*Department of Microbiology, Central University of Haryana, Mahendergarh (123031), India*
[2]*Department of Microbiology (COBS & H), CCS Haryana Agricultural University, Hisar (125004), India*
[3]*School of Environmental Sciences, Jawaharlal Nehru University, New Delhi (110067), India*

Abstract: The use of microbial antagonists (MAs) against phytopathogens is a cost-effective, environmentally sustainable strategy that successfully enhances crop yield. In this study, we evaluated the in-planta efficacy of multistress-tolerant MAs isolated previously from the cotton rhizosphere showing high antagonistic activity against *Macrophomina phaseolina* and *Fusarium oxysporum*. During pathogenicity testing, *M. phaseolina* was found more aggressive compared to *F. oxysporum* as indicated by disease area percentage on cotton seeds but the use of MAs lowered the seed mortality rate (0–20%) in the pot experiment compared to pathogen control (47–60%) indicating their high antagonistic potential. The mode of antagonism was investigated by identifying antifungal metabolites and volatile organic compounds secreted by these agents using HPLC–MS and GC–MS coupled with SPME fiber, respectively, which revealed compounds like iturins, surfactins, mixirins, fengycins, undecanone, involved in the activation of induced systemic resistance (ISR) along with the antifungal activity. The increased levels of two defense enzymes, polyphenol oxidase [110–180% increase over absolute control (IOC)] and phenylalanine ammonia-lyase (22–58% IOC), and three antioxidant enzymes, catalase (36–98% IOC), peroxidase (44–71% IOC), and superoxide dismutase (72–145% IOC) in MA-treated plants confirmed the activation of ISR against both pathogens. The proline, total phenolic, and glycine betaine contents also increased in the MAs-treated plants, whereas decreased malondialdehyde content was observed. These results indicate that these MAs are reliable and sustainable options for enhancing crop growth and that their bioformulations can be used to control fungal pathogens and help plants endure biotic and abiotic stresses.

Keywords: *Biocontrol, Induced systemic resistance, Iturins, Phytopathogens, Root rot, Surfactins*

PMI-42 (Poster)

Assessment of Soybean Genotypes for *Agrobacterium*-Mediated Transformation Efficiency

Shruti Shukla[1, 2*], Anita Rani[2], Meeta Jain[3], Vineet Kumar[2] and Lilly Ganju[1]
shrutirps2092@gmail.com

[1]*Malwanchal University, Index City, Near Khudel, Nemawar Road, Indore (452016), Madhya Pradesh, India*
[2]*ICAR-Indian Institute of Soybean Research Centre, Khandwa road, Indore (452016), Madhya Pradesh, India*
School of Biochemistry, Devi Ahilya Vishwavidyalaya, Indore (452001), Madhya Pradesh, India

Abstract: To see the effect of genotypes on *Agrobacterium*-mediated transformation using half-seed explant type, 83 soybean genotypes were selected, and co-cultivated for 5 d in dark with *Agrobacteriumtumefaciens* strain EHA105 carrying the binary vector pCAMBIA1305.1 containing the *hptII* and *GUSPlus* genes. We observed differential genotypic variation of susceptibility in soybean towards *Agrobacterium-tumefaciens* infection. Based on the rate of transient GUS expression, these genotypes were categorized as highly, moderately, and weakly susceptible. Five genotypes, namely, KHSb2; Pusa-16; DS 228; NRC 149, and JS 72-280, were found to be highly susceptible showing >70% transient GUS expression whereas 30 genotypes were moderately susceptible (30–70%); and 48 genotypes showed very low transient GUS expression (<30%) and were categorized as weakly susceptible. The analysis revealed that different soybean genotypes have variable susceptibility to *Agrobacterium-tumefaciens* infection. Rate of transient GUS expression was significantly higher in KHSb2, Pusa-16, DS 228, NRC 149, and JS 72–280 as compared to other genotypes. The finding can lead to identification of susceptible soybean genotypes which could be used for successful transformation protocol.

Keywords: Soybean; *Agrobacterium*; *GUSPlus*; Transformation; Genotypes; Half seed; Transgenic

PMI-43 (Poster)

Unveiling the Role of Bacterial Endophytic Diversity in Promoting Plant Growth and Secondary Metabolites Synthesis in *Pelargonium graveolens*

Nikky Deepa [1,2]
deepasinghlalan@gmail.com

[1]*Division of Crop Production and Protection, CSIR-Central Institute of Medicinal and Aromatic Plants, Lucknow (226015), India*
[2]*Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, India*

Abstract: The diverse microbial endophytic communities associated with plants, also known as the "second genome," exemplify the efficiency of co-evolution. The maintenance of plant health and enhanced adaptation to dynamic environment conditions are greatly aided by this Co-evolutionary existence. Henceforth, studying the diversity of the endophytic microbes linked to specific host plants is crucial for understanding the deep insights of plant-microbe interactions. The present study focused on identifying the endophytic bacterial diversity associated with the root and shoot portion of *Pelargonium graveolens* through both culture dependent and independent (metagenomics) approach. The study identified a total of 614 and 620 operational taxonomic units (OTUs) across 291 and 229 genera in the shoot and root tissues, respectively. Moreover, 15 extremely prevalent phyla were identified by the subsequent classification of OTUs, with Proteobacteria predominating in both root and shoot tissues. Interestingly, the shoot tissue showed a significantly higher abundance of the Firmicutes phylum compared to the root. Furthermore, a similar pattern of diversity distribution between *P. graveolens's* root and shoot was shown by the molecular characterisation of 30 bacterial endophytes that were isolated from the petiole, leaves, stem, and root. Rigorous screening revealed that *Pseudomonas oryzihabitans* exhibited key plant growth-promoting traits, including nitrogen fixation and phosphate solubilization, leading to a two-fold increase in essential oil content with a notable rise in geraniol and citronellol levels. In-depth analysis of *P. oryzihabitans'* genetic makeup in detail revealed many genes that both directly and indirectly support the endophyte's capacity to successfully colonise host plants. In conclusion, findings from metagenomic and culture-dependent approaches, supported by glasshouse trials and phytochemical analysis highlight promising bacterial endophytes for field applications aimed at boosting crop yields and enhancing in planta secondary metabolite production.

Keywords: Culture-dependent, Metagenomics, *P. graveolens*, Endophytes, Secondary metabolite, Genetic makeup

PMI-44 (Poster)

Evaluating the Impact of Phytonim on Nitrogen Availability and Its Influence on Microbial Population in Paddy Soil

Sriram Lakshmanan**, Devi Priya Arumugam** and Sivakumar Uthandi*
devipriyaarumugam24@gmail.com

Biocatalysts laboratory, Department of Agricultural Microbiology, Tamil Nadu Agricultural University, Coimbatore (641003), India.

Abstract: Nitrification inhibitors (NIs) are a group of chemical compounds which used to slow down the nitrification process, improve the available nitrogen (N) concentrations, and reduce N losses in the soil. Phytonim, a plant extract from neem is formulated as a nitrification inhibitor and coated with fertilizers for direct application in soil which serves as alternative for regular fertilizers. An incubation study was conducted to estimate the potential inhibition rates of nitrification using phytonim coated fertilizers like urea and ammonium sulphate (AS) at different concentrations viz., 100% and 65% of the recommended dosage (RD) and additionally ammonifying bacteria (AB) was also added with urea fertilizer as one of the treatment. Samples were taken at 13 different intervals in a 45-day incubation period. Applying phytonim coated fertilizers slow down the nitrification process for 35 days, thereby improving the available N in the soil. Ammonia oxidation rate, nitrite oxidation rates and nitrate reductase activity were reduced by 14%, 35% and 17% in phytonim coated urea followed by 11% and 23% in phytonim coated urea + AB and 16% in phytonim coated AS over uncoated

fertilizers. Soil urease activity was inhibited in phytonim coated urea (100% RD and 65% RD) of 9.6% and 7.4%, respectively whereas 5.7% and 6.7% increased urease activity were observed in coated urea + AB (100% RD and 65% RD). Increased soil dehydrogenase activity and fluorescein diacetate (FDA) hydrolysis of 20% and 15% were observed in phytonim coated urea followed by 15% and 18% in NI coated urea + AB (100% RD) over uncoated fertilizers. This study concludes that, application of phytonim inhibited the nitrification and denitrification rates, affected the urea hydrolysis, and resulted in a positive effect on the microbial population.

Keywords: Ammonia oxidation, Microbial population, Phytonim, Soil enzymes, Soil incubation.

PMI-45 (Poster)

Studies on Development of a Phyllosphere Consortia for Plant Growth Promotion.

Bhavana M[1] and C R Patil [2]
bhavanagrv@gmail.com

[1]*Ph.D. first year, Division of Microbiology, ICAR-IARI, New Delhi (110012), India*
[2] *Professor and Head, Department of Microbiology, College of Agriculture, University of Agricultural Sciences, Dharwad (580005), Karnataka, India*

Abstract: Plant growth-promoting bacteria have emerged as promising approach for sustainable agriculture by enhancing soil and plant health. There is a need for developing a consortium with reduced microbial strains which reduce cost of production and less time consuming. Hence, an attempt was made to develop seven consortia from four microbial strains in liquid formulations without losing their efficacy. The microbial strains used were collected from the Institute of Organic Farming (IOF), UAS, Dharwad. Biochemical and functional characterization tests were conducted to evaluate their plant growth-promoting traits and to reduce the number of strains from eleven to four. Compatibility between the isolates was tested by Cross streak method. The results showed that among the six actinobacterial strains, PSA 7 produced the maximum IAA (15.31 µg/ml broth) and GA (2.56 µg/25 ml broth) respectively and PSA 5 showed highest *invitro* nitrogen fixation (3.48 N_2/ g of carbon utilized), where as among the PPFM strains, PPFM 33 produced the maximum amount of IAA (12.29 µg/ml broth) and GA (2.51 µg/25ml broth) respectively and the highest percent of nitrogen was fixed by PPFM 33 (2.88 N_2/ g of carbon utilized). Among the LAB strains, LAB 75 produced the maximum amount of IAA (8.39 µg/ml broth) and GA (2.31 µg/25ml broth) respectively. All four isolates were found to be compatible.So, using these four strains seven consortia was developed and other four were formulated individually. An effective formulation with lesser number of strains contributing to multiple PGPR activities and with high bio efficacy is desirable character of microbial inoculants, was achieved in this study. The formulated consortia can be commercialized further for plant growth in different crops in the field.

Keywords: Phyllosphere, Consortia, Compatibility, *invitro* nitrogen fixation, IAA & GA, Liquid formulation.

PMI-46 (Poster)

Plant Growth Promoting Rhizospheric Actinomycetes as Potential Bioinoculants

Priya Tanwar[1*]**,** Shaik Tabasum1 and Leela Wati[2]
priyatanwar0012@gmail.com

[1]*Ph.D. student, Department of Microbiology, College of Basic sciences & Humanities*
[2]*Principal Scientist, Department of Microbiology, College of Basic sciences & Humanities*
Chaudhary Charan Singh Haryana Agricultural University, Hisar (125004), Haryana, India

Abstract: Plant growth promoting rhizobacteria (PGPR) are a class of natural inhabitant, free-living bacteria that colonize the rhizosphere of plants which confers the ability to enhance plant growth and yield by providing nutrition and protection through direct and indirect mediated mechanisms. Actinomycetes are widely distributed in the rhizosphere of plants and prominent producers of diverse bioactive compounds. Due to its potent antimicrobial activities and soil-dominant saprophytic nature along with plant growth promotion, actinobacteria has received a lot of attention in agricultural context. In the current investigation, 6 actinomycetes isolates AK-6, AK-11, AK-19, AK-15, AK-26, AK-40 were screened for plant growth promoting activities. Most of the

actinomycetes isolates exhibited phosphate and zinc solubilization on Pikovskaya and Zinc minimal media and maximum zone index was in AK-11 (1.93) and AK-26 (3.02) after 72h of incubation. The actinomycetes isolates were solubilizing mica powder as insoluble potassium source on the modified Aleksandrov medium with maximum solubilisation index in AK-6 (2.73) after 72h of incubation. Out of the six actinobacterial isolates screened, AK-6, AK-11 and AK-19 recorded positive for HCN production after 5 days of incubation in King's B broth. All the actinobacterial isolates exhibited Indole acetic acid (IAA) production and ammonia excretion ranged from 15.66 to 32.01 µg/ml and 16.37-20.74 µg/ml. The above results indicate that the plant growth promoting rhizospheric actinomycetes could be used as bioinoculants due to their intensified PGP activities that involve the production of IAA, HCN, phosphate, potassium and zinc solubilisation and ammonia excretion.

Keywords: Actinomycetes, Bioinoculants, Bioactive compounds, Plant growth promoting bacteria and Solubilisation

PMI-47 (Poster)

Investigation of Endophytes in Tissue Cultures of *Syngonium podophyllum*

Syed Zaid Ali, Divyanshi Solanki, Monica Jainand and Sheetal Bhasin
syedzaiidali@gmail.com and divyanshisolanki005@gmail.com

Maharaja Ranjit Singh College of Professional Sciences, Indore, Madhya Pradesh, India

Abstract: Microbial endophytes and plant tissues symbiosis has been an interesting field of research, as microbes impact on various aspects of growth in plants. In this study we investigated the presence of endophytes in petiole derived tissue cultures of *Syngonium podophyllum* and leaves of the mother plant. Tissue cultures are supposed to be aseptic cultures but various bacteria or fungus may reside in latent form inside the tissues. The petioles segments of 1cm were inoculated in Murashige and Skoog medium supplemented with 1-naphthaleneacetic acid (NAA) and 6-benzylaminopurine (BAP). The callus obtained from these tissues was selected for endophyte study. Isolation of bacterial and fungal endophytes was performed by culturing short segments of callus and leaves in nutrient agar (NA) and potato dextrose agar (PDA). In another method the callus tissues and leaf segments from the mother plant, were crushed and the extract was used to isolate the endophytes on NA and PDA. The results obtained show the presence of variety of microbial endophytes in tissue culture derived callus and the mother plant of *Syngonium podophyllum.* The study can be used further to identify plant growth promoting beneficial microbes that help plants grow and produce more or help with plant disease management and nutrient mobilization.

Keywords: Endophytes, *Syngonium podophyllum*, 1-naphthaleneacetic acid (NAA), 6-benzylaminopurine (BAP).

PMI-48 (Poster)

Plant-Soil-Microbe Interactions in Sustaining Ecosystem Stability and Coordinated Biogeochemical Turnover amidst Environmental Change

Rohit Nain[*1] and Shweta Laura[2]
rnain099@gmail.com

[1]*Msc, Department of Soil Science, Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana (125004), India*
[2]*Msc, Department of Agricultural Economics, Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana (125004) India*

Abstract: Plant-soil-microbe interactions are fundamental to maintaining ecosystem stability and driving biogeochemical processes, which are critical for nutrient cycling and overall ecosystem functioning. As

environmental conditions change, particularly under the influence of climate change, these interactions are increasingly challenged. Elevated temperatures, CO2 levels and altered precipitation patterns affect plant growth and microbial communities, leading to shifts in nutrient availability and energy flow. Soil microbes play a crucial role in mediating plant responses to environmental stress, influencing plant productivity and resilience. At the same time, plants can alter microbial community composition through root exudates, shaping the microbial processes that regulate nutrient turnover. These reciprocal interactions underpin the capacity of ecosystems to adapt to changing conditions, sustaining their stability and functional integrity. However, climate-induced disturbances, such as drought and heat stress, disrupt these feedback mechanisms, potentially leading to declines in ecosystem health and productivity. The interactive relationship between plants and soil microbes is critically important for structuring terrestrial ecosystem. The anticipated climate change is aggravating the living conditions for soil microbes and plants. The environmental insecurity and complications are not short-term and limited to any particular type of organism. We have appraised effects of climate change on the soil inhabiting microbes and plants in a broader prospect.

Keywords: Plant-soil-microbe interactions, Ecosystem stability, Biogeochemical processes, Climate change, Nutrient cycling, Environmental stress responses

PMI-49 (Poster)

Screening of Chilli Rhizosphere Bacterial Isolates for their Beneficial Traits and Volatile Bioactive Compounds

Mohankumar Udagi[1*], Nagaraj M. Naik[1], Mahadevaswamy[2], Pampangouda[3], and Prabhuraj A[1]
mohanudagi44@gmail.com

[1]*Pesticide Residue and Food Quality Analysis Laboratory, University of Agricultural Sciences, Raichur, Karnataka, India*
[2]*Department of Microbiology, University of Agricultural Sciences, Raichur, Karnataka, India*
[3]*Agricultural Research Station, Bheemarayanagudi, University of Agricultural Sciences, Raichur, Karnataka, India*

Abstract: Microorganisms are important components of soil that directly or indirectly influence soil properties through their beneficial activities such as organic matter breakdown, nutrient cycling, plant growth promoting activities and antimicrobial properties. Volatile bioactive microbial compounds or metabolites are the naturally active components produced by many bacteria. These bioactive metabolites are produced in trace amounts by microbiota but have high-grade applications such as antibiotics, antibacterial, antitumor and antifungal. This study aimed to screen beneficial traits and bioactive compounds isolated from chilli rhizosphere. Among 25 isolates of PSB, PSB18 registered the highest P solubilization (359.25 mg/L). Out of 25 isolates of *Azospirillum*, AZS25 recorded the highest *in-vitro* nitrogen fixation (44.19 mg/g malate). The isolates PSB18 and AZS25 were registered compatible with Fipronil 5% SC and Diafenthiuron 50% WP pesticide at half of recommended dose, recommended dose, and double of recommended dose of concentrations. Efficient isolates were subjected for GC-MS analysis for detection of bioactive compounds (BAC). Based on peak area percentage, retention time and structure, 59 compounds of PSB18 and 80 compounds of AZS25 were identified. Among 59 BAC of PSB18 isolate, the 2,3-Butanediol showed the highest peak area percentage (58.60%). 2,3-butanediol triggers the secretion of root exudates that modulate soil fungi, rhizosphere bacteria and induces systemic acquired resistance in the plant. For AZS25 isolate Phenol, 2,4-bis(1,1-dimethylethyl)-, phosphite had the highest peak area percentage (48.06%). Phenol, 2,4-bis(1,1-dimethylethyl)-, phosphite responsible for antifungal activity. Hence, these beneficial traits and bioactive compounds present in the isolates play an important role as growth promoters and inducers of plant defences system.

Keywords: Bioactive compound, GC-MS, Chilli rhizosphere, *Azospirillum*, PSB.

