AMI-INSCR

Microbial World: Recent Developments in Health, Agriculture and Environmental Sciences

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> If I set out to prove something I am no real scientist, I have to learn to follow where the facts lead me, I have to learn to whip my prejudices
>
> - Spallanzani

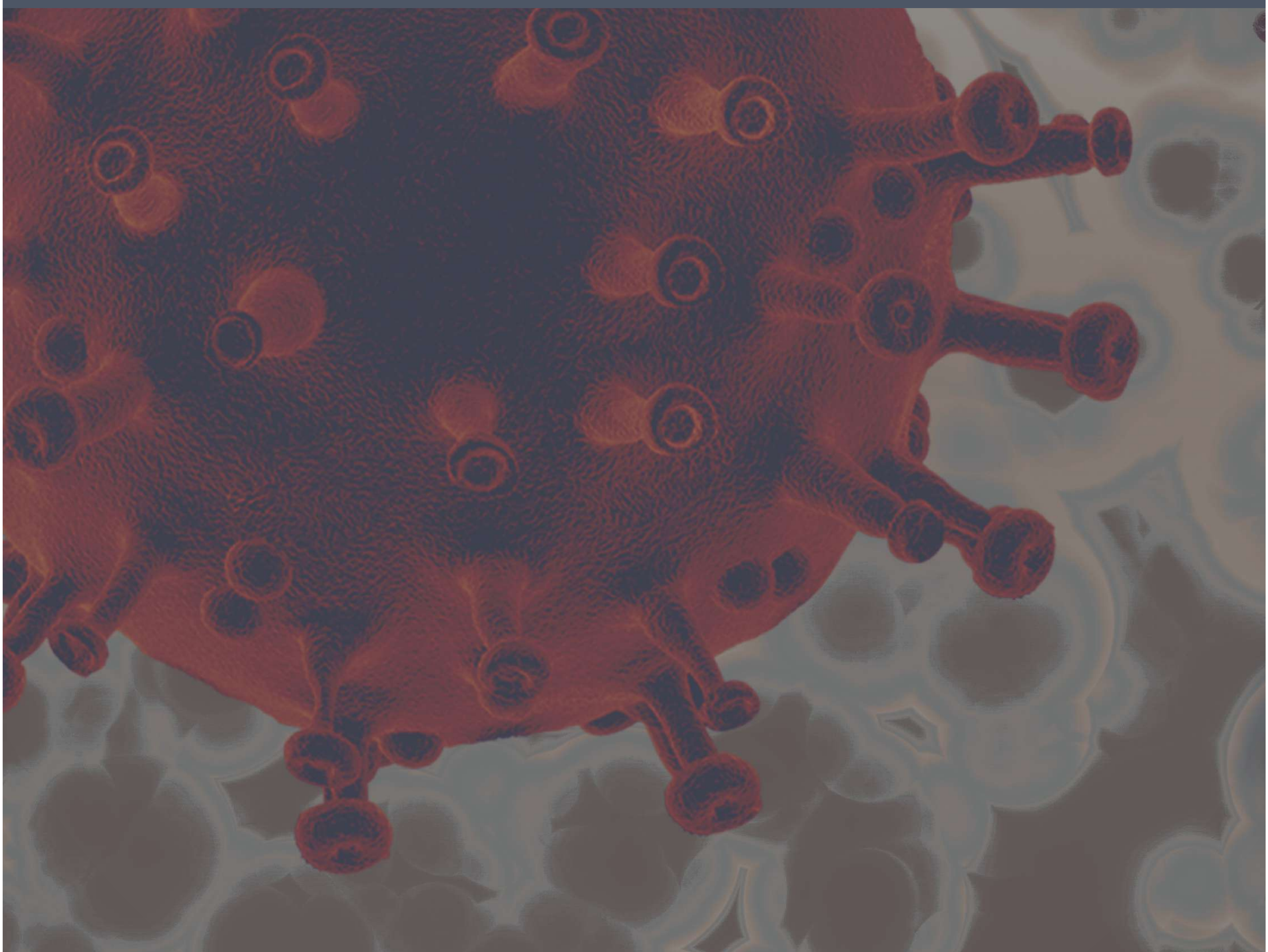
61ST ANNUAL INTERNATIONAL CONFERENCE

03-05 FEBRUARY 2021

econferenceami@gmail.com
+91-1203679147

61ST INTERNATIONAL CONFERENCE

Annual International Conference of