PMI-50 (Poster)

Metagenomic Profiling of Soil Bacterial Communities to Study the Impact of Nitrification Inhibitors on Functional Gene Diversity and Nitrogen Cycling

Sriram Lakshmanan, Devi Priya Arumugam and Sivakumar Uthandi*
*usiva@tnau.ac.in

Biocatalysts Laboratory, Department of Agricultural Microbiology, Tamil Nadu Agricultural University, Coimbatore (641003), Tamil Nadu, India

Abstract: Nitrogen is an important nutrient for plant growth and agricultural production more particularly for crops like paddy which is majorly cultivated as a wetland crop with a nitrogen uptake of 30 to 50% of the applied fertilizer and the remaining is lost through denitrification, nitrous oxide emission, runoff, and leaching. To overcome this, nitrification inhibitors (NI) can be used along with conventional fertilizers to slow down the nitrification process, improve the available N concentrations, and reduce the N losses in the soil thereby reducing the amount of applied fertilizers. The present study investigated the effect of botanical-based NI in paddy soil to observe the diversity of the bacterial community in the soil and functional genes responsible for nitrification and other processes in nitrogen metabolism through 16s metagenomic sequencing. The results showed that proteobacteria, acidobacteriota, gemmatimonadota, chloroflexi, myxococcota, bacteroidota, desulfobacterota, and actinobacteriota were dominantly present in the soil. The functional genes responsible for nitrification, denitrification, assimilatory and dissimilatory nitrate reduction, ammonification, nitrogen fixation, and glutamate synthesis have been reduced significantly in the nitrification inhibitor applied treatments. Hence it has been concluded that applying NIs along with conventional fertilizers could reduce the abundance of genes responsible for nitrogen metabolism, which leads to a lowered nitrifying bacterial population in the long term and could improve N uptake by plants resulting in good yields in agriculture.

Keywords: Bacterial Diversity, Gene Abundance, Metagenomic Analysis, Nitrification Inhibitor, Nitrogen uptake

PMI-51 (Poster)

Studies on the Physicochemical Parameter's Optimization of Indole-3-Acetic Acid Using Cost-Effective Medium by Pantoea Agglomerans CPHN2 One Factor at a Time Approach

Chetna Rathi, Simran Rani, Priyanka Dahiya and Pooja Suneja*
chetnarathi25@gmail.com

Department of Microbiology, Maharshi Dayanand University, Rohtak, India

Abstract: Phytohormone indole-3-acetic acid (IAA), being the most active physiological member of functional auxins, is produced by various plant growth promoting bacterial endophytes. The present study was aimed to optimize the cost effective medium for IAA production by PGPEB Pantoea agglomerans CPHN2 using one factor at a time (OFAT) approach. The low cost substrates such as glycerine, soybean flour, chickpea flour, cassava flour, and mungbean flour were used as a substitutes for carbon and nitrogen sources in yeast extract mannitol(YEM) broth. A maximum yield of 270.99 µg/ml of IAA was achieved at a tryptophan concentration of 800 µg/ml with 10 g/L glycerine as carbon source, and 1 g/L soybean flour as nitrogen source on 1 st day of incubation at pH 9 with an agitation speed of 150 rpm. The production of IAA under optimized conditions was also confirmed by TLC analysis. The optimization resulted in a 10-fold decrease in the production cost as compared to the YEM broth. The results demonstrate that this medium can be used for large scale production of IAA in bioreactors.

Keywords: Phytohormone, Biofertilizer, Cost-effective, TLC analysis

PMI-52 (Poster)

Enhanced Nutrient Uptake in Saline Conditions with Mycorrhizal Soil Application in Wheat (*Triticum aestivum*)

Sujata Yadav[1*], Anita Mann[1], Priyanka Chandra[1], Ashwani Kumar[1] and Parvender Sheoran[2]
sujatakaninwal@gmail.com

[1]*ICAR- Central Soil Salinity Research Institute, Karnal (132001), India*
[2]*ICAR- Agricultural Technology Applications Research Institute, Ludhiana (141004), India*

Abstract: The experiment was carried out in two contrasting wheat varieties, KRL 283 (salinity tolerant) and HD 3226 (salt sensitive), to observe the effect of AMF mitigating salt stress at ECiw 10dS/m and enhancing the nutrient uptake. Mycorrhizal seed treatment was given at the time of sowing for all the treatment combinations, along with one set of experiment without mycorrhizal inoculation under saline treatment. Salt stress primarily impacts plant growth and development through osmotic stress and ion toxicity. High salinity leads to excessive accumulation of sodium (Na^+) and chloride (Cl^-), which disrupts nutrient uptake, particularly affecting essential ions like potassium (K^+) and phosphorous (P) due to competitive interactions. This imbalance can result in nutrient deficiencies, oxidative stress, and ultimately reduced crop yields and quality. Mycorrhiza application increased P uptake by 16.90 percent, while N and K uptake increased to 12.12% and 34.71% respectively in the wheat varieties. AMF improved the P uptake due to better soil enzyme activity (alkaline phosphatase & acid phosphatase) activities, thereby, maintaining ionic content in plant leaves. With salt stress, the soil enzymes alkaline phosphatase and acid phosphatase activities decreased to 37.8; 41.9% in the case of KRL 283 and 38.2; 41.9% in HD 3226 which were improved increased up to 29.76 and 30.89 % with AMF. The dehydrogenase activity reduced to 181µg TPF g-1 during salt stress which increased to 211µg TPF g^{-1} with AMF inoculation. Simultaneously, the mycorrhizal colonization was higher in HD 3226 (37.45%) than in salt-tolerant KRL 283 (33.69%). Similarly, arbuscular abundance was also lower (21.91%) in KRL 283 compared to HD 3226 (25.33%). These results show that AMF application created favorable soil conditions and better nutrient uptake in the salt-sensitive variety, HD 3226 to cope with the harmful effects of salt stress.

Keywords: Wheat, Salinity, AMF, Nutrients, Soil enzymes

PMI-53 (Poster)

Deciphering Plant Growth-Promoting Traits in Rhizobial Endophytes across Diverse Soybean Genotypes (*Glycine max*) Cultivated in Central India

Hirudhaya Ravi[1], Kirti Suman[2], Pushpendra Sharma[3], Meena Rathore[4] and Rajeev Kaushik[5]
ravihirudhaya@gmail.com

Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi, India

Abstract: Soybean (*Glycine max*), one of the world's most vital commercial crops, boasts a global production of approximately 388.01 million metric tons. As soybean cultivation expands into new regions, farmers face growing challenges in maintaining sustainable yields, particularly under evolving climatic conditions. Addressing these challenges requires innovative nutrient management strategies and approaches to combat abiotic stress. Various rhizobial genera are known to nodulate soybeans across diverse soil types and promote plant health through mechanisms such as antibiosis against plant pathogens, enzyme activity, phytohormone production, organic acid secretion, and secondary metabolite synthesis. In this study, a total of 60 endophytic rhizobial isolates were obtained using CRYEMA medium from root nodules of seven widely cultivated soybean varieties (RUS1135, JS2098, NRC142, NRC136, JS9560, and NRC37) grown across different regions of India. Initial confirmation of these rhizobial isolates was performed through biochemical tests (Hoffer's alkaline solution, glucose-peptone, and ketolactose), and their nitrogen-fixing abilities were assessed using Leonard jar tests, leading to the identification of isolates with positive nodulation potential. The isolates were further evaluated for their plant growth-promoting abilities, including nutrient solubilization (N, P, K, Fe, Zn), ammonia production, exopolysaccharide (EPS) formation, and hormone production (IAA, cytokinin, gibberellic acid, and ethylene). Top-performing strains were also screened for abiotic stress tolerance, focusing on moisture stress using PEG 8000 assays, proline and glycine betaine estimation, and biofilm formation. Molecular identification

of key rhizobial isolates was carried out through 16S rRNA gene sequencing. The results revealed significant variation in microbial populations within the nodules, depending on the genotype and cultivation environment. Additionally, the study confirmed that rhizobial endophytes have strong plant growth-promoting potential, which can improve soybean growth and nodulation efficiency. Integrating these microbial formulations into soybean farming practices is crucial for achieving a sustainable and resilient future in global food production.

Keywords: Rhizobial endophytes, Soybean, Plant growth promotion, Nodulation efficiency.

PMI-54 (Poster)

Diversity of Arbuscular Mycorrhiza (AM) fungi and their Application for Sustainable Cultivation of Some Endangered Medicinal Plants of Meghalaya

Nilufa Afruza[1]*and Dhritiman Chanda[1]
afruznilufa@gmail.com
*[1]*Nilufa Afruza; Ph.D Scholar, Department of Botany, University of Science and Technology Meghalaya (793101), India*
[1]*Assistant Professor, Department of Botany, University of Science and Technology Meghalaya (793101), India*

Abstract: Arbuscular Mycorrhizal (AM) plays an important role for the development of soil parameters which in turn useful for the growth and yield of the plants. Medicinal plants are integral part of rural and tribal lives of India for traditional uses especially for the treatment of various diseases. Due to increase in population and extensive need of medicine, the medicinal plants are becoming endangered for the supply of drugs. Inoculation of Arbuscular Mycorrhizal (AM) fungi during an early stage of plant growth has become an alternative strategy for improved plant survival and growth. AM association has been reported to have function in improving the growth of medicinal plants and productivity of medicinal plants and medicinal compound. Meghalaya is home to very rich floral diversity because of its favourable climatic condition, leading the availability of a wide range of medicinal and aromatic plants. Our study reports the use of native AM fungal strain for the conservation of endangered medicinal plants of Meghalaya. We have studied the mycorrhizal diversity and its association on six selected medicinal plants *Alternanthera brasiliana*, *Ageratum conizoides*, *Curcuma zedoeria*, *Zinziber montanum*,and *Ricinus cumminis.* The molecular characterization of dominant AM strain also carried out for further characterization. This work also emphasizes the scope of mass cultivation of endangered medicinal plants using native AM inoculum and thereby enhancing the entrepreneurial opportunities in this region. *Glomus* spand *Acaulospora* sp were found to be dominant AM strain isolated from the selected medicinal plants which can be used as AM inoculum for the cultivation and preservation of rare and endangered medicinal plants of Meghalaya.

Keywords: Medicinal plants, endangered, *Arbuscular mycorrhiza,* Physico-chemical properties, *Glomus* sp. *Acaulospora* sp

PMI-55 (Poster)

Exploring the Structural Diversity of Root-Colonizing and Soil-Inhabiting Arbuscular Mycorrhizal Fungi in Acidic Soils of North-East India

Priya M*, Subrata Nath Bhowmik and Rajeev Kaushik
*mpriyamurugesan97@gmail.com

Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi, India

Abstract: Soil acidity poses a significant challenge to plant growth and productivity, with approximately 90% of India's land being affected, predominantly in the North-Eastern Region where 54% of the acidic soils are concentrated. Arbuscular mycorrhizal fungi (AMF), which form symbiotic relationships with 80% of terrestrial plant species, are especially effective at phosphorus uptake, a nutrient often scarce in acidic soils. This research aimed to examine the AMF communities colonizing native acidic soil of disturbed and undisturbed agroecosystem of North-East India using next-generation sequencing. DNA was extracted from AMF-colonized

root samples and amplified via nested PCR with primers specific to AMF genera. Soil samples were gathered from undisturbed and cultivated sites in upland (Mizoram) and lowland (Tripura) areas to serve as inocula for trap cultures using maize as a host plant. After four months, DNA from root samples was analysed, identifying six ASVs across the four sites. The highest Shannon and Simpson diversity indices were observed at undisturbed sites in both Mizoram and Tripura, while the lowest was recorded at the cultivated site in Tripura. Two ASVs belonging to the Glomeromycetes and Glomerales orders were detected as core genera across all sites. Unique to Mizoram's undisturbed site was the Archaeosporaceae family, and to the cultivated site was Acaulospora. ASVs from the Glomeraceae family were found in three root samples, except in the cultivated Tripura site. Understanding the composition of AMF communities colonizing plant roots is crucial for developing effective AMF biofertilizers to enhance nutrient uptake and crop productivity in acidic soils.

Keywords: Soil Acidity, Arbuscular Mycorrhizal Fungi (AMF), North-East India, Phosphorus Uptake, Next-generation sequencing, AMF trap cultures

PMI-56 (Poster)

A Comparative Transcriptomic Approach to Unravel the Molecular Basis of Cotton's Response to CLCuD

Ramandeep Kaur[1], Satish Kumar Sain[2] and and Priyanka Siwach[1]
priyankasiwach@cdlu.ac.in

[1]*Department of Biotechnology, Chaudhary Devi Lal University, Sirsa (125055), Haryana, India*
[2] *ICAR-Central Institute of Cotton Research, Regional Station, Sirsa, Haryana (125055), India*

Abstract: Cotton leaf curl disease (CLCuD), caused by cotton leaf curl viruses (CLCuVs), is one of the most destructive diseases impacting cotton production. *Gossypium hirsutum*, the primary cultivated cotton species, is highly susceptible to CLCuD, while its diploid progenitor, *Gossypium arboreum*, exhibits strong natural resistance. Despite various molecular and breeding strategies, *G. hirsutum* remains vulnerable, primarily due to the high recombination rates of CLCuVs, which accelerate the breakdown of host resistance. To unravel the molecular mechanisms governing cotton-CLCuV interactions, we conducted a comparative transcriptomic analysis utilizing the publicly available RNA-Seq datasets from the NCBI Sequence Read Archive (SRA) for both CLCuD-resistant *G. arboreum* and CLCuD-susceptible *G. hirsutum*. The datasets were processed using Tophat for read alignment and Cuffdiff for quantifying gene expression, enabling the identification of differentially expressed genes (DEGs) between the resistant and susceptible species. Further characterization and phylogenetic analysis of the DEGs provided insights into their evolutionary significance and their potential role in conferring resistance. Network and enrichment analyses highlighted key molecular pathways involved in cotton's response to CLCuVs, including those related to defense signaling and stress responses. These findings enhance our understanding of the molecular mechanisms underlying virus-host interactions, identifying crucial targets for functional validation and breeding efforts to develop CLCuD-resistant *Gossypium hirsutum* species.

Keywords: Cotton leaf curl disease, Cotton, Expression, Phylogenetic, Signaling, Enrichment.

PMI-57 (Poster)

Understanding Microbial Contributions to GABA Dynamics in Tomato Rhizosphere

Ejeoghene Rita Ogbimi[1, 2], Tanushri Kaul[1] and Rashmi Kaul[1]
eogbimi@oauife.edu.ng, e.rita@icgeb.res.in

[1.] *Nutritional Improvement of Crops Group, Plant Molecular Biology Division, International Centre for Genetic Engineering and Biotechnology (ICGEB), New Delhi (110067), India,*
2. Obafemi Awolowo University (220101), Ile – Ife, Nigeria

Abstract: This review examines the influence of rhizosphere microbiota on gamma-aminobutyric acid (GABA) metabolism in tomato plants. Plant growth-promoting rhizobacteria and mycorrhizal fungi stimulate GABA biosynthesis, enhance stress signaling, and improve nutrient uptake. Key findings highlight the potential of microbial inoculants as biostimulants for sustainable agriculture. Further research is needed to explore the molecular interactions between soil microbiota and plant metabolic pathways.

The role of gamma-aminobutyric acid (GABA) in modulating plant responses to biotic and abiotic stresses is well established. In tomato plants (*Solanum lycopersicum*), GABA biosynthesis is intricately linked to stress mitigation pathways, growth regulation, signaling, and metabolism. Recent advances emphasize the significance of rhizosphere microbiota, specifically bacteria and fungi, in modulating GABA metabolism through root-associated interactions.

Plant growth-promoting rhizobacteria (PGPR), such as *Bacillus* and *Pseudomonas*, and *mycorrhizal* fungi like *Trichoderma*, have been found to influence GABA levels in tomatoes. These microorganisms directly stimulate GABA biosynthesis, trigger systemic resistance, and enhance plant stress signaling pathways. For instance, *Pseudomonas fluorescens* has been reported to increase GABA content under drought stress by upregulating glutamate decarboxylase activity, a key enzyme in GABA production.

Mycorrhizal associations also boost GABA accumulation by enhancing the plant's nutrient uptake and stress resilience. Furthermore, microbial-induced modulation of the GABA shunt offers new insights into carbon and nitrogen metabolism under stress conditions. This complex interplay highlights the critical role of the rhizosphere microbiota in regulating GABA metabolism.

The potential application of microbial inoculants as biostimulants for enhancing GABA-mediated stress tolerance in tomatoes presents a promising avenue for sustainable agriculture. To fully harness this potential, future research should explore the molecular dialogues between soil microbiota and plant metabolic pathways, uncovering innovative strategies for crop management. By elucidating these interactions, scientists can develop effective, microbiome-based approaches to improve crop resilience and productivity.

Keywords: GABA, Metabolism, Rhizosphere, Microbiota, Tomato, Stress

PMI-58 (Participate only)

Thermal Stress Adaptability Study in Whiteflies in Relation to Climate Resilience- A Review

Prabhat Kumar[a], Rishi Kumar[b], Debashis Paul[b], **Priyanka Siwach[a]***, Sunita[b] and Rahul Kumar[b]
Priyankasiwach@cdlu.ac.in

[a]*Chaudhary Devi Lal University, Sirsa, Haryana, India*
[b]*ICAR-Central Institute for Cotton Research, Regional Station, Sirsa, Haryana, India*

Abstract: The current rise in mean temperature due to climate change hampers the economic status of agricultural productivity globally. Due to this surge in temperature, the abundance, distribution, and population dynamics of *Bemisia tabaci* (order: hemipteran) commonly called whitefly, a pest of worldwide concern were altered. Whiteflies having a wide host range also attacks cotton crop, besides sucking the sap from the host plant also vectored viruses of Cotton Leaf Curl Disease which significantly impact the productivity of cotton. Whiteflies exhibit thermotolerance, a biological trait linked to their capacity to endure elevated temperatures. This affects its fitness traits including fecundity, survival and developmental duration. Additionally, thermal stress in whiteflies leads to alteration of different biomolecules like catalase, superoxide dismutase, alkaline phosphatase, total amino acid and total sugar content. Existing research underscores the variability in whitefly life cycles contingent upon temperature, relative humidity, and its interaction with host plants. However, the enduring effects of prolonged high-temperature stress on the fitness and population dynamics of *B. tabaci* remain poorly understood. Past studies also reveal that this thermo-tolerance positively correlates with insecticide resistance. Results from the studies on induced and basal thermotolerances would be very useful in monitoring pest dynamics, distribution, dispersal and eventually for developing sustainable integrated strategies for managing the pest in the context of climate change.