The Association of Microbiologists of India (AMI) &
Indian Network for Soil Contamination Research (INSCR)
in association with
The Energy and Resources Institute (TERI),
University of Delhi (DU),
Indian Agricultural Research Institute (IARI) &
Indian National Science Academy (INSA)



भारतीय जीवाणुतत्ववेत्त संगठन
Association of Microbiologists of India

Indian Network for Soil Contamination Research

ABSTRACT BOOK

ANNUAL INTERNATIONAL CONFERENCE

61

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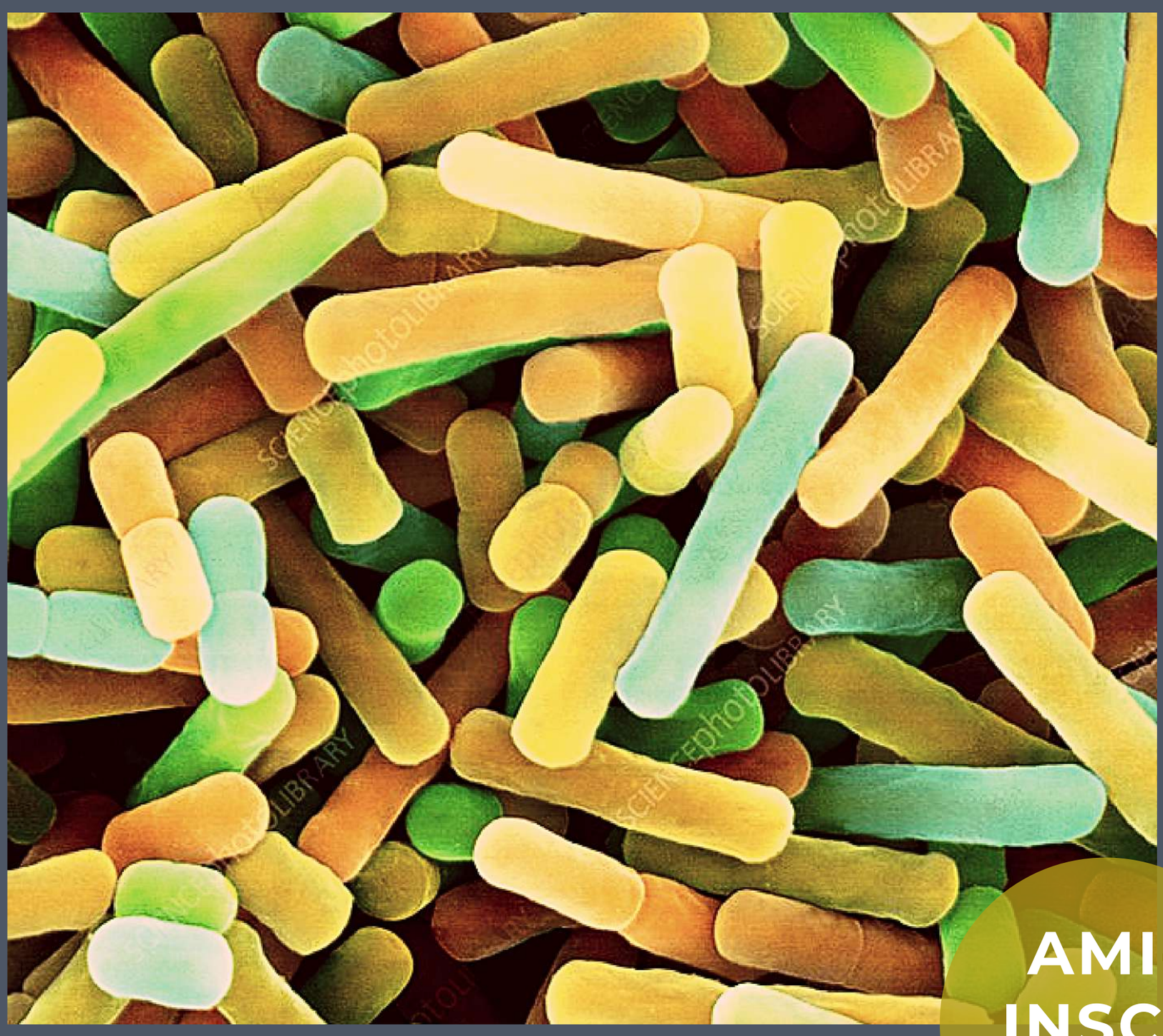

AMI-INSCR 2021

Microbial World: Recent Developments in Health, Agriculture and Environmental Sciences

WORKSHOPS
1-2 FEBRUARY 2021

03-05 FEBRUARY 2021

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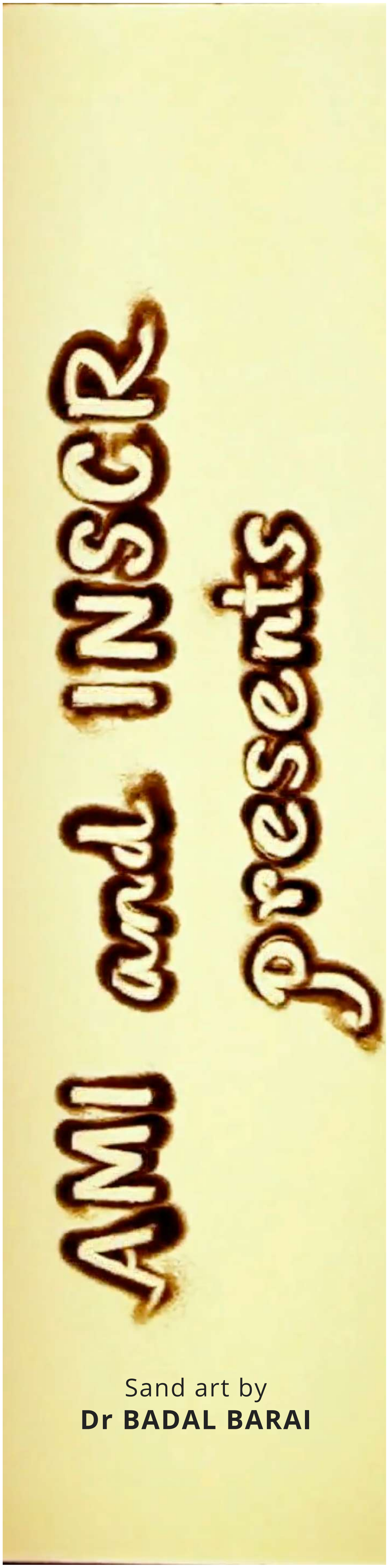
AMI.INSCR.CO.IN