Keywords: Climate resilience, Thermotolerance, Whitefly, Fecundity, Cotton

VDL-1 (Oral)

Web-based Predictions and Experimental Validations of T cell and Antibody Epitopes In *Mycobacterium tuberculosis*-Specific Proteins

Abu Salim Mustafa
abu.mustafa@ku.edu.kw

Department of Microbiology, College of Medicine, Kuwait University, (24923), Safat (13110), Kuwait

Abstract: The proteins encoded by the genes located in of *Mycobacterium tuberculosis*-specific genomic regions absent/deleted in the vaccine strains of *M. bovis* BCG could be useful in subunit vaccine design against tuberculosis. Among these proteins, PE35, PPE68, ESXA, ESXB, and ESXV have been shown to have T cell epitopes using both web-based prediction methods and experimental validations. Hence, these proteins have been considered useful for vaccine applications. However, recently conducted studies have indicated that, in addition to T cells, antibodies also play a role in protection against tuberculosis. In this work we have performed studies to identify antibody epitopes in the above proteins by applying web-based prediction methods and experimentally validated them in antigen-specific antibody responses using sera from experimental animals and humans. The antibody reactivities against the above-mentioned proteins were predicted by using seven web-based methods available at IEDB Analysis Resource. To experimentally confirm the antibody reactivities, serum samples were tested from immunized mice, rabbits, and humans using enzyme-linked immunosorbent assays (ELISA). All the seven web-based prediction methods suggested the presence of multiple antibody epitopes in PE35, PPE68, ESXA, ESXB, and ESXV proteins. The predicted epitopes were present at various positions in each protein. The ELISA results with sera from rabbits showed positive antibody reactivity with all the five immunizing proteins, their synthetic peptide pools, and multiple peptides of each protein. The sera from mice showed positive antibody reactivity with all proteins but only to one peptide of PE35 and two peptides of PPE68. In humans, three peptides of ESXV and five peptides of PPE68 showed positive reactivity with sera from both tuberculosis patients and healthy subjects.
Conclusions: The web-based prediction methods and experimental studies confirm the presence of multiple T cell and antibody epitopes in each protein, which suggest their usefulness in vaccine design against tuberculosis.

Keywords: *M. tuberculosis*, Specific-proteins, T cell epitopes, Antibody epitopes, Subunit vaccines

VDL-2 (Oral)

F gene Based Genetic Characterisation of Newcastle Disease Virus Isolated from *Pavo cristatus*

Anubha Sharma[1-3], Aman Kumar[2*], Sushila Maan[2] and Namita Singh[1*]
anubhasharma222@gmail.com

[1]*Department of Biotechnology, Guru Jambheshwar University of Science and Technology, Hisar, India*
[2]*Department of Animal Biotechnology, Lala Lajpat Rai University of Veterinary and Animal sciences, Hisar, India*
[3]*Department of Medical Lab Technology, School of Allied Health Science, JECRC University, Jaipur, India*

Abstract: Newcastle disease virus (NDV) affects a variety of avian species and has caused significant financial losses for the poultry sector. It is categorised as an avian paramyxovirus type 1 (AMPV-1), which is a member of the family Paramyxoviridae, order Mononegavirales, and genus Avulavirus. Six structural genes that encode nucleocapsid (N), matrix protein (M), phosphoprotein (P), fusion protein (F), haemagglutinin-neuraminidase protein (HN), and large polymerase protein (L) are flanked by the 55 nt leader at the 3′ end and the 114 nt trailer at the 5′ end of the typical NDV genome. The two surface glycoproteins, F and HN, are antigens that neutralise viruses and are in charge of the virus's attachment and fusion with the membrane of the host cell. Analysing the full-length F gene sequence of NDV derived from peafowl was the goal of this investigation. The isolate modified from Vero cells was passaged further in the allantoic cavity of specific-pathogen-free (SPF) chicken eggs that had been embryonated. The NDV in allantoic fluid was verified by hemagglutination (HA) testing. RT-PCR was used to amplify the full-length F gene, which was further cloned in a pJET cloning vector. Sanger's sequencing technique was successfully used to sequence the purified recombinant plasmid. The full sequencing of the 1662 bp F gene, which codes for 553 amino acids, was verified by the in-silico investigation

in which the Swiss Prot Modeler produced only two models, with a GMQE value of 0.68 and 0.54 and a Q mean value of 0.75 ± 0.05 and 0.61± 0.05 respectively. A Ramachandran plot was created from the rampage site in order to ascertain the stereochemical features of the F protein. It was found that 89.59% of residues had phi/psi angles that fell in the most preferred regions, 1.97 % had phi/psi angles that fell in Ramachandran outliers, 0.52% had rotamar outliers. The secondary structure characteristics showed alpha helices (40%) dominated the secondary structure elements, followed by Beta strands (22%), TM helix (8%) and disordered region (7%). The F protein was predicted to have an average molecular weight of 59039.48daltons and calculated isoelectric point (pI) value of 8.89 indicated that it was naturally basic. Asp + Glu accounted negatively charged residues in F protein, whereas Arg + Lys made up positively charged residues. The F protein molecule consists of 8434 atoms with the atomic composition $C_{2600}H_{4305}N_{699}O_{805}S_{25}$. The extinction coefficient (EC) of F protein for a wavelength of 280 nm in water is calculated by Expasy's Protparam. With all pairs of Cys residues becoming cystines, its EC value ranges from 31580 Abs 0.1% (=1 g/l) 0.535 to 30830 Abs 0.1% (=1 g/l) 0.522, assuming all Cys residues are reduced. The F protein in question had an instability score of 35.77, indicating that it was unstable under in vitro conditions. For F protein, the aliphatic index was 109.17. By summing the hydropathy values of each amino acid residue and dividing by the total number of residues or sequence length, the GRAVY value of the F protein was determined. F protein has a negative value of 0.184, which suggests that it is more hydrophilic. The estimated half-life for F protein was calculated as 30 hours (mammalian reticulocytes, in vitro), >20 hours (yeast, in vivo) and >10 hours (*Escherichia coli*, in vivo). Thus, the identity of the protein and nucleotide sequences was determined to be 89.6%-97.65% and 96.45-97.69%, respectively. ^{112}K-R-Q-K-R-F^{117} was the inferred amino acid sequence of the F protein's cleavage site. The isolate was identified as NDV genotype II by phylogenetic analysis OF F gene. The NDV isolate's pathogenicity was validated by the presence of many basic amino acids at the cleavage site. The variations in the genomic sequence of NDV with low and high virulence from year to year reveal that different NDV genotypes are simultaneously emerging at various geographic locations globally. Many NDV control programmes and vaccination programmes are already running but this issue should be addressed by concerned authorities for the effective control of NDV infections as the problem persist and effecting poultry industry to a great extent. Comprehensive molecular epidemiology investigations of NDVs with large sample sizes are required to have a better understanding of the transmission mechanisms of virulent NDV strains.

Keywords: NDV, Fusion gene, Phylogenetic analysis, In silico study, Genome.

VDL-3 (Poster)

Evaluating Inflammation in In Vivo Zebrafish Model: A Promising Therapeutic Approach

H Thamarai Kannan and Ieshita Pan
thamaraikannanh22002.sse@saveetha.com

Institute of Biotechnology, Department of Medical Biotechnology and Integrative Physiology, SIMATS Engineering, Saveetha Institute of Medical and Technical Sciences, Chennai (602105), Tamil Nadu, India.

Abstract: Copper sulfate (CuSO4), commonly used in various industrial processes, often finds its way into aquatic environments as a pollutant, either intentionally through disposal practices or unintentionally through runoff. Once in water bodies, CuSO4 can accumulate in aquatic organisms, including fish, posing significant environmental and health risks to human. Its widespread use makes it hazardous to non-target species, leading to harmful effects such as oxidative stress and cognitive impairment in fish populations. The presence of CuSO4 in aquatic habitats can induce the production of reactive oxygen species (ROS), causing oxidative damage to tissues and impairing neurological function. Small humanin-like peptide-6 (SHLP6) is a mitochondrial-derived peptide known for its anti-aging and anticancer properties. However, its potential protective role against CuSO4 induced toxicity and neurological impairment in vivo remains largely unexplored. To investigate this, we examined the effects of CuSO4 on zebrafish larvae exposed to various concentrations of SHLP6 (10, 20, 30, 40, and 50 µg/ml). The study focused on evaluating the toxicity of CuSO4 treated with SHLP6 by measuring survival rates and heart rate, along with assessing the occurrence of malformations, mortality, and oxidative stress in the larvae. Our results revealed that SHLP6 exhibited a protective effect against CuSO4-induced oxidative damage. SHLP6 showed the protective effect in the zebrafish larvae at 40 µg/ml and 50 µg/ml, survival rates improved significantly to 83.6% and 90%, respectively. Molecular analysis confirmed that SHLP6 mitigates CuSO4 toxicity by downregulating pro-inflammatory genes (COX-2, NLRP3, cav1, TNF-α, and IL-1α) and upregulating antioxidant genes (SOD, GPx, GST, and GSH). These findings suggest that SHLP6 holds

promise as a protective and therapeutic agent against CuSO4-induced inflammation and toxicity in fish, offering a novel approach for mitigating environmental pollutants impact on human health and aquatic life.

Keywords: Zebrafish larvae, SHLP6, CuSO4, Oxidative stress, Inflammation, Toxicity

VDL-4 (Poster)

The Therapeutic Vaccine Potential of Live Recombinant *Lactococcus Lactis* Secreting Murine Ifnλ3 against Influenza Type A Virus (IAV) Infection

Sandeep Yadav and Amirul Islam Mallick*
sy22rs043@iiserkol.ac.in

Host-Pathogen Interaction Lab, Department of Biological Sciences,
Indian Institute of Science Education and Research Kolkata, Mohanpur, Nadia (741246), India

Abstract: Probiotic bacteria in the gut directly or indirectly help maintain overall health by contributing to growth, metabolism, absorption, and non-specific immunity against microbial pathogens. In addition to generalized health benefits, recent studies highlight their potential as effective delivery vehicles for a range of therapeutic and prophylactic molecules. This is mainly because of their non-toxic nature, GRAS category, ease of growing, and ability to withstand harsh physiological conditions. Considering these intrinsic benefits, bioengineering of food-grade LAB vectors for targeted delivery of biomolecules directly in the mucosal surface has attracted significant attention across the globe.
In the present study, we bioengineered food grade Lactic acid-producing bacteria (LAB), *Lactococcus lactis (L. lactis),* to secrete functionally bioactive recombinant murine IFNλ3 (MuIFNλ3) directly at the host-mucosal interface to combat influenza Type A virus (IAV) infection. To engineer *L. lactis* cells as a preferred mode of mucosal delivery of MuIFNλ3, we utilized the nisin-controlled gene expression system, known for its ability to express heterologous proteins in a tightly controlled manner. Assessment of the bio-therapeutic potential of recombinant MuIFNλ3 secreted by rLAB vector against IAV infection was performed using both *in vitro* and *in vivo* models. Using murine B16F10 cells we demonstrated that pre-treatment with MuIFNλ3 secreted by r*L. lactis* can upregulate the expression of several antiviral genes, including Interferon Regulatory Factors (IRFs) and Interferon-stimulated genes (ISGs) to protect the cells from IAV infection. Finally, we showed that mucosal delivery of rLAB vector expressing MuIFNλ3 in BALB/c mice can endure significant immune protection in terms of viral clearance against mice-adapted influenza virus, A/PR/8/1934 (H1N1) infection.Based on these results, our study illustrates how exogenous application of IFNλ3 using a live vector-based delivery platform can modulate the host immune responses and serve as a promising therapeutic vaccine modality against IAV infections by augmenting the antiviral state in the host.

Keywords: Murine IFNλ3 (MuIFNλ3), *Lactococcus lactis* (*L. lactis*), Influenza type A Virus (IAV), Immune protection

VDL-5 (Poster)

Reverse Vaccinology-Machine Learning (RV-ML) Based Discovery of a Highly Protective Protein-Based Vaccine Antigen against Methicillin Resistant *Staphylococcus aureus* (MRSA)

Pranaya M. Mishra[1], Suman Chaudhary[12], Ravi S. Manhas[1], Diksha Sharma[13], Manoj K.Baranwal[3] and Ravi P.N. Mishra[1, 2*]
ravi.mishra@imtech.res.in

[1]*Vaccine & Biotherapeutics Research laboratory, CSIR-Institute of Microbial Technology, Chandigarh, India.*
[2]*Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, India*
[3]*Thapar Institute of Engineering and Technology (TIET), Patiala, Punjab, India*

Abstract: The methicillin resistant *Staphylococcus aureus* (MRSA) is a notorious nosocomial pathogen that causes an array of illnesses ranging from wound infections to the potentially fatal conditions such as sepsis, pneumonia, endocarditis and meningitis. MRSA presents a significant medical challenge due to its rapid

increase in multi-drug resistance and the absence of an effective vaccine, posing a serious threat to global health. In the present study, we discovered a novel staphylococcal hypothetical protein antigen (named hereafter IMTS8) using supervised machine learning and reverse vaccinology algorithms. The gene encoding IMTS8 protein was found to be well conserved in major clinical strains of *S. aureus*, well expressed by bacteria and localized on the bacterial surface. The administration of mice with two doses of recombinant purified, adjuvanted IMTS8 protein was shown to be highly immunogenic, and conferred excellent protection of mice against MRSA lethal challenge, in sepsis model. The overall findings from this study strongly support that IMTS8 may serve as potential vaccine candidate against staphylococcal mediated sepsis.

Keywords: Methicillin resistant *Staphylococcus aureus* (MRSA), Adjuvanted IMTS8 protein, Endocarditis, Pneumonia

VDL-6 (Poster)

Immunoinformatics Approach for Designing a Multi-Epitope Peptide Vaccine against Drug-Resistant *Acinetobacter Baumannii*

Shiv Nandan Sah[1], Neha Bhardwaj[1], Neena Capalash[2] and Prince Sharma[1]
sahshivnandan96@gmail.com

[1]*Department of Microbiology, Panjab University, Chandigarh, India*
[2]*Department of Biotechnology, Panjab University, Chandigarh, India*

Abstract: *Acinetobacter baumannii*, an opportunistic and notorious nosocomial pathogen, is implicated in many infections affecting soft tissues, skin, lungs, bloodstream, and the urinary tract, contributing to over 722,000 cases annually. Despite significant therapeutic options advancements, no approved vaccine for this pathogen remains. In response to this critical gap, the present study concentrated on the rational design of a vaccine utilizing advanced bioinformatics approaches. Three outer membrane proteins with significant immunogenic potential and favorable vaccine candidate properties were selected to identify epitopes based on their strong antigenic characteristics, non-allergenicity, high binding affinity, and low IC50 values. These epitopes were sequentially linked using appropriate linkers to construct a multi-epitope peptide (MEP). The ClusPro 2.0 and C-ImmSim web servers were employed to perform docking analyses with TLR2/TLR4 receptors and to simulate immune responses, respectively. The accuracy of the MEP model was confirmed by the Ramachandran plot, which indicated that 100% of the residues were located in the most favored and allowed regions. The construct exhibited high antigenicity, stability, non-allergenicity, non-toxicity, solubility, and demonstrated optimal population coverage. Molecular docking studies revealed strong binding interactions between the designed MEP vaccine and TLR2/TLR4 receptors. In silico immunological simulations showed substantial increases in T-cell and B-cell populations. Furthermore, codon optimization and in silico cloning were carried out using the pET-28a (+) plasmid vector to assess the efficiency of the vaccine peptide's expression and translation in *Escherichia coli*. This MEP vaccine design aims to facilitate and expedite the development of a potent vaccine against multidrug-resistant *Acinetobacter baumannii*.

Keywords: Immunoinformatics, *Acinetobacter baumannii*, Multi-epitope peptide, Immune-simulation, Molecular docking, Vaccine

VDL-7 (Poster)

Investigating the Role of Protein Phosphate 5 Catalytic Subunit PPP5C Gene in Vesicular Stomatitis Virus (VSV) Lifecycle Using Short Hairpin RNA (Shrna)- Mediated Knockdown

Himanshi Bilwal
bilwalhimanshi0@gmail.com

Malwanchal University, NH-59-A, Nemawer Road, Indore (452001), India

Abstract: The protein phosphate 5 catalytic subunit (PPP5C) of human gene, which encodes serine/threonine protein phosphate 5, is a regulatory enzyme involved in several critical cellular process, including stress

responses/ cell cycle regulation, apoptosis, and signal transduction. Vesicular Stomatitis Virus (VSV), an RNA Virus, relies on host cellular machinery for replication, and PPP5C has emerged as a potential key player in this process. By inhibiting apoptosis, particularly apoptosis induced by oxidative stress, PPP5C may promote viral persistence and survival, making it essential for VSV replication.
This study aims elucidate the role of the PPP5C gene in VSV replication. To investigate this, we utilized an shRNA-mediated knockdown approach to silence PPP5C in Baby Hamster Kidney (BHK) cells. Following transfection, the cells were infected with GFP-tagged VSV-EGFP, allowing us to monitor viral infection and replication dynamics in real-time. Our results indicate that PPP5C knockdown significantly reduces viral replication and gene expression, suggesting that PPP5C is crucial for the VSV life cycle.
By uncovering the mechanisms through which PPP5C influences viral propagation, this study provides new insights into host-virus interactions and highlights the potential of targeting PPP5C for therapeutic intervention in viral infections.

Keywords: Vesicular Stomatitis Virus, Protein Phosphate 5 Catalytic Subunit, shRNA Knockdown, VSV Life cycle

VDL-8 (Poster)

From COVID to Cancer: The Role of mRNA Technology in Oncology

Ayushi Malik, Annu
ayushimalik982@gmail.com

Department of Biotechnology
Guru Jambheshwar University of Science & Technology, Hisar, Haryana, India

Abstract: The rampant growth of normal cells which have lost the property of apoptosis are said to be called as cancerous cells. It is one of the leading causes of death in today's time due to the absence of proper cure. Mutations due to the over-exposure to chemicals like benzopyrene, benzene; UV or X-ray radiations are some of the major contributing factors leading to transformation of normal cells to cancerous ones. These mutations can also be due to the genetic disposition. The development of cancer often occurs in stages including the initial tumor stage which starts from being benign to develop further as malignant. Currently, some of the available cancer treatments include surgery, radiation, and chemotherapy. These treatments, however, are not very efficient for all types of cancer and its advancements as cancer cells mutate at a high rate.
At present, studies are done on the fighting potential of our immune system against cancer cells. Immunotherapy can serve for a potential cure which is still under study. Earlier aspects of cancer vaccine were based on therapeutics in which TAA or TSA were being targeted by our immune system. Comparatively, it is more reliable than chemotherapy with less side-effects as it specifically targets the cancer antigens. New studies have shifted the focus from peptide vaccine to m-RNA vaccines witnessing the success in COVID. The trials for lung and breast cancer are going on in which m-RNA and DNA based vaccines are being used for treatment.

Keywords: Cancer, Mutations TAA/TSA, Immunotherapy, m-RNA, COVID

LS-1

Screening and Assessment of Rhizospheric PGPR Strain of *Chakhao*, With Different PGP Characteristics

Sushma Khaidem and Menaka Devi Salam
sushmakhaidemtony@gmail.com

Amity Institute of Microbial Technology, Amity University, Sector 125, Noida (20130), Uttar Pradesh, India

Abstract: Plant growth-promoting rhizobacteria (PGPR) possessing beneficial characteristics has the potential to be a cost-efficient and environmentally sustainable substitute for chemical pesticides and fertilizers. They can play a great role in plant growth and health directly or indirectly. It is commonly recognized that PGPRs directly increase plant development by producing phytohormones and increasing the availability of nutrients in the soil. A total four different rhizospheric sample of *chakhao* were collected and 113 rhizobacterial strains were isolated. Only 10 out of 113 isolates were found positive in all the screened PGP attributes which includes phosphate solubilizing activity, potassium solubilizing, nitrogen fixing ability, siderophore production, ammonia production, ACC deaminase activity, IAA production and zinc solubilizing activity. Among these 10 isolates, SAY12 and SPS9 were found to be highest in phosphate solubilizing index (SAY12 – 2.8 , and SPS9 – 2.5) and solubilizing phosphorus of 343 mg/L and 305 mg/L, potassium solubilizing index with 5 in SAY12 and 2.5 in SPS9. SAY12 was found to be maximum IAA producer with 410 mg/L and SPS9 produces 162 mg/L. These two isolates were further checked for seed germination percentage in which it is found to be 90% for SAY12, 86% for SPS9 when compared with control uninoculated on with 64%. The two bacterial isolates were identified using 16S rRNA gene sequencing technique and found to be *Enterobacter cloacae* strain SAY12 and *Pseudomonas aeruginosa* strain SPS9. With this defined PGPR strain, biofertilizers with improved soil fertility and crop production could be developed.

Keywords: *Chakhao,* Rhizosphere, Soil microbes, PGPR, Phosphate solubilizers, IAA.

LS-2

Effect of Adenine Sulphate on Growth and Secondary Metabolites Profile of Callus Cultures of *Ficus Religiosa* L.

Anita Rani Gill[1*] and Priyanka Siwach[2]
*shineanitagill@gmail.com

[1]*Department of Biotechnology, Guru Jambheshwar University of Science & Technology, Hisar*
[2]*Department of Biotechnology, Chaudhary Devi Lal University, Sirsa, India*

Abstract: *Ficus religiosa* L. having a wide spectrum of applications and has got **mythological**, **religious** and **medicinal** importance in Indian culture. But irony is that because of great religious importance it restricts its pruning or cutting for any purpose, also regarded as inauspicious and so the medicinal properties remains unrevealed. Callus tissue provides an alternative *in vitro* source for the production of various metabolites for further medicinal applications. Till date there is not even a single report available for the callus studies in *Ficus religiosa* and secondary metabolite accumulation as well. The present study aimed to optimize various conditions for efficient callus induction and proliferation. MS medium supplemented with 2.0mg/l thidiazuron and 0.5mg/l indole-3-acetic acid alongwith moderate concentration of ADS was found to induce callus with maximum frequency of 100%. For long term maintenance of callus, 100mg/l ADS was more suitable than other concentrations of ADS. Standard biochemical tests for the qualitative and quantitative estimation of various phytochemicals revealed the enhanced production in the *in vitro* source (callus tissue) as compared to that in the *in vivo* source (stem segments of mother plant). The present work is an attempt to highlight the importance of callus tissue, proving an alternative source for further biochemical investigation about the medicinal aspects of this tree.

Keywords: *Ficus religiosa* L., adenine sulphate, Alzeihmer's disease, callus, secondary metabolite

LS-3

Isolation of Endophytic Fungi from *Cichorium Intybus* and Determination of Their Phosphate Solubilization Ability

Abdusamatov Sokhibjon[1,2], Numonjon Sultanov[2], **Jabborova Dilfuza[1,2*]**
*dilfuzajabborova@yahoo.com

[1]*Institute of Genetics and Plant Experimental Biology, Uzbekistan Academy of Sciences, Kibray 111208, Uzbekistan*
[2]*Faculty of Biology, National University of Uzbekistan, Tashkent 100174, Uzbekistan*

Abstract: *Cichorium intybus* is a plant species belonging to the *Asteraceae* family, commonly known as chicory. This plant is considered a highly promising object in traditional medicine, modern medicine, and various other fields due to its many beneficial properties discovered through extensive research. Its leaves and roots are used worldwide, with the leaves consumed in Poland, Southern India, Italy, and Greece, while its roots are commonly used as a coffee substitute. *Cichorium intybus* L. Possesses many properties that affect human metabolism, including antifungal, antibacterial, analgesic, anticancer, and antidiabetic properties. Additionally, different parts of the chicory plant are widely used in the folk medicine of various countries to treat a variety of conditions. For instance, it is used to treat diarrhea, prostate and other reproductive organ disorders, lung cancer, bile duct cleaning, liver disorders, spasms, high cholesterol, rheumatism, jaundice, hepatoprotection, hemorrhoids, and urinary disorders. Chicory is a plant rich in chemical compounds, and studies conducted by scientists have led to the isolation of several bioactive substances from its various organs, including aliphatic compounds and their derivatives, terpenoids, saccharides, methoxycoumarins, chicoryin, flavonoids, essential oils, and anthocyanins. The research aimed to isolate endophytic fungi from different organs of *Cichorium intybus* and investigate their determination of phosphorus solubilizing ability. PDA and Czapek-Dox Agar media were used for the isolation of endophytic fungi. The plant organs were divided into segments, sterilized, and then inoculated onto nutrient media containing antibiotics that restrict bacterial growth. These inoculated samples were incubated at 25°C for 5 days. The resulting colonies were transferred and purified through classical subculturing methods. A total of 13 endophytic fungal isolates were isolated. To investigate their determination of phosphorus solubilizing ability, all isolates were inoculated onto Pikovskaya agar medium containing 0.04% bromocresol purple and incubated at 25°C for one week. It was observed that the isolates turned from reddish to yellow, indicating their ability to dissolve phosphate salts. Among the isolates, CIR 2, CIR 4, CIS 2, and CIL 1 demonstrated the highest phosphate solubilizing activities.

Keywords: *Cichorium intybus,* Chicory, endophytic fungi

LS-4

Immunohistochemical Detection of *Pasteurella Multocida* in Ruminants with Respiratory Illness

Rakshita Sharma, Gulshan Narang, **Paras Saini***, Babu Lal Jangir, Deepika Lather and Vikas Nehra
sainiparas700@gmail.com

Department of Veterinary Pathology, College of Veterinary Sciences, Lala Lajpat Rai University of Veterinary and Animal Sciences, Hisar (125004), Haryana, India

Abstract: The present study was undertaken to examine the immune histo chemical detection of *Pasteurella multocida* (*P. multocida*) associated with respiratory affections in the ruminants. The study was conducted on the ruminant carcasses which had the history of respiratory illness, presented for necropsy to the Post-mortem Hall of the Department of Veterinary Pathology, College of Veterinary Sciences, Lala Lajpat Rai University of Veterinary and Animal Sciences, Hisar. Lung tissue samples were collected during necropsy and fixed in 10% neutral buffer formalin. Immunoperoxidase staining technique was used for detection of *P. multocida* in paraffin-embedded lung tissue sections in a total of 49 cases (including 19 buffaloes, 8 cattle, 6 sheep and 16 goats) having pneumonic lesions. Immunohistochemistry (IHC) by using hyperimmune sera (1:500) raised against *P. multocida* in mice was able to detect *P. multocida* in 31 (12 buffaloes, 3 cattle, 4 sheep, 12 goats) out of 49 cases (63.26%). The immune positive reaction was presented as brown colour staining of variable intensity in the tissue sections. Positive immune peroxidase staining associated with *P. multocida* was detected within the

epithelial cells of bronchi, bronchioles and alveoli. The bacterial antigens were also detected in the desquamated cellular debris present in the lumen of bronchi, bronchioles and alveoli, degenerating neutrophils and macrophages. Apart from this, positive reaction was also observed in the cytoplasm of inflammatory cells. In the corresponding negative controls, no immune reactivity was noticed. The present findings suggest that IHC using hyperimmune sera can be a valuable tool for localizing, understanding the pathogenesis, and diagnosing *P. multocida* infection. Detecting specific bacterial antigens in tissue sections through IHC is recognized as a key method both for diagnosing bacterial infections as well as for studying the pathogenesis of bacterial diseases

Keywords: Immunohistochemistry, lung, *Pasteurella multocida*, ruminant and respiratory affections

LS-5

Isolation and Characterization of Endophytic Bacteria from *Capparis Spinosa* L.

Jabborova Dilfuza[1,2*], Namita Singh[3], Baljeet Singh Saharan[4]
*dilfuzajabborova@yahoo.com

[1]*Institute of Genetics and Plant Experimental Biology, Uzbekistan Academy of Sciences, Kibray 111208, Uzbekistan*
[2]*Faculty of Biology, National University of Uzbekistan, Tashkent 100174, Uzbekistan*
[3]*Department of Bio and Nano Technology, Guru Jambheshwar University of Science and Technology,*
[4]*Department of Microbiology, Chaudhary Charan Singh Haryana Agricultural University, Hisar, India*

Abstract: *C. spinosa* L.is one of the most important herbal plant in the Capparidaceae family. *C. spinosa* possesses several biological activities such as antidiabetic, antioxidant, anticancer hepatoprotective, neuroprotective, anti-inflammatory, anti-arthritic, insecticidal and antibacterial effects. The active compounds associated with these effects mainly include phenolic acids, alkaloids, flavonoids, volatile oils, polysaccharides and. fatty acids. The present investigation highlights the isolation of endophytic bacteria from the medicinal plant (*Capparis spinosa* L.) growing Surkhandarya region and their potential role salt tolerance, antifungal activity, and plant growth-promoting traits. A total of 22 endophytic bacteria were isolated from *Capparis spinosa* L.by standard microbiological culture methods. Eighteen endophytic bacterial isolates showed salt tolerance up to 10% NaCl concentration. Four isolates showed salt tolerance up to 6-8% NaCl concentrations. Studies on plant growth-promoting activity suggested that twelve endophytic bacterial isolates were positive for IAA production, siderophore production, and phosphate solubilization activity. Sixteen endophytic bacterial isolates were screened for the production of enzymes. While studying the antifungal activity of the bacterial isolates, it was determined that sixteen isolates showed antifungal activities against *Fusarium* species.The results showed that endophytic bacteria were isolated from *Capparis spinosa* L. with salt-tolerant and plant growth-promoting activities that were reported, that could be used as inoculants to establish a sustainable *Capparis spinosa* L. production system.

Keywords: *Capparis spinosa,* antidiabetic, siderophore, hepatoprotective

LS- 6

Isolation of Endophytic Fungi from Different Organs of *Rosa Canina L.* and Determination of their Some Extracellular Enzyme Activities

Abdusamatov Sokhibjon[1,2],Numonjon Sultanov[2], **Jabborova Dilfuza[1,2*]**
*dilfuzajabborova@yahoo.com

[1]*Institute of Genetics and Plant Experimental Biology, Uzbekistan Academy of Sciences, Kibray 111208, Uzbekistan*
[2]*Faculty of Biology, National University of Uzbekistan, Tashkent 100174, Uzbekistan*

Abstract: *Rosa canina* L. commonly known as dog rose, is a shrub that grows naturally in Uzbekistan and has been used in traditional medicine for many years to treat and prevent various diseases. Research conducted by scientists has identified several bioactive compounds in different organs of the plant, particularly in its fruits,

which are considered beneficial for human health. Due to its rich content of vitamin C and phenolic compounds, the fruit of *Rosa canina* is highly valued as an effective antioxidant for preventing and even treating various diseases. This plant is also recognized for its antibacterial and antidiabetic properties. Numerous studies confirm that *Rosa canina* helps reduce heart and cardiovascular diseases by lowering blood pressure and cholesterol levels without causing any adverse effects. Additionally, it is effective in treating inflammatory diseases such as osteoarthritis and rheumatoid arthritis. The fruit has shown potential in combating certain types of cancer. Therefore, *Rosa canina* is indeed a valuable and beneficial natural resource, with important medicinal properties confirmed by various studies. However, there is limited research on the endophytic fungi of *Rosa canina*, and the aim of this study is to isolate endophytic fungi from various organs of the plant and characterize their different properties. Samples were collected from the Chotqol nature reserve area in the Bostanliq district of Tashkent region and brought to the laboratory for examination. Microbiological analyses were carried out using standard microbiological methods. The plant organs (roots, stems, leaves, and fruits) were cut into pieces and placed on nutrient agar plates. Czapek-Dox Agar and PDA media were used for the isolation of fungi. The inoculated Petri dishes were incubated at 25°C for 5 days. The resulting colonies were subcultured to obtain pure cultures. A total of 11 fungal isolates were isolated. The extracellular enzyme activities, including cellulase, protease, lipase, catalase, and amylase, were qualitatively analyzed for the isolated strains. The results showed that the isolates *RCR 1* and *RCF 2* exhibited activity for the enzymes mentioned above.

Keywords: Antioxidant, *Rosa canina,* Endophytic fungi

LS-7

Therapeutic Potential of Gut Microbiota-derived p-Cresyl Sulfate for the Treatment of Colorectal Cancer

Manish Kushwaha[1*,2], Akhilesh Kumar Singh[2], Jyoti Jaiswal, Anil Kumar[1]

[1]*Gene Regulation Laboratory, National Institute of Immunology, New Delhi 110067, India*
[2]*School of Life Science, Department of Biotechnology, Mahatma Gandhi Central University, Motihari, Bihar, India*

Abstract: P-Cresyl sulfate (pCS), a gut-derived uremic toxin, is implicated in cellular dysfunction and cancer biology. This study examines the cytotoxic and genotoxic effects of pCS on both colon cancer cells (HCT116) and normal colon epithelial cells (CCD 841) through various in vitro assays. pCS treatment resulted in dose-dependent cytotoxicity, with concentrations ranging from 0.1 to 10 mM. In HCT116 cells, pCS induced significant oxidative stress, leading to DNA damage, cell membrane disruption, and lactate dehydrogenase (LDH) release, culminating in cell death. Additionally, pCS caused cell cycle arrest in the S phase, reducing the colony-forming ability of cancer cells. A time- and dose-dependent reduction in intracellular ATP content was observed after 24, 48, and 72 hours of treatment. Notably, pCS exhibited selective toxicity, with threefold less detrimental effects on normal colon cells compared to cancer cells, suggesting a potential role in selective anticancer activity. Mechanistic insights revealed that pCS disrupts mitochondrial function, leading to elevated oxidative stress and cellular damage. These findings underscore the role of gut microbiota-derived metabolites, such as pCS, in contributing to colorectal cancer pathogenesis and overall gastrointestinal health. The selective impact on cancer cells highlights pCS as a potential target for therapeutic intervention. Further research is necessary to elucidate the molecular pathways involved and to explore therapeutic strategies aimed at mitigating pCS-induced cellular damage in cancer and normal tissues.

Keywords: p-Cresyl Sulfate, Gut Microbiota, Colorectal Cancer, uremic toxin

LS-8

Targeting Dephospho Coenzyme A Kinase (DPCK) in *Leishmania donovani*: Discovery and Validation of steroidal alkaloids as Potent anti-leishmanial drugs

***Naveena Menpadi,** *Pranjal Chandra, *Vikash Kumar Dubey
*naveenamenpadi.rs.bce19@itbhu.ac.in

**School of Biochemical Engineering, Indian Institute of Technology (BHU), Varanasi (221005), Uttar Pradesh, India*

Abstract: Leishmaniasis, commonly known as "kala-azar," remains a critical health challenge in India, indicated by rising drug resistance among parasites. In our research, we targeted the Dephosphocoenzyme A kinase (LdDPCK) of *Leishmania donovani* to inhibit Coenzyme A synthesis, aiming to eliminate theparasite. Using molecular docking and simulations, Veratramine and Hupehenine were screened from a natural products database, which was demonstrated by strong binding affinities for LdDPCK. The *in-silico* findings were further verified by *in-vitro* assays, which revealed that IC_{50} of Hupehenine and Veratramine as 7.34 ± 0.37 µM and 12.46 ± 2.28 µM, respectively. Through a series of *in-vivo* validations, we confirmed that the inhibitory effects of Hupehenine and Veratramine are primarily mediated through the induction of autophagy, a cellular process where cells degrade and recycle their components. Unlike other drugs, which show typical cell death by apoptosis, evidence indicates cell death involving autophagy, which was further, validated using CYTO-ID staining. This study shows the potential of Veratramine and Hupehenine as effective anti-leishmanial agents and attributes the importance of DPCK as a drug target against *Visceral Leishmaniasis*. Our conclusions are supported by flow cytometry, which confirmed the absence of apoptosis markers; ultrastructural imaging, which provided visual evidence of toxicity; and fluorescence imaging, which highlighted the visual evidence of autophagic vacuole formation. Furthermore, the upregulation of ATG genes, revealed by real-time PCR, provides molecular confirmation of autophagy induction. This study identifies steroidal alkaloids, Veratramine and Hupehenine as potent inhibitors of the LdDPCK enzyme, providing a new mechanistic insight into their action through autophagy-mediated cell death. These findings pave the way for developing novel therapeutic strategies against Visceral Leishmaniasis, particularly in overcoming the challenge of drug resistance in *Leishmania* parasites.

Keywords: *Leishmania donovani*, *Visceral Leishmaniasis*, Coenzyme A, Dephospho-coenzyme A kinase, Hupehenine, Veratramine

LS-9

Potential Plant Growth-Promoting Rhizobacteria Ccumula the Cadmium Stress Tolerance in Tomato (*Solanum lycopersicum* L.)

Rajganesh Marappa[1], Rahul Krishnappa, Renuga Selvakumar, Srinivas Chowdappa
*rajaganesh035@gmail.com

Fungal Metabolite Laboratory, Department of Microbiology, Biotechnology, and Food Technology, JnanaBharathi Campus, Bangalore University, Bangalore (560 056), India

Abstract: Accumulation of cadmium (Cd) in the soil is an increasing ecological threat to field crops and is frequently listed as the main obstacle to global agricultural production. Furthermore, it is anticipated that they will become more prevalent and serious in the future. Plant-growth-promoting rhizobacteria (PGPR) can alter the bioavailability of heavy metals. Consequently, in the current study, we screened novel strains of *Bacillus firmus* and *Bacillus subtilise*, which we applied to tomato seedlings. The germination percentage ,vigouras index and seedling growth were enhanced in pgrpr treated Cd(0.40 M) stress conditions and pot trial experiments conducted in greenhouse conditions revealed that Cd (50 mg/kg after 15 days) experienced a positive effect on pgprs treated tomato plant was comparatively better, germination percentage, vigorosindexas and the biomass, Cd tolerance index, balancing the micro, macro elements and decrease in the Cd ccumulation in *Bacillus firmus* (35.98, 458.39 ppm), *Bacillus subtilise* (41.68, 282.39ppm) compared to controle (60.14 ,643.97 ppm) in leaf and root respectively, Therefore, the application of multifunctional plant-growth-promoting bacteria

exhibiting resistance to Cd may result in better growth of tomato under stress. This may also improve the remediation of contaminated sites by alleviating Cd-induced phytotoxicity and promoting the growth of plants.