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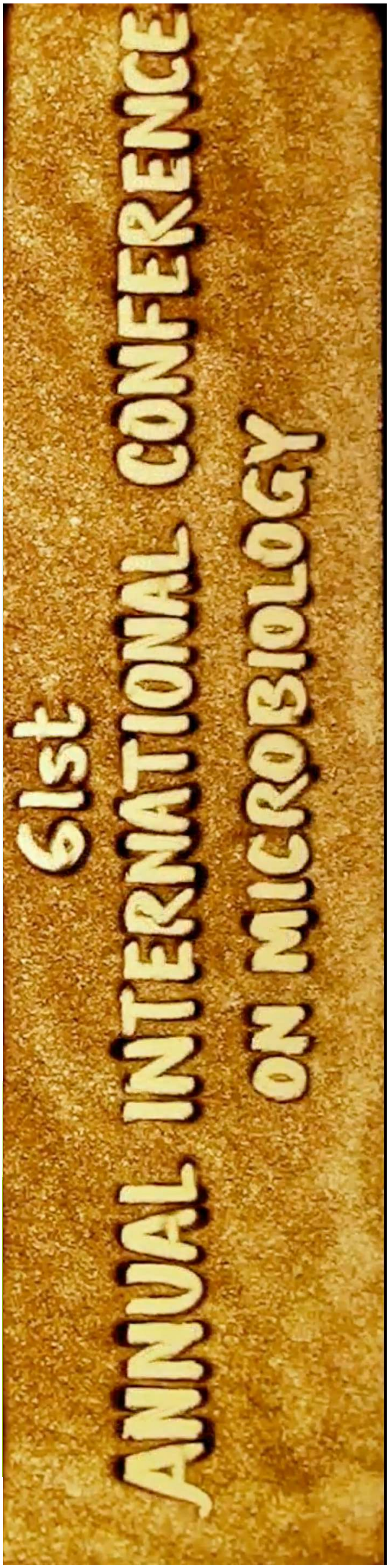
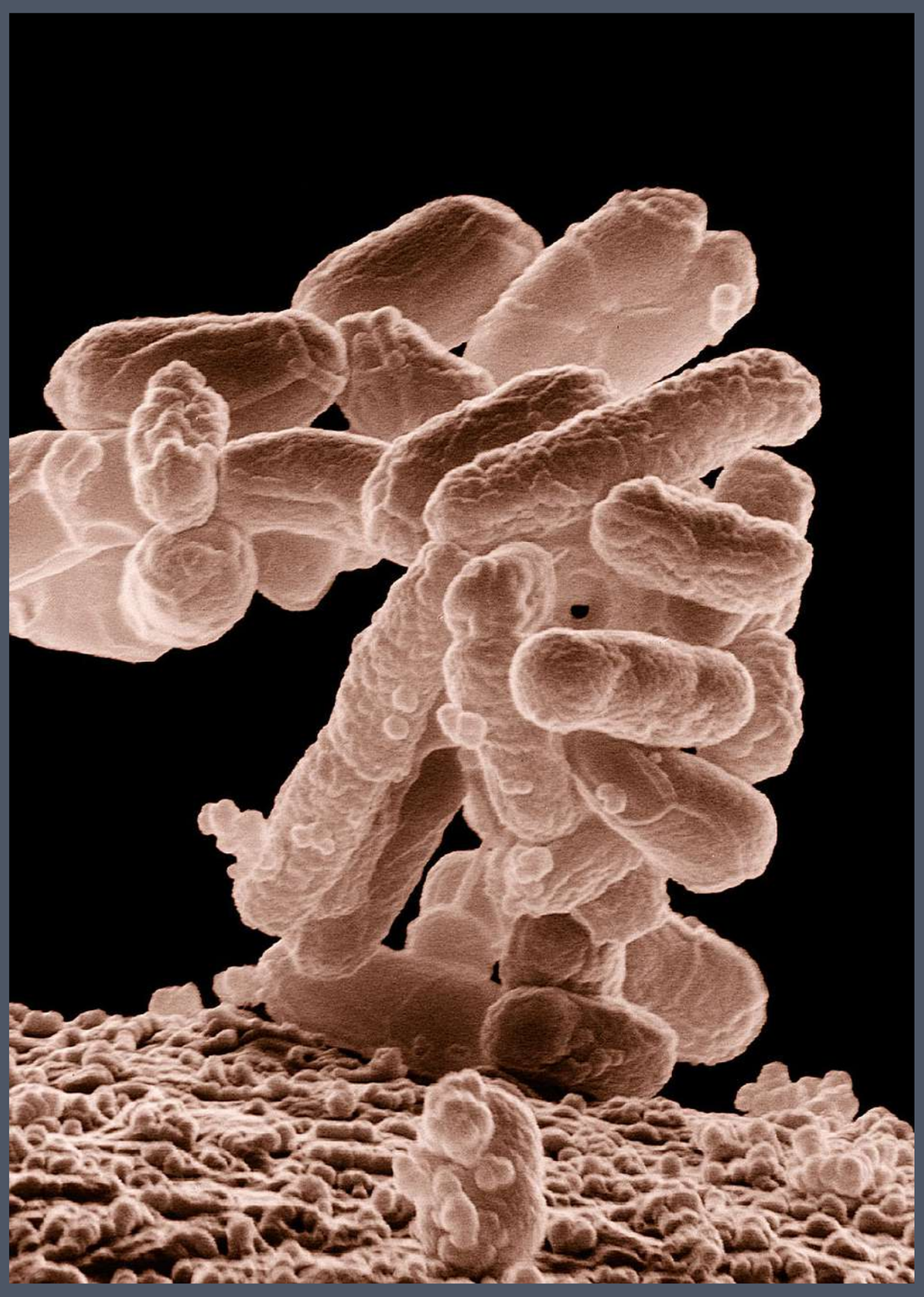