Keywords: Cadmium, PGPRs, *Bacillus firmus*, *Bacillus subtilise.*

LS-10

Green Synthesis of Zinc Oxide Nanoparticles from *Clitoria ternatea* and its Bioactive Potential

Rahul Krishnappa, Rajganesh Marappa, Renuga Selvakumar, **Srinivas Chowdappa***
srinivasbub@gmail.com

Fungal metabolite laboratory, Department of Microbiology, Biotechnology and Food Technology, Jnana Bharathi Campus, Bangalore University, Bangalore (560056) India

Abstract: Green synthesis of zinc oxide nanoparticles (ZnO NPs) has been promoted as an environmentally-friendly, cost-effective and high yield method. The present study reports the biosynthesis of zinc oxide nanoparticles (ZnO NPs) using *Clitoria ternatea* plant extract and examination of their antibacterial activity. The change in color of the reaction mixture from violet to yellow colour indicated the formation of ZnO NPs. The synthesized silver nanoparticles were characterized by UV-Vis spectroscopy, FTIR, SEM, EDS, TEM, and XRD. The formation of ZnO NPs was confirmed by the appearance of a maximum absorption peak at 360 nm in the UV-visible spectrum. The XRD pattern corresponding with the JCPDS card for ZnO showed the presence of pure crystalline ZnO NPs. FTIR spectra confirmed the stretching vibrations of C=O, C–O–H, and O–H groups involved in the reduction of ZnO NPs. The size and surface morphology of the ZnO NPs were confirmed by Transmission Electron Microscopy (TEM). Furthermore, the antibacterial activity of ZnO NPs showed significant inhibitory activity against *Escherichia coli* and *Staphylococcus aureus* bacteria.

Keywords: Biosynthesis, Zinc oxide nanoparticles, Characterization, XRD, Antibacterial Activity.

LS-11

Isolation and Identification of *Stenotrophomonas maltophilia* from Upper Respiratory Tract of Equines

Sumanshu[1], Ritu Rani[1], Jyoti Bakshi[1], Taruna Anand[1], R.K. Vaid[1,*]
sumanshunarwal@gmail.com, *rk_vaid@yahoo.com

[1]*National Centre for Veterinary Type Culture Collection, ICAR-NRCE, Hisar, Haryana (125001)*

Abstract: *Stenotrophomonas maltophilia*, a Gram-negative, glucose non-fermenter, is one of the most underestimated multidrug resistant bacteria in both human and animal populations. Since it has been recently associated with lower airway disease in the horse and has been considered an emerging opportunistic nosocomial pathogen of humans, we therefore studied the prevalence of *S. maltophilia* in equines and pattern of antimicrobial resistance in isolates from nasal swabs of horses from north Indian states received in this laboratory. A total of 83 nasal swab samples of equines were processed during the period of last 7 months. Samples were cultured on 5% sheep blood agar, nutrient agar and MacConkey lactose agar. Suspected colonies were characterized through Gram staining and further identification of the isolates was performed using biochemical tests and API Kit. The resistance pattern against 14 antibiotics was determined using the Kirby-Bauer disk diffusion method. Out of 83 nasal swabs processed for bacteriological examination, a total of (132) bacterial isolates were picked up for identification. A total of 13 *S. maltophilia* (9.84%) isolates were identified alongwith a few significant pathogens viz. *Streptococcus* spp, *Staphylococcus* spp, *Nocardia* spp. Most of the *S. maltophilia* isolates were resistant to carbapenems, cephalosporins, beta-lactams and aminoglycosides including one of the isolates intermediate to Co-trimoxazole. Intermediate pattern against Co-trimoxazole can be point of concern as it is the drug of choice for treatment. Since *S. maltophilia* is reported from humans with chronic respiratory disease, e.g. cystic fibrosis or chronic obstructive pulmonary disease, its presence underscores the

need for biosecurity measures in stables and veterinary practices to prevent potential zoonotic transmission. This study highlights the importance of monitoring *S. maltophilia* in equine populations, as its identification in nasal swabs can be indicative of underlying respiratory pathology.

Keywords: *S. maltophilia*, Antimicrobial resistance, Equines, Respiratory disease, Zoonosis, Biosecurity.

LS-12

Influence of Chemicals and Bioagents on Physiological Parameters under Drought Stress in Upland Cotton (*Gossypium hirsutum L.*)

Ande Aravind Reddy*, Shiwani Mandhania, Vikram Singh, Rashi Datten, and Arman Khan
*aravindande143@gmail.com.

**Department of Biochemistry, Division of Basic Sciences and Humanities, Chaudhary Charan Singh Haryana Agricultural University, Hisar-125004, India*

Abstract: Climate change significantly lowers the productivity of crops and plants, exposing them to various biotic and abiotic stresses, which in turn diminishes their yield and the economic returns for farmers. Cotton, often referred to as 'White Gold' due to its value, faces two primary abiotic stresses: salinity and drought. In this study, cotton is subjected to drought stress, and at the crop's full bloom stage, different chemicals such as trehalose, acetic acid, abscisic acid, and chitosan, along with their combinations, are sprayed at varying concentrations to examine their effects on mitigating physiological losses. We evaluated the impact of drought stress on several physiological parameters, including total chlorophyll content, anthocyanin content, plant height, and specific leaf weight, using various instruments. Our findings indicate that drought significantly reduces cotton yield, but acetic acid treatment shows the most promise among all the treatments tested, promising further investigation.

LS-13

Monascus purpureus: A Potential Source for Natural Pigment

Nikita[1], Aastha Dewan[1*]
23aastha10@gmail.com

Department of Food Technology
Guru Jambheshwar University of Science and Technology, Hisar, Haryana

Abstract: There is upsurge in natural edible colors due to substantial health concerns associated with artificial colors. *Monascus purpureus*, a red mold that grows on starchy substrates, traditionally cultivated through solid state fermentation of rice in East Asia since at least the first century A.D. Optimum growing conditions occurs at 28°C - 30°C and a pH range of 4.5-8.5, with maximum biomass at pH 4.5, where yellow-orange pigment dominates. However, the highest red pigment production occurs at room temperature with pH 5.5. The typical representatives of this group are the pigments produced by the mold *Monascus* spp. which includes orange pigments (Monascorubin and Rubropunctatin), yellow pigments (Monascin and Ankaflavin), and red pigments (Monascorubramine and Rubropunctamine).
Commercial red certified FD&C dyes like Erythrosine and Allura Red are commonly used in processed foods but have been linked to negative health effects such as DNA damage, colonic inflammation, and altered gut microbiota. Switching to microbial colors can mitigate these hazardous effects while also providing health benefits like antioxidant, antimicrobial, and antifungal properties. *Monascus* pigment demonstrates thermal stability below 50°C under neutral and alkaline pH conditions. It is widely used in food products like candies, bread, beer, yogurt, and meat, serving as a health-friendly biocolor without compromising sensory and functional attributes. However, issues such as toxic effects, interactions with metallic ions, and regulatory hurdles need further investigation. To deduce, *Monascus* pigment seems to be a promising pigment which can be employed in food for its colorant function and positive health benefits.

Keywords: Antioxidant activity, Colonic inflammation, DNA damage, *Monascus* pigment.

LS-14

In silico bio-prospecting and Chemoinformatics Screening of Potential Inhibitors against Drug Resistant *Acinetobacter baumanii* and *Pseudomonas Aeruginosa*

Sinosh Skariyachan
23aastha10@gmail.com

Department of Microbiology, St. Pius X College Rajapuram, Kasaragod-Kannur University, Kerala, India

Abstract: Multidrug-resistant *Acinetobacter baumannii* (MDRAb) and *Pseudomonas aeruginosa* (MDRPa) were declared as priority-I & II pathogens, respectively by WHO (2019) and screening of potential therapeutic agents have profound scope and applications. This study aimed to identify natural lead molecules as potential inhibitors against MDRAb and MDRPa by *in silico* bioprospecting. Based on the metabolic pathway analysis, protein RecA (RecA) and orotate phosphori bosyl transferase (PyrE) were identified as potential drug targets for MDRAb. The three-dimensional structure of RecA and PyrE were computationally predicted. A library natural molecules were constructed and subjected to virtual screening, molecular docking, and molecular dynamic simulation. The therapeutic potential of computationally predicted molecules was validated by *in vitro* studies. Computational screening suggested that out of 236 molecules selected from the library, 06 leads were qualified for drug likeliness, and pharmacokinetic features, and one molecule-natural epiesteriol exhibited significant binding towards RecA and PyrE in comparison with the binding of faropenem and polymyxin E towards their usual targets. MD simulations suggested that epiesteriol-receptor complexes demonstrated stability throughout the simulation. The *in vitro* assay substantiated the finding. Similarly, Celastrol in *Celastrus paniculatus* and Rotiorinol in *Chaetomium cupreum* showed better binding with GacA (binding energy -7.2 kcal/mol) and RhlR (binding energy -8.0 kcal/mol) of MDRPa, respectively, when compared to the binding of Meropenem and its target. MD simulation studies and the *in vitro* studies confirmed the inhibitory potential of these molecules ($p \leq 0.05$). The present study suggested that natural molecules screened by *in silico* bioprospecting can be used as potential binders towards the identified targets of MDRAb and MDRPa.

Keywords: Drug-Resistant *Acinetobacter baumannii, Pseudomonas aeruginosa, In Silico* Bioprospecting, Chemoinformatics, Molecular Docking, Molecular Dynamic Simulation

LS-15

Development of Whey-Kodo Millet Based Probiotic Product and Its Bioactivities

Nikita Yadav*, Aayushi Rohilla, Savi Khurana, Navnidhi Chhikara
navnidhi24@gmail.com*Department of Food Technology,*

Guru Jambheshwar University of Science & Technology, Hisar, India

Abstract: Millets are considered as sustainable solution to nutritional and food security and have been recommended as "ShriAnna". Kodomillet contains around carbohydrates (65-70%), proteins (6-8%), fat (1-2%), ash (2-3%) along with substantial amount of various bioactive compounds. The present study was planned to prepare a novel synbiotic product using kodo millet as prebiotic source and whey protein as protein source. A mixture of the defatted kodo millet flour (15%), whey protein (5%), with TSS at 11°brix was subjected to lactic acid fermentation using *lactobacillus acidophilus* at 37°C for 24 hrs in incubator. *Lactobacillus acidophillus* was selected as probiotic microorganism for this study based on superlative experiments. After fermentation, probiotic product reported 10.18% protein content with 61.98% *in-vitro* protein digestibility. This might be due to structural breakdown of complex proteins into smaller oligopeptides, reduction in various anti-nutritional factors and enhanced proteolytic activity resulting in conversion of insoluble protein fragments into soluble proteins. The fermented kodo millet extract exhibited significant increase in radical scavenging activity from 26.64% to 81.34% as assessed through 2,2 diphenyl 1-picrylhydrazyl activity. The fermented kodo millet flour ethanolic extract was found to be effective against *Escherichia coli* and *Staphylococcus aureus* as evident from inhibition zones. The substantial increase in various bioactive and functional compounds is well supported by Fourier Transform Infrared Spectroscopy. The study advocated the potential of kodomillet in functional food formulation and possibilities to meet sustainable development goals.

Keywords: Millets; Nutritional security, Antimicrobial activity, Digestibility, Sustainability

AWARDEES CITATIONS

ASSOCIATION OF MICROBIOLOGISTS OF INDIA

AMI-Life Time Achievement Award

(2024)

Prof. Kamla Chaudhary

Prof. Kamla Chaudhary belongs to Hisar, Haryana. She had her early education from Government Primary School sector 23, Chandigarh 1955-60 and GGHS School, Sector 18C, Chandigarh, 1960-1965. She completed her B.Sc. degree in Medical from Government college (Panjab University) Hisar in 1968. She joined M.Sc Microbiology at Punjab Agricultural University, Hisar Campus (later on in 1970 HAU Hisar) and completed M.Sc Microbiology in 1970. Prof. Chaudhary joined Microbiology department as Research Assistant/Lecturer in 1970 and started research on Citric acid fermentation by *Aspergillus niger* using cane molasses and taught UG students practical course of Basic Microbiology. Later on a solid state fermentation process was developed for citric acid production and published a number of papers in national and international journals. She joined Ph.D in 1976 and worked on cellulase production by *Trichoderma reesei.* She completed her Ph.D in 1981 and continue to Microbiology courses and do research in Microbiology department till 1997. Later on, she joined the department of Biotechnology and Molecular Biology in 1997 and became HOD in 1998. She continued to teach Biotechnology and Molecular biology courses and do research in department till 2008. After superannuation she joined back the BMB department as Emeritus Scientist ICAR, 2008. She worked as Emeritus Fellow UGC, Department of Bio-Nanotechnology, Guru Jhambheshwer University of Science and Technology, Hisar; from 2009 to 2011 and later on as Professor Emeritus, Department of Microbiology, Maharshi Dayanand University, Rohtak, Haryana, till 2017. She has more than 100 publications in national and international journals which include research papers, book chapters and practical manuals. She has granted 03 patents which highlight innovative contributions in the fields of agricultural biotechnology and bioenergy, focusing on sustainable solutions for pest control, ethanol production, and biomass fractionation.

In view of the contributions in area of Agriculture Microbiology, which are of both fundamental and applied values, Prof. Kamla Chaudhary efforts are recognised by AMI in conferring her AMI-Lifetime Achievement Award on 16 November, 2024.

Namita Singh

Prof. Namita Singh
General Secretary

Sr. No.-AMI-Award 2024/

Dr. S.K. Khare
President

ASSOCIATION OF MICROBIOLOGISTS OF INDIA

AMI-Life Time Achievement Award

(2024)

Dr. (Mrs.) Praveen Rishi

Dr. Praveen Rishi is a distinguished Professor (Retd.) from the Department of Microbiology at Panjab University, Chandigarh. She holds extensive experience in the field of Medical Microbiology, with over 25 years of academic and research expertise. Her primary research areas include antimicrobial resistance, biotherapeutics, immunosensors/biosensors, and the development of diagnostic tools, particularly in relation to enteric fever (such as typhoid and paratyphoid). She has been involved in pioneering work on combating emerging antibiotic resistance through the development of innovative strategies that include the use of antimicrobial peptides, enzymes, probiotics, and vaccines. Her research on biosensors for diagnosing enteric fever has led to her obtaining a patent for the technology and establishing a Memorandum of Understanding (MoU) with the industry to advance the development of a diagnostic kit. In addition to her research accomplishments, She has a robust publication record, with 170 publications in high-impact journals, including review articles (6), book chapters (6), and research articles (158). She is also a book editor, having contributed to significant publications like Probiotic Research in Therapeutics: Modulation of Gut Flora (2021) and Role of Microbes in Sustainable Development: Human Health and Diseases (2023). She has supervised 30 Ph.D. candidates, with one ongoing project. She is recognized for her leadership roles and has served as the First Woman Dean of the Faculty of Science at Panjab University (2015-2017). She has been an active contributor to academic and professional societies, including serving as the President of the Association of Microbiologists of India (AMI) in 2022. Furthermore, she has been a member of the Central Council of AMI since 2017. Dr. Rishi's other administrative contributions include her role as Chairperson of the Department of Microbiology at Panjab University (2014-2017) and as the CET-UG Admissions Coordinator for two consecutive years. She also serves as an editor for leading academic journals, such as the Indian Journal of Microbiology and Plos ONE.

In view of the contributions in area of Medical Microbiology, which are of both fundamental and applied values, Dr. (Mrs). Praveen Rishi efforts are recognised by AMI in conferring her AMI-Lifetime Achievement Award on 16 November, 2024.

Namita Singh

Prof. Namita Singh
General Secretary

Sr. No.-AMI-Award 2024/

Dr. S.K. Khare
President

ASSOCIATION OF MICROBIOLOGISTS OF INDIA

AMI-Life Time Achievement Award

(2024)

Prof. Narsi Ram Bishnoi

Prof. Narsi Ram Bishnoi, born on June 8, 1961, in Jandwala, Haryana, has over 30 years of experience in research and teaching. He served as a Professor of Environmental Science and Engineering at Guru Jambheshwar University of Science and Technology (GJUST), Hisar, for more than 15 years. Prof. Bishnoi has held key administrative roles at GJUST, including Head of the Department, Dean of multiple faculties, and Dean of Research.With expertise in cleaner technologies, he has supervised 22 Ph.D. theses, 78 M.Tech. dissertations, and published nearly 170 research papers. He has completed R&D projects funded by UGC, AICTE, and HSCST, and coordinated the DST-FIST program at GJUST. Prof. Bishnoi also managed the university's Central Instrumentation Laboratory for four years.He holds an M.Sc. and Ph.D. in Plant Physiology from CCSHAU, Hisar, and is ranked among the top 2% of scientists globally (Stanford University, 2020-2022). He has over 6,300 Google citations, an h-index of 43, and an i10 index of 84. His awards include the NESA Fellowship (2021), Best Scientist Award (2015), and Rashtriya Gaurav Award (2010).

Prof. Bishnoi has served on various academic councils, professional bodies, and committees, and collaborated with international and national institutions.

Administrative Experience:

- Dean of Research w.e.f. September 2nd, 2019 to June 30th, 2021.
- Dean of Colleges w.e.f. April 1st, 2016 to May 26th, 2019.
- Dean of Law from w.e.f August 24th, 2017 to December 10th, 2018.
- Dean of faculty of Non-conventional sources of Energy and Environmental Sciences from March 15th, 2008 to March 14th, 2011.
- Chairman, Department of Environmental Sciences and Engineering from August 14th, 2008 to August 13th, 2011.

No. of Publications:

175 with Google H-index 44, Google citation 6564, Google i-10 index 86, Scopus H-index 36 and Scopus citation 4118 Books Published: 4 (on Religion and Environment) Thesis Supervised: Ph.D. awarded-21 and in progress-04 M.Tech awarded-77

Awards and Achievements:

- NESA Fellowship of The Year Award-2021 by National Environmental Science Academy, New Delhi.
- Ranked among top 2% of the world scientist listed by Standford University, USA in 2020 & 21.
- Dr. S.A. Salgare's Best Scientist Award-2019 conferred by Indian Academy of Environmental Sciences, Hardwar.
- Best Scientist Award-2015 conferred by National Environmental Science Academy, New Delhi.
- Certificate of Honor by the Department of Plant Breeding, CCS HAU, Hisar for development of Hybrid HHB 94 of Bajra in January, 2001.
- Certificate of Honor by the Department of Plant Breeding, CCS HAU, Hisar for development of Composite of HC 10 of Bajra in January, 2001

In view of the contributions in area of Agriculture Microbiology, which are of both fundamental and applied values, Prof. Narsi Ram Bishnoi efforts are recognised by AMI in conferring his AMI-Lifetime Achievement Award on 16 November, 2024.

Namita Singh

Prof. Namita Singh
General Secretary

Sr. No.-AMI-Award 2024/

Dr. S.K. Khare
President

भारतीय जीवाणुतत्ववेत्त संगठन
Association of Microbiologists of India

ASSOCIATION OF MICROBIOLOGISTS OF INDIA

Prof. Sarman Singh

Prof. Sarman Singh is a medical scientist, with more than 40 years of experience in the field of medicine. He joined AIIMS, Delhi in 1988, and in 2018, he was selected as Director of AIIMS, Bhopal. He superannuation in November 2021 from AIIMS. He was also founder Director-in-Charge of AIIMS, Hyderabad. Currently he is Director of Medical Research, at AVMC&H, Pondicherry. He holds 7 Fellowships and 25 memberships of various Academies and Societies. He has received more than 30 national and international awards. He has 8 patents, and one technology was taken up by Govt of India which played significant role in kala-azar elimination from India. Prof. Singh has supervised 32 PhDs, 40 DM/MD/MS and more than 40 MSc. students. His outstanding publication record includes 6 books, 52 chapters and 375 research papers in reputed journals, with a total citation of 15200, i10 index of 244 and H-index of 64, he is listed in the world's top 2% Scientist by Stanford University /Elsevier for the last 5 consecutive years. He is editor-in-chief of Journal of Laboratory Physicians (JLP), Editor of Medicine, PLoS-One, PLoS-NTD and TRT, besides being on the editorial boards of more than 40 national and international journals.

In view of the contribution in several area of microbiology, which are of both fundamental and applied value, Prof. Sarman Singh efforts are recognised by AMI in conferring him fellow of Academy of Microbiological Sciences on 16 November, 2024.

Namita Singh

Prof. Namita Singh
General Secretary

Sr. No.-AMI-Award 2024/

Dr. S.K. Khare
President

भारतीय जीवाणुतत्ववेत्त संगठन
Association of Microbiologists of India

ASSOCIATION OF MICROBIOLOGISTS OF INDIA

Prof. Sunil Pabbi

Prof. Sunil Pabbi, Former Principal Scientist was professionally employed at ICAR-Indian Agricultural Research Institute, New Delhi & served for over 37 years. His research contributions are in applied microbiology/phycology on use of microalgae/cyanobacteria as biofertilizer and other value-added products. Dr. Pabbi has developed a commercially viable technology for year-round production of quality BGA biofertilizer with high titer, longer shelf life and lesser application dose. The technology has been licensed to six private companies. BGA based liquid formulation was also developed and validated. These technologies have greater acceptance among farmers and commercial houses. BGA technology is now a recommended practice in INM and organic farming. He isolated several indigenous cyanobacteria that showed enhanced phycobiliprotein production with pharmaceutical and analytical grade purity and outperformed Arthrospira in C-phycocyanin (C-PC) production. These novel strains were deposited to culture collections for future use and upscaling, the molecular sequences deposited in public database GenBank, NCBI. The identification of potential cyanobacteria and process optimization has economized high value C-PC production having application in food, feed, pharmaceuticals and nutraceuticals. A patent was granted for this novel process. Spirulina enriched functional foods were also developed by him leading to nutritional and functional fortification without any detrimental changes in textural/sensory attributes. Dr. Pabbi has so far carried out 16 research projects, has over 164 publications, authored two and edited 7 books. He was Co-ordinator of DBT, GoI funded multi-institutional project on cyanobacterial biopigments and also CCPI of other multi-institutional and overseas collaboration projects. He visited USA, EU, Israel etc. on scientific assignments and received overseas fellowships. He is recipient of Prof. Y S R K Sarma Memorial Award 2013 and Distinguished Scientist Award 2019 by Society for Plant Research and Prof. S R Vyas Memorial Award 2018 of Association of Microbiologists of India (AMI). He has guided several M.Sc./Ph.D. students and was awarded Best Teacher Award of ICAR-IARI for excellence in teaching and Best Professor in Microbiology Award by Agriculture Innovation Congress and CMO Global. Dr. Pabbi also served as member of Specialized Products Sectional Committee (FAD 24), Bureau of Indian Standards (BIS) and Sub-technical Committee of Central Bio-stimulant Committee, MA&FW, Govt. of India. He is also nominated as Distinguished Honorary Advisor and Member, Board of Studies of several universities in India and is immediate Past PRESIDENT, Association of Microbiologists of India. He was involved in development of PG course of Indo-Myanmar- Advanced Centre for Agricultural Research & Education at Yezin Agricultural University, Myanmar and has successfully completed HRD projects funded by NATP, ICAR and DST, GoI as PI and conducted 28 training programs as Course Director/Coordinator. Dr. Pabbi spearheaded and facilitated popularization, demonstration, licensing and commercialization of microbial technologies and generated handsome revenue for the Institute.

In view of the contribution in several area of microbiology, which are of both fundamental and applied value, Prof. Sunil Pabbi efforts are recognised by AMI in conferring him fellow of Academy of Microbiological Sciences on 16 November, 2024.

Namita Singh

Prof. Namita Singh
General Secretary

Dr. S.K. Khare
President

Sr. No.-AMI-Award 2024/

भारतीय जीवाणुतत्ववेत्त संगठन
Association of Microbiologists of India

ASSOCIATION OF MICROBIOLOGISTS OF INDIA

AMI Prof. S R Vyas Award

Dr. Reddy Shetty Prakasham

Dr. Reddy Shetty Prakasham, Emeritus Scientist and Ex Chief Scientist at CSIR-Indian Institute of Chemical Techonology (CSIR-IICT), Hyderabad. He completed his Doctoral Degree from North-Eastern Hill University, Shillong on Cyanobacterial Biological Nitrogen Fixation in 1990 and subsequently served in Centre for Cellular and Molecular Biology as Research Associate and developed Anti-sense RNA for TMV.

Dr Prakasham started his independent research carrier at CSIR-North East Institute of Scientist and Technology, Jorhat in 1991 and contributed on Microbial Enhanced Oil Recovery. Upon joining at CSIR-IICT, Hyderabad continued to explore the microbial systems for their application at industrial sectors through understanding the basics mainly modulation of microbial metabolic principles in improving the productivity either by adapting new nutritional or physiological environment with the utilization of renewable resources.

Dr Prakasham was instrumental in development of bioprocess for alkaline protease – a leather industry useful enzyme, recombinant L-asparaginase – an anticancer enzyme use in the treatment of lymphoblastic leukemia, recombinant Uricase and showed its application at Gout treatment, alfa glucans – a neutraceutical and sustrainable drug release compound as well as wound healing product, xylanase enzyme complex – for production of xylooligosaccharides for colon cancer abatement, xylitol – a diabetic and non-insulin based sweetner by using isolated microbial systems from different virgin environments. One of his notable research activities is isolation of mutanase producing *Paracoccus* strain and its application as biocontrol as well as dental carries reduction. His contributions led to development of a couple of industrial friendly technologies.

Dr Prakasham published more than 200 research articles in peer reviewed scientific journals and has 12 patents to his credit. Throughout his carrier, he was involved in human resource development and supervised several Ph.D., M.Phill students and more 250 M.Sc. /M.Tech/M.Pharm project students. He established collaborative research activities at international level with UK, Canada and USA along with national research institutions such as ICRISAT, DSR, IMTECH, different IITs etc.

Dr Prakasham received several recognitions at National and International level as visiting professor at Rothemsted Institute, UK, NSERC, Canada, etc and received several awards like Eminent Teacher, Established Scientist, Pharmaceutical award, Talent Industrial Biotechnology, Gaurav Samman etc. He is a fellow of several scientific academies viz. AP Academy of Sciences, Telangana Academy of Sciences, ABAP, Society of Biological Sciences, Society of Applied Biotechnology, etc.

The Association of Microbiologists of India is pleased to honor Prof. Dr Reddy Shetty Prakasham with AMI-Prof. S R Vyas Award for 2024 for his outstanding credentials and contributions to the profession of Microbiology.

Prof. Namita Singh
General Secretary

Dr. S.K. Khare
President

Sr. No.-AMI-Award 2024/

भारतीय जीवाणुतत्ववेत्त संगठन
Association of Microbiologists of India

ASSOCIATION OF MICROBIOLOGISTS OF INDIA

AMI- Louis Pasteur Award

Prof. Namita Singh

Prof. Namita Singh is a Professor at the Department of Biotechnology at Guru Jambeshwar University of Science & Technology, Hisar, Haryana. She is the Dean of International Affairs at GJUST, Hisar. She is the General Secretary of the Association of Microbiologists of India from 2020 to till date.

She started her career as an Assistant Professor at the Department of Biotechnology at Guru Jambheshwar University of Science and Technology, Hisar, presently serving as a professor of Microbial Biotechnology at the Department of Biotechnology, Guru Jambeshwar University of Science & Technology, Hisar, Haryana. She has more than 22 years experience in teaching, administration, and research.

She has supervised nearly 22 Ph.D. thesis and mentored more than 300 M.Sc/M.Tech and under-graduate students. She authored more than 200 reseearch articles in peer reviewed scientific journals, 03 patents, 05 textbooks, 18 technical reports in his credit

She is the part of organizing committee of 12 International Conference as Convenor, Core committee member, Organizing Secretary, co-organizing secretary etc. She also organized 08 international workshop, more than 100 national workshop and more than 200 webinars. She develop 08 technical course. She guided more than 08 Entrepreunar for establishment of their unit under her mentorship. She has been successfully able to receive and complete around 26 Government funded projects and has made several academic visits both nationally and internationally. She has delivered more than 100 lectures in the area of Biotechnology, Microbiology, and Metagenomics at various national and international platforms.

Prof. Namita Singh specialized in the area of microbial diversity, Algal Biotechnology, Microbial Biotechnology, Bioremediation, Enzyme production, Biofuel Production, food science, and technology and product/process development. She has extensively explored the application of microbes in the field of Food Feed and Environment (published over more than 250 bacterial species), sequenced more than 10 bacterial genomes, carried out comparative genomics (more than 2 projects) and metagenome analysis (five metagenomes/microbiome). Her research has led to the identification and functional characterization by using metagenomic approaches for the characterization of Microbial consortium isolated and developed for environmental application. Her group has also explored microbial diversity and its role in the degradation of food waste for biohydrogen production and PAH degradation.

Professor Singh was Chairperson of the Department of Biotechnology, (2014-2017), Chairman BOSR (2014-2017), Coordinator DBT-HRD Program (2014-2017), Coordinator DBT-BIF Program, Deputy Coordinator SAP DRS-I and II, Dean of International Affairs (2023 to date) Member of Executive Council and Academic Council and member of several national and international bodies. She is a member of various committees of UGC, DBT, CSIR, DST, MOEF, FSSAI, FAO, AMI. One GIAN program for 21 days. International workshops etc. She is the first woman General Secretary of a leading scientific organization ie. Association of Microbiologists of India (2020-2023, 2023- to date). Under her tenure AMI-Hisar Unit awarded Best Unit Award consecutively 04 times.

She has been awarded several prestigious honors by the UNESCO-American Society for Microbiology, the EP Odum Gold medal by the International Society for Ecological Communication, Hungary, Jacob Bloustine Post-Doctoral Fellowship, ISRAEL, Young Scientist Award by MPCST, Bhopal, and multiple best presentation awards in. several national as well as international conferences. Her contribution to the field of microbiology is well recognized and appreciated across the country.

The Association of Microbiologists of India is pleased to honor Prof. Namita Singh with AMI- Louis Pasteur Award for 2024 for her outstanding credentials and contributions to the profession of Microbiology.

Namita Singh

Prof. Namita Singh
General Secretary

Dr. S.K. Khare
President

Sr. No.-AMI-Award 2024/

भारतीय जीवाणुतत्ववेत्त संगठन
Association of Microbiologists of India

ASSOCIATION OF MICROBIOLOGISTS OF INDIA

AMI- Louis Pasteur Award

Dr. Mahesh S Dhar

Dr. Mahesh Dhar is currently working as Vice-President (Research) at Sunny Corporation Pvt Ltd since March, 2022. Earlier he served as Assistant Director (Microbiology) at National Centre for Disease Control, MoH&FW where he established the Covid-19 testing & SARS-CoV2 sequencing facility. He drafted the constitution of Indian National SARS-CoV2 Genomics Consortium also called INSACOG in December 2020 and later was the highest contributor of the SARS-CoV2 genome sequence database in India. Before joining NCDC in May, 2019, he was working as an Assistant Professor at Amity University. Dr. Mahesh has successfully completed two research projects including the highly competitive Biotechnology Ignition Grant from BIRAC and DST-SERB Young investigator startup grant. He completed his Doctorate from Microbial Pathogenicity Lab, Dept. of Microbiology, University of Delhi in 2014. Dr. Mahesh is a Life Member of AMI since 2013. He has authored more than 20 research articles in reputed Journals like Nature, Science and Nucleic Acid Research with a citation score of more than 2300; and has been bestowed with AMI-Young Scientist Award in 2019 and Dr. R. S. Rana memorial Best poster prize in 2023.

Dr. Mahesh's lab contributed to the understanding of SARS-CoV-2 epidemiology and helped in the disease surveillance of various variants across India. As the first fully automated Covid-19 testing lab, his team catered to samples from 10 states and UTs and sequenced samples from 14 states. He played a pivotal role in establishing two relief centers for evacuees coming to India from abroad during first Covid-19 wave. As a Microbiologist, his contribution to the society have been acknowledged through this award.

The Association of Microbiologists of India is pleased to honor Dr. Mahesh S Dhar with AMI- Louis Pasteur Award for 2024 for his outstanding credentials and contributions to the profession of Microbiology.

Prof. Namita Singh
General Secretary

Dr. S.K. Khare
President

Sr. No.-AMI-Award 2024/

भारतीय जीवाणुतत्ववेत्त संगठन
Association of Microbiologists of India

ASSOCIATION OF MICROBIOLOGISTS OF INDIA

AMI-G. S. Rangasamy Memorial Award

Dr. Livleen Shukla

Dr. Livleen Shukla received a B.Sc. degree in (Chemistry, Botany and Zoology) from University of Delhi in 1986; M.Sc. Microbiology from South Campus, University of Delhi, New Delhi and a Ph.D in Microbiology from ICAR-Indian Agricultural Research Institute, Pusa, New Delhi-110012. Dr Shukla is presently working as Principal Scientist at Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi, India. She joined as a Scientist at IARI, New Delhi w.e.f. 10th November 1993. She is a life member of the Association of Microbiologist of India (AMI) and International Society for Molecular Plant-Microbe Interactions. She has been working on Recycling of Agri-Residue management (ex-situ & in-situ). During her research experience she has developed a microbial/fungal consortium popularly known as Pusa Decomposer especially for in-situ management of paddy straw. She has guided 2 M.Sc & 16 Ph.D students and actively involved in research, teaching & extension activity. She has published more than seventy research articles including research, review, book chapters in the leading International Journals or Books and also edited one book title Microbes based approaches for the management of hazardous contaminants" publisher John Wiley & Sons. She has wide area of research experience, especially in the field of Plant-Microbe Interactions, Agro-waste recycling. She has been awarded Outstanding women researcher award at 7th Asian PGPR International Conference, Malaysia, 2022. She has been awarded Excellence in research award for Excellent contribution in the field of Agriculture & Allied Sector in 2020 by Dr. Ram Avatar Shiksha Samiti (DRASS). She has also gone 3 month training at Centre for Environmental Risk Assessment and Remediation, University of South Australia, Adelaide, SA, Australia. She is also serving as guest editors in several leading international journals like Journal of Basic Microbiology, Antioxidants, Indian Journal of Agriculture Sciences, Agriculture, Sustainability, Applied Microbiology etc. She attended several International and National Seminars, Symposia, Conferences and chaired technical sessions and presented papers in them..

In view of the contribution in area of Agriculture Microbiology, which are of both fundamental and applied values, Dr. Livleen Shukla is recognised by AMI in conferring her AMI-Prof G S Rangaswamy Award on 16 November, 2024.

Namita Singh

Prof. Namita Singh
General Secretary

Dr. S.K. Khare
President

Sr. No.-AMI-Award 2024/

भारतीय जीवाणुतत्ववेत्त संगठन
Association of Microbiologists of India

ASSOCIATION OF MICROBIOLOGISTS OF INDIA

AMI- Soshil Kumar Jain Panacea Biotech Award

Dr. Narottam Acharya

Dr. Narottam Acharya is a distinguished scientist from the Department of Infectious Disease Biology at Institute of Life Sciences, Bhubaneswar. Dr. Acharya has been awarded his PhD degree from Indian Institute of Science, Bangalore in the year 2003. He holds extensive experience in the field of Molecular Microbiology, with over 20 years of research experience. His primary research areas include DNA replication in Fungi, Antifungal Drug resistance, Antifungal Drug Discovery, and Vaccine development, and trained immunity, particularly with respect to systemic *candidiasis.* He has also been an elected fellow of "NATIONAL ACADEMY OF SCIENCES" for his contribution in DNA replication and antifungal vaccine development. Dr. Acharya's laboratory has generated several DNA polymerase knockout strains with live whole cell vaccine potential and several of those strains have been patented. In addition to his research accomplishments, he has a robust publication record, with 61 publications in high-impact journals, including review articles (5), book chapters (1), and research articles (55) in peer reviewed journals like EMBO Molecular Medicine, eLife, mBio, JBC, Molecular Microbiology, etc. He has supervised 8 Ph.D. students and 7 students are being currently supervised. He has been a life member of various academic and professional societies like Society of Biological Chemistry, Electron microscope of India, and Association of Microbiologists of India (AMI). He also serves as an editor for leading academic journals like Micobial Cell and Frontiers in Fungal biology.

The Association of Microbiologists of India is pleased to honor Dr. Narottam Acharya with AMI- Dr. Soshil Kumar Jain Panacea Biotech Award for 2024 for his outstanding credentials and contributions to the profession of Microbiology.

Namita Singh

Prof. Namita Singh
General Secretary

Dr. S.K. Khare
President

Sr. No.-AMI-Award 2024/

भारतीय जीवाणुतत्ववेत्त संगठन
Association of Microbiologists of India

ASSOCIATION OF MICROBIOLOGISTS OF INDIA

AMI- Soshil Kumar Jain Panacea Biotech Award

Dr. Goutam Ghosh

Dr. Goutam Ghosh is the Founder Director of Vaxfarm Life Sciences - a unique research-based Vaccine Company based at New Delhi. He has served as the Vice-Chancellor of Gandhi Institute of Engineering and Technology University; Dr. Ghosh has also served the leadership role in Research & Development, Technology Management and Scientific Administration in the Corporate and the Government. He has also served several years as Senior Vice President & Head of Vaccines & Biological at leading Indians Vaccine & Biopharmaceutical company where he lead the development of number of vaccines candidates including the India's first Dengue Vaccine which is currently under phase Phase III trial at Panacea Biotec. Currently his company is also working on some of novel vaccines such as Chikungunya, Hepatitis-E and others. Dr. Ghosh is an alumnus of IIT Kharagpur and IIT Delhi. As a World Bank Scholar, Dr Ghosh has also carried out his research at leading European University. Dr Ghosh had been the Vice President of Asian Federation of Biotechnology, Seoul and members of other scientific agencies.

The Association of Microbiologists of India is pleased to honor Dr. Goutam Ghosh with AMI- Dr. Soshil Kumar Jain Panacea Biotech Award for 2024 for his outstanding credentials and contributions to the profession of Microbiology.