ABOUT

THE ASSOCIATION OF MICROBIOLOGISTS OF INDIA (AMI)



A cluster of Escherichia coli bacteria magnified 10,000 times

AMI

TThe AMI society was established in the year 1938 and is currently one of the oldest and reputed scientific organizations of India. Since its inception, it has contributed significantly towards development of microbiology, particularly in areas of research and teaching in country. This association publishes a quarterly journal known as "Indian Journal of Microbiology" for the last 45 years and organizes a National convention annually at one of the well-established centres of microbiology in the country. At present, this society has more than 4200 life and annual members along with 450 corporate members. The journal of this society has been acquired as respectable status among national and international scientific research periodicals in the world.

INSCR

INDIAN NETWORK FOR SOIL CONTAMINATION RESEARCH

Established in early 1999, in the wake of organising an international conference, on the subject of environmental pollution, conference was organised at Hotel Radisson in New Delhi, during December 1999. The network brought together several key researchers working on different aspects of contamination in soil environment spread across various academy, agricultural and industrial research institutions.

The December 1999 conference was a huge success attracting as many as 200 renowned scientists from various countries, i.e., Australia, New Zealand, Japan, China, Sweden, UK, U.S.A and elsewhere. Indian Network for Soil Contamination Research-INSCR is a registered society under the society's registration act XXI of 1860. You can join us and be next supporter to save environment.

MANIKARAN HOTSPRINGS

MICROBIAL WORLD:

RECENT DEVELOPMENTS IN HEALTH, AGRICULTURE AND ENVIRONMENTAL SCIENCES

The Event

The world is currently dealing with a pandemic caused by SARS-CoV-2. The ongoing pandemic has influenced our lifestyle, work cultures, and hygiene perspective. Sooner or later, the common people will understand the importance and cosmopolitan nature of these microbes. Thus, this year's conference aims to target the recent development in the microbial world. The horizon of the event has been extended by inviting students from different schools across India to propagate microbiology and raise awareness at the grass-root level. As this conference is operating in e-mode, we are fortunate enough to bring renowned scientists from across the globe on the same platform to discuss microbial advancements and to provide potential solutions to the current challenges related to health, agriculture, and the environment.

THE MESSAGES

Microscope A601160. Model of Hooke’s microscope as shown in 1665 edition of Micrographia, made by W.G. Turner, English, circa 1915
© Science Museum

PATRON

Ajay Mathur

Web www.teriin.org

teri The Energy and Resources Institute

Darbari Seth Block
I H C Complex
Lodhi Road
New Delhi – 110 003

Tel. 2468 2151 or 2468 2152
E-mail dg@teri.res.in
Fax 2468 2144
India +91 • Delhi (0) 11

Regional centres within India

North-Eastern Regional Centre
Guwahati
Tel. (361) 233 4790
E-mail terine@teri.res.in
Fax (361) 233 4869

Southern Regional Centre
Bangalore
Tel. (80) 2535 6590 (5 lines)
E-mail terisrc@teri.res.in
Fax (80) 2535 6589

Goa
Tel. (832) 245 9306 or 245 9328
E-mail terisrc@teri.res.in
Fax (832) 245 9338