Namita Singh

Prof. Namita Singh
General Secretary

Sr. No.-AMI-Award 2024/

Dr. S.K. Khare
President

भारतीय जीवाणुतत्ववेत्त संगठन
Association of Microbiologists of India

ASSOCIATION OF MICROBIOLOGISTS OF INDIA

AMI-K.K. Dadarwal Memorial Talk

Dr. Hukam Singh Gehlot

Dr Hukam Singh Gehlot is professor of Botany with over 30 years of experience in teaching and research specialization in Plant Physiology, Microbiology, Biotechnology, Molecular Biology, and Microbial Genomics. He served as Head of the Department of Botany at JNV University (2012-2014). He also served as Coordinator for Center for Advanced Study under UGC-SAP and Coordinator Center for Potential Excellence in Particular Area (UGC-CEPEPA) programs. He recognized with multiple international awards, including the Crawford Fund Training Award (2009, Australia) and participation in the UGC-Indo-Hungary Educational Exchange Program (2014). Has designed and guided academic curricula, and supervised over 15 Ph.D. students and more than 50 students for dissertation program. He contributed to more than 75 research publication in high-impact publications and served on various academic selection committees viz. : UPSC (Uttarakhand Public Service commission, Haridwar); Subject Expert in state Civil service interview; lecturer recruitment in college education at IIT Jodhpur; technical post and he is the life member of prestigious society including Indian Botanical Society; The American Society of Microbiologists; Association of Microbiologists of India (AMI) and Society for promotion of higher education.

The Association of Microbiologists of India is pleased to honor Mr. Hukam Singh Gehlot for AMI- K.K. Dadarwal Memorial Talk Session delivered during 65th AMI Annual International Conference.

Namita Singh

Prof. Namita Singh
General Secretary

Sr. No.-AMI-Award 2024/

Dr. S.K. Khare
President

भारतीय जीवाणुतत्ववेत्त संगठन
Association of Microbiologists of India

ASSOCIATION OF MICROBIOLOGISTS OF INDIA

AMI-Young Scientist Award

(Environmental Microbiology)

Dr. Nirjara Singhvi

Dr. Nirjara Singhvi is currently working as Assistant Professor and Research Coordinator at Dev Bhoomi Uttarakhand University, Dehradun. She completed her PhD in 2021 from Department of Zoology, University of Delhi under the supervision of renowned microbiologists Prof. Yogendra Singh and Prof. Rup Lal. In her doctoral research, she has majorly focused on the proteomic architecture of rifamycin producer, *Amycolatopsis mediterranei* and decipher the molecular mechanism of antibiotic export in the mutated strains. She has been awarded with travel grant by International society for microbial ecology, Netherlands to attend AMI annual conference 2018. She was awarded with INSCR best poster and ISME best oral presenter awards. She is also the member of microbiology societies like Association of Microbiologists of India, and Indian Network for Soil Contamination Research and Society for Ethanophamacology. She is actively working in field of proteomics, comparative genomics, system biology and structural biology and conducted more than 40 hands-on training session for young students across the country in collaboration with AMI-ISME-INSCR societies and various institutes. She was invited to Tribhuvan University, Nepal for conducting the workshop on proteomics. She has also been an active part of the Microbial literacy campaign and spreading the importance of microbiology among young students in remote areas. She has published her research work in various reputed and peer reviewed journals like Journal of Proteomics, mSystems, Journal of Biomolecular Structure and Dynamics, Infection, Genetics and Evolution and many more. Dr. Singhvi has been appointed as the Treasurer-cum-Secretary for the AMI-Dehradun Unit.

The Association of Microbiologists of India is pleased to honor Dr. Nirjara Singhvi with AMI- Young Scientist Award (Environmental Microbiology) for 2024 for her outstanding credentials and contributions to the profession of Microbiology.

Namita Singh

Prof. Namita Singh
General Secretary

Sr. No.-AMI-Award 2024/

Dr. S.K. Khare
President

भारतीय जीवाणुतत्ववेत्त संगठन
Association of Microbiologists of India

ASSOCIATION OF MICROBIOLOGISTS OF INDIA

AMI-Young Scientist Award

(Industrial Microbiology)

Mr. Sandeep Kumar Singh

Mr. Sandeep Kumar Singh is currently working as a Senior Research Fellow at Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi, 110012, India. He obtained his Master's & Bachelor degree in Botany from Banaras Hindu University, Varanasi in 2016 & 2018. He is pursuing Ph.D from Amity University. He is a life member of the Association of Microbiologist of India (AMI); Asian Society of PGPR, Association for Conservation of Microbes and Application (ACMA) and International Society for Molecular Plant-Microbe Interactions. He has awarded AMI Springer Nature awards for best poster award 2023 in the field of Agriculture Microbiology at 64th Annual International Conference of the Association of Microbiologist of India (AMI). He has worked in three different projects in IARI, New Delhi as a Senior Research Fellow. He has been engaged in various research activities on plants–microbes interaction, recycling of waste, plant growth promoting bacteria, plant disease management, Plant Taxonomy, and published many book chapters and various research papers in journals of international repute. In his research tenures, Singh has published more than 100 scientific contributions in the form of research and review articles, book chapters with the leading International Journals or Publishers. He has an h-index of 24 with a total citation of over 4600. His current research interest lies in management of Lignocellulosic Waste and Bioremediation of Chlorpyrifos (DT50) contaminated sites, microbial diversity, plant growth-promoting microbes, and soil microbial community analysis. In addition he also act as guest editors in several leading international journals like in Frontier in Microbiology, Heliyon, Antioxidants, Water, Pharmaceuticals, Plants, Coatings, Sustainability, Applied Sciences, Microorganisms, Metabolites, Agriculture, Forests, Horticulturae, Tropical Medicine and Infectious Disease, Agronomy, International Journal of Molecular Sciences etc.

The Association of Microbiologists of India is pleased to honor Mr. Sandeep Kumar Singh with AMI- Young Scientist Award (Industrial Microbiology) for 2024 for his outstanding credentials and contributions to the profession of Microbiology.

Namita Singh

Prof. Namita Singh
General Secretary

Dr. S.K. Khare
President

Sr. No.-AMI-Award 2024/

भारतीय जीवाणुतत्ववेत्त संगठन
Association of Microbiologists of India

ASSOCIATION OF MICROBIOLOGISTS OF INDIA

AMI-Young Scientist Award

(Dairy and Food Microbiology)

Dr. Somenath Das

Dr. Somenath Das is a distinguished researcher and microbiologist, currently serving as Assistant Professor in Department of Botany, Burdwan Raj College (Affiliated to The University of Burdwan), West Bengal, India. He did his M.Sc. and Ph.D. from Department of Botany, Banaras Hindu University.

Dr. Das has exceptional contributions to the understanding of food systems, their contamination through fungi and microbes, and mitigation techniques by using nanotechnology. He did his Doctor of Philosophy on study of fungal and mycotoxin contamination of stored rice samples from different regions of India and their control by some higher plant products. His promising research on food microbiology not only advanced scientific knowledge but also ensures the nutritious food availability, address the food security challenges, and can fulfill the sustainable development goals. He has demonstrated exceptional scientific acumen and a strong commitment to food research. He has been playing pivotal role to avoid synthetic preservatives posing negative impact on human health and environment as well as engaged for isolation of essential oils and synthesis of green nanoformulations for mitigation of microbial infection, fungal inhabitation and mycotoxin contamination in different stored foods and fresh fruits.

Dr. Das is having 8 years of experience in Research and 4 years of experience in teaching (UG and PG) in Botany (including Microbiology). His ability to apply cutting-edge green nanotechnological techniques for food preservation has placed him at the forefront of the microbiological research. He has attended several International and National seminars and conferences and life member in many Professional Bodies. His active participation in scientific communities is characterized by a deep passion for discovery, a collaborative spirit, and a dedication to the advancement of microbial knowledge. In addition to his impressive research output, Dr. Das has shown a remarkable ability to mentor and inspire the postgraduate students and junior researchers in their academic and research work on food microbiology. His work of food science has been cited by Google Scholar (citation 2525), Scopus (citation 2085), Web of Science (citation 1254), and Research Gate (citation 2368) at different points of the world.

Dr. Das received many prestigious awards like Young Scientist from Botanical Society of Bengal, West Bengal and National Environmental Science Academy, New Delhi, India. He has also awarded Certificate of Excellence for outstanding paper from West Bengal State Science and Technology Congress and Certificate of Reviewing from internationally reputed journals. Considering his potentiality for excellent review he has been included in Editorial Board Member of Scientific Reports (Nature Portfolio, Section Food) and recognized as Bentham approved Reviewer. He has published about 58 Research and Review articles in reputed International and National journals with high impact factors and 24 Book chapters of International repute.

The Association of Microbiologists of India is pleased to honor Dr. Somenath Das with AMI- Young Scientist Award (Dairy and Food Microbiology) for 2024 for his outstanding credentials and contributions to the profession of Microbiology.

Namita Singh

Prof. Namita Singh
General Secretary

Sr. No.-AMI-Award 2024/

Dr. S.K. Khare
President

भारतीय जीवाणुतत्ववेत्त संगठन
Association of Microbiologists of India

ASSOCIATION OF MICROBIOLOGISTS OF INDIA

AMI-Young Scientist Award
(Agricultural Microbiology)

Dr. Gaurav Raturi

Dr. Gaurav Raturi is a Postdoctoral Research Associate at the Institute of Genomics for Crop Abiotic Stress Tolerance at Texas Tech University, USA. His research advances sustainable agriculture by harnessing the potential of beneficial microorganisms, including *Arbuscular mycorrhizal* fungi (AMF) and Rhizobium, to reduce reliance on chemical fertilizers. His work is instrumental in developing effective microbial formulations and elucidating the genomic interactions between plants and these beneficial microbes.

Dr. Raturi holds an M.Sc. in Microbiology and a Ph.D. in Biotechnology. With a research focus spanning Agriculture and Environmental Microbiology/Biotechnology, he has published over 28 scholarly articles, including research, review papers, and book chapters, reflecting his significant contributions to the field.

Among his numerous awards, Dr. Raturi earned the prestigious National Eligibility Test (NET) - JRF with an all-India rank of 66, awarded by the CSIR-UGC. He also received the "Swachhta Saarthi Fellowship (SSF) 2021" from the Government of India's Waste to Wealth Mission, NET-LS AIR 30, ICAR-NET and the Best Poster Award at the International Conference on Pulse Research (ICPR-2022), organized by the Society for Plant and Agricultural Sciences (SPAS), India.

In addition to his research, Dr. Raturi is an editorial board member of several journals, including BMC Plant Biology, Frontiers in Genome Editing in Plants, International Journal of Microbiology and Biotechnology, Cellular Microbiology, and BioMed Research International. He is an active member of various scientific societies and networks, contributing to advancements in microbiology and biotechnology on a global scale. Dr. Raturi's work continues to make a meaningful impact on agricultural science, bridging the gap between fundamental research and real-world agricultural solutions that promote environmental stewardship and food security.

The Association of Microbiologists of India is pleased to honor Dr. Gaurav Raturi with AMI- Young Scientist Award (Agricultural Microbiology) for 2024 for his outstanding credentials and contributions to the profession of Microbiology.

Namita Singh

Prof. Namita Singh
General Secretary

Sr. No.-AMI-Award 2024/

Dr. S.K. Khare
President

GURU JAMBHESHWAR UNIVERSITY OF SCIENCE AND TECHNOLOGY HISAR , HARYANA

(Established by State Legislature Act 17 of 1995)

(A+ Grade NAAC Accredited)

Post Graduate Programmes

M.Tech. (Computer Science & Engineering)
M.Tech. (Environmental Science & Engineering
M.Tech. (Electronics & Communication Engineering)
M.Tech. (Printing Technology)
M.Tech. (Food Technology)
M.Tech. (Mechanical Engineering)
M.Tech. (Mechanical Engineering) For Working Professionals
M.Tech. (Geo-informatics)
M.Pharma. (Pharmaceutical Chemistry)
M.Pharma. (Pharmaceutics)
M.Pharma. (Pharmacology)
M.Pharma. (Pharmacognosy)
Master of Physiotherapy (Orthopedics)
Master of Physiotherapy (Sports)
Master of Physiotherapy (Cardiothoracic & Pulmonary-Disorders)
Master of Physiotherapy (Neurology)
M.Sc. (Physics)
M.Sc. (Chemistry)
M.Sc. (Mathematics)
M.Sc. (Biotechnology)
M.Sc. (Microbiology)
M.Sc. (Environmental Sciences)
M.Sc. (Food Technology)
M.Sc. (Yoga Science and Therapy)
M.Sc. (Artificial Intelligence & Data Science)
M.Sc. (Economics)
M.Sc. (Psychology)
M.Sc. (Geography)
Master of Computer Applications (MCA)
Master of Business Administration (MBA)
MBA (Finance)
MBA (Marketing)
MBA (International Business)
MBA (Business Analytics)
MBA (Health Care)
M.A. (Mass Communication)
M.A. (English)
M.A. (Hindi)
M. Com

P.G. Programmes as per NEP 2020

M.Sc. Botany
M.Sc. Zoology
M.Sc. Computer Science (Artificial Intelligence and Data Sciences)
M.A. Education
Master of Library and Information Science

P.G. Diploma Programmes

Advance Diploma in Child Guidance and Counselling
P.G. Diploma in Yoga Science & Therapy
P.G. Diploma in Guidance & Counselling
P.G. Diploma in Rehabilitation Psychology

KNOW MORE ABOUT ADMISSIONS

SCAN ME

Under Graduate B.Tech. Programmes for Working Professionals (Evening)

B.Tech. (Mechanical Engineering)
B.Tech. (Computer Science and Engineering)

Under Graduate B.Tech. Programmes in Hindi Medium

B.Tech. (Computer Science and Engineering)
B.Tech. (Information Technology)
B.Tech. (Electronics & Communication Engineering)
B.Tech. (Mechanical Engineering)

Under Graduate B.Tech. Programmes

B.Tech. (Computer Science & Engineering)
B.Tech. (Computer Science & Engineering) Artificial Intelligence & Machine Learning
B.Tech. (Artificial Intelligence and Data Science)
B.Tech. (Information Technology)
B.Tech. (Electronics & Computer Engg.)
B.Tech. (Electronics & Communication Engineering)
B.Tech. (Electronics and Biomedical Engineering)
B.Tech. (Electrical Engineering)
B.Tech. (Mechanical Engineering)
B.Tech. (Civil Engineering)
B.Tech. (Printing Technology)
B.Tech. (Packaging Technology)
B.Tech. (Food Technology)

Under Graduate Programmes

Bachelor of Pharmacy
Bachelor of Physiotherapy
Bachelor in Medical Laboratory Technician
B.Sc. Radiography & Imaging Technology
Post Basic B. Sc. Nursing
B. Sc. Nursing
B.Sc. Aviation
B.Sc. B.Ed. – 4 Year programme under ITEP
B.A. B.Ed. – 4 Year programme under ITEP
B.A. LL.B. (Hons.) – 5 Year programme

Under Graduate and Integrated B.Sc. (Hons. /Hons with Research)-M.Sc. Programmes

Intergrated B.Sc. (Hons. /Hons. with Research)- M.Sc. Computer Science (Artificial Intelligence and Data Science)
Integrated B.Sc. (Hons./Hons. with Research) -M.Sc. Geography
Integrated B.Sc. (Hons./Hons. with Research) -M.Sc. Psychology
Integrated B.Sc. (Hons./Hons. with Research) -M.Sc. Economics
Integrated B.Sc.(Hons./Hons. with Research) Yoga Science and Therapy – M.Sc. Yoga Science and Therapy
Integrated B.Sc. (Physical Sciences) -M.Sc.(Physics/Chemistry/ Mathematics)
Integrated B.Sc. (Life Sciences) -M.Sc.(Botany/Biotechnology/ Microbiology/Zoology/ Chemistry)
Integrated BBA (Hons./Hons. with Research) – MBA
Integrated B.Com. (Hons./Hons. with Research)–M.Com
Integrated BCA – MCA
Integrated B.A. - M.A. (Mass Communication)
B.Voc. (Food Processing and Engineering)

OPEN & DISTANCE LEARNING (ODL)/ONLINE MODE

P.G. PROGRAMMES (ODL & ONLINE)

M.A. Mass Communication
M.A. Mass Communication (Lateral Entry)
MBA
M.Com
MCA

U.G. PROGRAMMES (ODL & ONLINE)

B.Com

P. G. PROGRAMMES (ODL)

M.Sc. Mathematics
M.A. English
M.A. Hindi

U. G. PROGRAMMES (ODL)

B.A. Mass Communication
B.A.

DIPLOMA COURSES (ODL & ONLINE)

Diploma in Computer Applications (Online)
Diploma in Computer Applications (ODL)
Diploma in Data Science (ODL)
Diploma in Business Analytics (ODL)
Diploma in Supply Chain Analytics (ODL)
Diploma in Financial Market (ODL)
Diploma in Banking and Finance (ODL)
Diploma in industrial Health and Safety (ODL)
Diploma in Guidance and Counselling (ODL)

CERTIFICATE COURSES (ONLINE)

Certificate in Information Technology (HS-CIT)
Certificate in Advanced Accounting
Certificate in AutoCAD
Certificate in IT Desktop & Hardware Support

CERTIFICATE COURSES (ONLINE)

Certificate in Office Assistance
Certificate in Coral Draw
Certificate in Graphic Designing
Certificate in Video Editing
Certificate in English Communication & Soft Skills
Certificate in Financial Accounting
Certificate in Advanced Excel
Certificate in IT Network Support
Certificate in IT Security Support
Certificate in Photo Editing
Certificate in Adobe (DTP)
Certificate in Web Designing
Certificate in C & C++ Programming

Doctor of Philosophy (Ph.D.) Programmes

Ph.D. (Printing Technology)
Ph.D. (Computer Science & Engineering)
Ph.D. (Electronics & Communication Engineering)
Ph.D. (Mechanical Engineering)
Ph.D. (Electrical Engineering)
Ph.D. (Chemistry)
Ph.D. (Mathematics)
Ph.D. (Environmental Science & Engineering)
Ph.D. (Biotechnology)
Ph.D. (Microbiology)
Ph.D. (Data Science)
Ph.D. (Food Technology)
Ph.D. (Physics)
Ph.D. (Haryana School of Business)
Ph.D. (Physiotherapy)
Ph.D. (Pharmaceutical Sciences)
Ph.D. (Economics)
Ph.D. (Mass Communication)
Ph.D. (Applied Psychology)
Ph.D. (Hindi)
Ph.D. (Commerce)

+91-70150-01907 01662-263139 admission@gjust.org www.gjust.ac.in

GURU JAMBHESHWAR UNIVERSITY OF SCIENCE AND TECHNOLOGY HISAR , HARYANA

(Established by State Legislature Act 17 of 1995)

(A+ Grade NAAC Accredited)

CENTRE FOR DISTANCE AND ONLINE EDUCATION

APPLY ONLINE

OPEN & DISTANCE LEARNING (ODL)/ONLINE MODE

P.G. PROGRAMMES (ODL & ONLINE)

M.A. Mass Communication
MBA
M.Com
MCA

P. G. PROGRAMMES (ODL)

M.Sc. Mathematics
M.A. Mass Communication (Lateral Entry)
M.A. English

DIPLOMA COURSES (ODL & ONLINE)

Diploma in Computer Applications (Online)
Diploma in The Srimad Bhagvad Gita (Online)
Diploma in Computer Applications (ODL)
Diploma in Data Science (ODL)
Diploma in Business Analytics (ODL)
Diploma in Supply Chain Analytics (ODL)
Diploma in Financial Market (ODL)
Diploma in Banking and Finance (ODL)
Diploma in industrial Health and Safety (ODL)
Diploma in Guidance and Counselling (ODL)
Diploma in Food Quality Assurance (ODL)
Diploma in Solid and Hazardous Waste Management (ODL)

KNOW MORE ABOUT ODL COURSE ADMISSIONS
SCAN ME

KNOW MORE ABOUT ONLINE COURSE ADMISSIONS
SCAN ME

U.G. PROGRAMMES (ODL & ONLINE)

B.Com

U. G. PROGRAMMES (ODL)

B.A. Mass Communication
B.A

CERTIFICATE COURSES (ONLINE)

Certificate in Information Technology
Certificate in Advanced Accounting
Certificate in AutoCAD
Certificate in IT Desktop & Hardware Support
Certificate in Office Assistance
Certificate in Coral Draw
Certificate in Graphic Designing
Certificate in Video Editing
Certificate in English Communication & Soft Skills
Certificate in Financial Accounting
Certificate in Advanced Excel
Certificate in IT Network Support
Certificate in IT Security Support
Certificate in Photo Editing
Certificate in Adobe (DTP)
Certificate in Web Designing
Certificate in C & C++ Programming
Certificate in Video Film Production (ODL)

+91-98123 99111 01662-263 638 01662-276735 01662-263141

01662-263158 01662-263157 cdoehkcl@gjust.org www.gjust.ac.in

SPONSORS

HIMEDIA®
For Life is Precious

HiMedia Laboratories Pvt. Ltd. - The Complete Bioscience Solution Hub

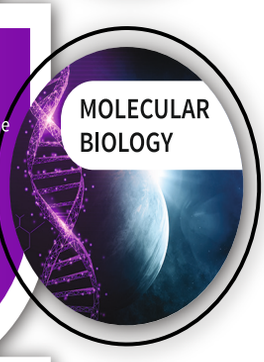
Vision... Strategy.. Results
50 Years of Scientific Excellence

MICROBIOLOGY


- Culture Media - Powders & Granulated, Encapsulated, HiVeg™ & HiCynth™
- Ready Prepared Media
- Antimicrobial Susceptibility Systems
- Animal & Vegetable Hydrolysates
- Culture Media Supplements & Bases

CELL BIOLOGY


- Cell Culture Platform
- Stem Cells & Primary Cells
- Cell Analysis & Detection Solutions
- Cell Culture Tested Chemicals
- Cell Culture Systems
- Filtration Solutions
- Skill Development Modules

MOLECULAR BIOLOGY


- HiPurA® Extraction Kits
- Hi-PCR® Kits
- Insta Q96® Series PCR Machine
- Insta NX® Series Extractor
- HiPer® Teaching Kits
- MB Chemicals & Buffers
- Insta-LF™ Rapid Kits
- Protein Purification Kits
- HiGx360® Sequencing & Bioinformatics Services

PLANT TISSUE CULTURE


- Plant Tissue Culture Media
- Gelling Agents
- Plant Growth Regulators
- Contamination Control Systems
- Plant Tissue Culture Tested Chemicals
- Plant Tissue Culture Systems / Accessories

HYDROPONICS SOILLESS FARMING


- Hydroponics Commercial Turnkey Project Solutions
- Hydroponics Hobby Systems
- Hydroponics Nutrients
- Hydroponics Accessories

CHEMICALS & BIOCHEMICALS


- Inorganic Chemicals
- Speciality Chemicals
- Hi-AR™/ACS, Hi-AR™, Hi-LR™, Hi-Cert™, UV & HPLC
- Chemicals Meeting Pharmacopeial Testing Specifications
- Acids & Solvents
- Filter Papers

LAB CONSUMABLES & INSTRUMENTS


- Culture Vessels - Microbiology, Culture Biology & Plant Tissue Culture
- Counting & Sampling Aids
- Liquid Handling
- Cryogenic Storage
- Instruments for Microbiology & Molecular Biology
- Disinfectant & Antiseptic Solutions

HIMEDIA Celebrating 50 Golden Years 1974 - 2024

www.himedialabs.com

ISO 9001-2015 CERTIFIED ISO 13485-2016 CERTIFIED WHO GMP CERTIFIED CE

• • • expect only quality from us™

info@himedialabs.com

+91-22-6147 1919

SPONSORS

SPONSORS

iNSERB DIA

सत्यमेव जयते

Department of Biotechnology

DRDO

DEFENCE R&D ORGANISATION

बलस्य मूलं विज्ञानम्

MINISTRY OF DEFENCE

HIMEDIA®

FOR LIFE IS PRECIOUS

HARYANA STATE COUNCIL FOR SCIENCE & TECHNOLOGY

योग: कर्मसु कौशलम्

Spectrum Technologies

Your partner in scientific discovery

QIAGEN

100 YEARS

विकसित भारत अभियान

1947 TO 2047

List of Ami Awardees

S. No.	Name
AMI-PROF. G. S. RANGASWAMY MEMORIAL AWARD	
1	Dr. Livleen Shukla
AMI-S. R. VYAS MEMORIAL AWARD	
1	Dr. Prakasham Reddy Shetty
AMI-SOSHIL KUMAR PANACEA AWARD	
1	Dr. Narottam Acharya Scientist F, Institute of Life Sciences, Bhubaneswar, Odisha
2	Dr. Gautam Ghosh Ex. Vice-Chancellor, Gandhi Institute of Engineering & Technology University Director, Vaxfarm Life Sciences, New Delhi
AMI-B.N. JOHRI AWARD	
	No Application Received differed for Next Year
AMI-LOUIS PASTEUR AWARD	
1	Dr. Mahesh S Dhar Vice-President (Research) Sunny Corporation Pvt. Ltd. Phase- I Okhla New Delhi, India
2	Prof. Namita Singh, Guru Jambheshwar University of Science and Technology, Hisar Haryana-125001
AMI-DR. J. V. BHATT AWARD	
Research Article:	Thongruck, K. and Maneerat, S., 2023. Enhanced production of gamma-aminobutyric acid (GABA) from Lactobacillus futsaii CS3 using agri-food industries by-products under batch and fed-batch fermentation. Indian Journal of Microbiology, 63(4), pp.467-482. Suppasil Maneerat suppasil.m@psu.ac.th Center of Excellence in Innovative Biotechnology for Sustainable Utilization of Bioresources, Faculty of Agro-Industry, Prince of Songkla University, Hat Yai, Songkhla 90110, Thailand
Review Article:	Thottarath Prasanthan, A., Damodaran, A., Kumar, N.S. and Viswanad, V., 2023. Deducing the interplay between gut flora and respiratory diseases: a new therapeutic strategy?. Indian Journal of Microbiology, 63(1), pp.1-17. Vidya Viswanad vidyanitin26@gmail.com; vidyaviswanad@pharmacy.amrita.edu Department of Pharmaceutics, Amrita School of Pharmacy, Amrita Vishwa Vidyapeetham, AIMS Health Science Campus, Kochi, Kerala, India

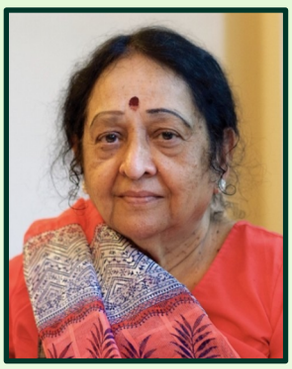
AMI-YOUNG SCIENTIST AWARD (AGRICULTURAL MICROBIOLOGY)	
3	Dr. Gaurav Raturia Post Doctoral Research Associate, IGCAST, Texas Tech University, USA
AMI-YOUNG SCIENTIST AWARD (DAIRY AND FOOD MICROBIOLOGY)	
2	Dr. Somenath Das (M.Sc, Ph.D.) Assistant Professor Department of Botany, Burdwan Raj College Burdwan 713104 West Bengal, India
AMI-YOUNG SCIENTIST AWARD (ENVIRONEMNTAL MICROBIOLOGY)	
1	Dr. Nirjara Singhvi, Devbhumi University, Uttrakhand
AMI-YOUNG SCIENTIST AWARD (INDUSTRIAL MICROBIOLOGY)	
1.	Mr. Sandeep Kumar, Dept. of Microbiology, ICAR-IARI, Pusa Campus, New Delhi
AMI-YOUNG SCIENTIST AWARD (MEDICAL AND VETERNARY MICROBIOLOGY)	
	No Application Received differed for Next Year
AMIYOUNG SCIENTIST AWARD (MOLECULAR MICROBIOLOGY)	
	No Application Received differed for Next Year
AMSc. FELLOW	
1.	Prof. (Retd) Sunil Pabbi, IARI-ICAR, New Delhi
2.	Prof. Sarman Singh, Ex Director,AIIMS Bhopal
AMI-BEST UNIT AWARD	
1.	AMI- Hisar Unit
2.	AMI- Banglore Unit
3.	AMI- Lovely Professional University Unit
AMI-LIFE TIME ACHIVEMENT AWARD	
1.	Prof. (Retd) Kamla Chaudhary, CCSHAU Hisar
2.	Prof. Praveen Rishi, Panjab University Chandighar
3.	Prof Narsi Ram Bishnoi, Vice Chancellor, GJUST Hisar Haryana
DR. MANVIKA SEHGAL MEMORIAL BEST POSTER AWARD	
1.	Mr. Lucky Duhan, Dept. of Biochemistry, MDU, Rohtak
DR. RANA MEMORIAL BEST POSTER AWARD	
1.	Ms. Renuka Sharma, Dept. of Biotechnology, GJUST, Hisar

AMI SPRINGER POSTER AWARDEES

NAME	EMAIL
Ms. Anushree Patra	shreeanu.004@gmail.com
Mr. Paras Saini	sainiparas700@gmail.com
Ms. Shweta Sinha	shweta7865sinha@gmail.com
Ms. Vijaysri D.	vijayashreed1997@gmail.com
Ms. Kritika Prasad	kp21rs064@iisekol.ac.in
Dr. Ruma Rani	rumasaharan@gmail.com
Ms. Shreya Maheshwari and Kanika	Shreyamaheshwari270203@gmail.com
Mr. Manoj S H	manojsh2810@gmail.com
Ms. Rajalakshmi S	rdsridharan@gmail.com
Mrs. Taruna Sheoran	tanusheoran@gmail.com
Mr. V. H. Vinuthana	vinuthana1998@gmail.com
Mr. Ramesh Kumar	

AMI SPRINGER ORAL AWARDEES

NAME	EMAIL
Dr Ankit	ankitzood522@gmail.com
Mr. Bandeppa S.	bgsonth@gmail.com
Ms. Rachana Arvind	rachana1.mitmpl2023@learner.manipal.edu
Mr. Katyal P.	drpkatyal@pau.edu
Dr. Anuj Rana	anujrana@hau.ac.in
Dr. Prafulla Shende	prafullashede@gmail.com
Ms. Bhagyashree Bora	bhagyabora09@gmail.com
Mrs. Rashmi Bharadwaj	bhardwajrashmi3@gmail.com
Ms. Anubha Sharma	anubha.sharma@jecrcu.edu.in
Ms. Shikha Mehta	shikhamicrobio@gmail.com
Ms. Jyoti Kaurav	jyotikaurav.gbu@gmail.com
Mr. Mandeep Kumar	nainmandeep70@gmail.com



A Tribute...

Prof. Manju Sharma (1940–2024)

(Padma Bhushan Awardee)

Past AMI President- 1999 (Term-Jan-Dec)

It is with profound sadness that we announce the passing of Dr. Manju Sharma, a trailblazer in India's biotechnology landscape and former Secretary of the Department of Biotechnology (DBT), who left us on October 31st, 2024, at the age of 84. Dr. Sharma's visionary leadership and relentless dedication to the field of biotechnology earned her a place among India's most respected scientists and administrators, with her legacy continuing to shape the sector for future generations.

Born in 1940 to a family deeply committed to education, Dr. Sharma was raised with a strong sense of intellectual curiosity and a belief in the transformative power of knowledge. She went on to earn her Master's and Ph.D. degrees in Botany, with a specialization in plant physiology—a field that captured her fascination and set her on a path toward a remarkable career. Her early research achievements and unwavering commitment to advancing science caught the attention of India's scientific community and led her to serve with distinction in the Government of India.

In 1986, Dr. Sharma joined the Department of Biotechnology, a newly established entity in Indian science administration, when the discipline of biotechnology was still in its formative stage in the country. As one of DBT's founding members, she played a pivotal role in creating policies, programs, and initiatives that laid the foundation for India's present-day biotech industry. Her efforts positioned India as a formidable player on the global biotechnology stage, marking the beginning of a transformative era in Indian science.

Dr. Sharma's impact on the biotechnology field was further increased in 1995 when she was appointed as the Secretary of DBT, becoming the first woman to hold this prestigious role. She held the position until her retirement in 2004, steering DBT through a period of substantial growth and diversification. Under her leadership, the department expanded its mandate to cover various essential areas, including agriculture, healthcare, environmental sustainability, and industrial biotechnology. Her commitment to fostering public-private partnerships and supporting both fundamental and applied research cemented DBT's reputation as a forward-thinking and inclusive institution.

Among her many contributions, Dr. Sharma was instrumental in establishing several significant initiatives, such as the National Biotechnology Development Strategy, which provided a blueprint for India's biotech growth. Her founding of 'Biotech Parks' and

'specialized biotechnology training programs' aimed at nurturing talent, exemplified her foresight and dedication to building a robust ecosystem for research and innovation. She also established the 'National Bioresource Development Board' (NBDB) in 1999, promoting the conservation, sustainable utilization, and commercialization of India's rich biodiversity.

A committed advocate for women in science, Dr. Sharma recognized the importance of creating supportive pathways for women to excel in scientific careers. She implemented numerous women-centric initiatives within DBT, which provided resources, mentorship, and opportunities for female scientists in an often male-dominated field. Her tireless advocacy inspired countless women to pursue careers in science and technology, and her efforts have had a lasting impact on gender equality within Indian research institutions.

Dr. Sharma's exceptional contributions were acknowledged with numerous awards and recognitions, most notably the Padma Bhushan in 2007, one of India's highest civilian honors. Her work earned international acclaim, and she served on several global scientific committees, where she fostered collaborations that brought Indian biotechnology to the world stage.

Beyond her professional accomplishments, Dr. Sharma is remembered by her colleagues for her warmth, humility, and generosity. She was known as a tireless worker with an indomitable spirit and a belief in the power of science to bring about societal change.

Upon her passing, the biotechnology community, along with industry leaders and scientific institutions across India, shared heartfelt tributes honoring her legacy. Kiran Mazumdar Shaw, Founder and Chairperson of Biocon, expressed, “Manju Sharma ji was such a torch bearer of Biotechnology. As Secretary of DBT, she gave wings to the biotech sector. Will miss her frequent calls to discuss various things.” Former DBT Secretary and Principal Scientific Advisor, Prof. K. Vijayaraghavan, also reflected, “Dr. Manju Sharma's passing is a big loss for the life sciences and biotechnology community. When at the Department of Science and Technology, she drove the creation of the National Biotechnology Board, which then became the Department of Biotechnology.”

Dr. Renu Swarup, former Secretary of DBT, remarked, “The end of an era. Dr. Manju Sharma has left a huge void which cannot be filled. Indian science, especially life sciences and biotechnology, and women in STEM have lost a strong pillar. We will miss her guiding light.”

Dr. Soumya Swaminathan, former Chief Scientist at the World Health Organization and Chairperson of MSSRF, noted, “Dr. Manju Sharma was a trailblazer, mentor to many, first woman DBT Secretary, and put DBT on a growth trajectory. A lifelong friend and trustee of MSSRF, she will be deeply missed. May her soul rest in peace.”

As the President of the Association of Microbiologists of India (AMI) in 1999, she played a key role in advancing microbiology research, contributing to her holistic approach to science and life sciences.

Dr. Sharma is survived by her family, whose support remained unwavering throughout her illustrious career. In honoring her memory, her family has announced plans to establish a foundation dedicated to providing scholarships for young women pursuing careers in biotechnology - a cause deeply meaningful to Dr. Sharma.

As India mourns the loss of this pioneering scientist, we remember Dr. Manju Sharma not only for her groundbreaking contributions to biotechnology but also for her dedication to a brighter, healthier future for all. Her vision, leadership, and passion have left an indelible mark on Indian science, and her legacy will live on through the institutions she built, the scientists she inspired, and the lives she touched.

Our Driving Force

Dr. Renu Singh

Dr. Saloni Gupta

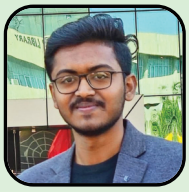
Ms. Renuka Sharma

Mr. Mandeep Nain

Ms. Taruna Sheoran

Ms. Chahat Bhatia

Ms. Meenakshi Mangal



Mr. Vipin

Ms. Shreya Maheshwari

Ms. Natasha Charaya

Ms. Menal Jain

Mr. Akshay Yadav

Mr. Yuvansh Anjna

Mr. Sahil Barak

Ms. Kanika

Ms. Annu

Ms. Kanishka Poonia

Mr. Ankit

Ms. Ayushi Malik

Ms. Aditi Singh

Ms. Pinki

Mr. Sujal Pruthi

Mr. Amit Tomar

Mr. Sandeep Kumar Singh

Mr. Sudhanshu Yadav

Mr. Prince

Mr. Prafull Srivastava

Mr. Tushar Sharma

AMI OFFICE BEARERS

President
Prof. Sunil K Khare

Chairman, (AMSc)
Prof. R.C. Kuhad

Immediate Past President
Prof. Sunil Pabbi

Past President
Prof. (Mrs.) Praveen Rishi

Past President
Prof. D.K.Singh

General Secretary
Prof. Namita Singh

Joint Secretary
Dr. Anil Panghal

Treasurer
Dr. Livleen Shukla

Central Council Member
Prof. Shamsher Singh Kanwar
ZONE - I

Central Council Member & EIC-INJM
Prof. Minakshi Prasad
ZONE - II

Central Council Member & EIC-INJM
Prof. Lilly L Ganju
ZONE - IV

Central Council Member
Prof. (Dr) Meenu Saraf
ZONE - V

Central Council Member
Prof.Dr.N.Vasudevan
ZONE - VI

65th International Conference of Association of Microbiologists of India

International Academic Partners

National Academic Partners