Western Regional Centre
Mumbai
Tel. (22) 2758 0021 or 4024 1615
E-mail terimumbai@teri.res.in
Fax (22) 2758 0022

Himalayan Centre
Mukteshwar
Tel. (5942) 286 433
E-mail praveen.sharma@teri.res.in
Fax (5942) 286 460/433

TERI Worldwide

TERI **North America**
Tel. (+91) 9811150290
E-mail
annapurna.vancheswaran@terina.org

Antwerp
TERI-VITO
Tel. (+32 3) 286 74 31
E-mail ihrehman@teri.res.in

TERI **Japan**
Tokyo
Tel. (+81 3) 3519 8970
E-mail teri@iges.or.jp
Fax +81 33 5195 1084

An ISO 9001:2008 certified organization

Ajay Mathur *Ph.D.*
Director-General

December 9, 2020

Letter from Patron

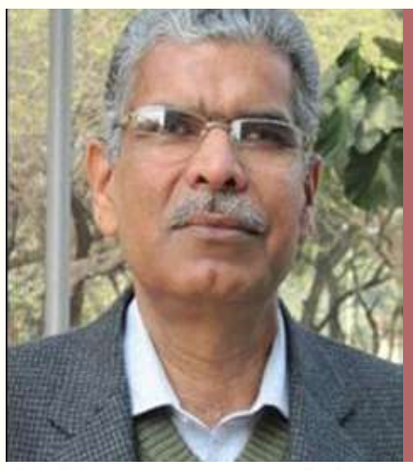
It gives me immense pleasure in writing this foreword for the book of abstracts of the papers to be presented at the 61st Annual Conference of Association of Microbiologists of India and 5th Annual Conference of Indian Network for Soil contamination Research, titled **"Microbial World: Recent Developments in Health, Agriculture and Environmental Sciences",** jointly organized by The Energy and Resources Institute, University of Delhi and IARI, under the aegis of Association of Microbiologists of India (AMI) and Indian Network for Soil Contamination and Research (INSCR) **from 3rd to 5th February 2021**.

This event is targeted towards researchers, professionals, educators, and students to share innovative ideas, issues, recent trends, and future directions in the fields one health, agriculture, and environmental sciences. The conference is preceded by two pre-conference workshops on Computational Biology and Art of Scientific Writing and Communication. Speakers from prestigious institutes around the globe and Indian scientists working in diverse fields of microbiology have given their consent to be a part of this conference.

While in this Conference, the major focus is on Microbes and Human Health, two Special Sessions on Viruses and Vaccine and Child-Centric Microbiology (Science & Society) are the major highlights. I am pleased to note that researchers from various Institutes/ Universities and Industries from different parts of the country and abroad are presenting their research on current aspects of Microbiome and One Health, Environmental & Agricultural Microbiology, Industrial Microbial Biotechnology, Advances in Microbial Systematics, Viruses & Vaccines (with special emphasis on SARS-CoV-2), Translating Innovative Ideas to Enterprise, Microbial Pathogenesis, and AMR.

I am sure that this Conference would greatly benefit researchers, students, and faculty. Young scientists and researchers will find the contents of the proceedings helpful to set roadmaps for their future endeavors. I take this opportunity to wish each and every one of you a very happy and prosperous 2021, and also wish great success of the International Conference of AMI and INSCR.

(Ajay Mathur)



PATRON
CHAIRPERSON

Ramesh C. Kuhad

हरियाणा केंद्रीय विश्वविद्यालय
महेंद्रगढ़--123031(हरियाणा), भारत
नैक द्वारा 'ए' ग्रेड प्राप्त विश्वविद्यालय

Central University of Haryana
Mahendergarh-123031 (Haryana), India
NAAC ACCREDITED 'A' GRADE UNIVERSITY

प्रो. आर. सी. कुहाड़, *कुलपति*
(एफएनएएससी, एफएनएएएस, एफबीआरएस)

Prof. R.C. Kuhad, *Vice-Chancellor*
(FNASc, FNAAS, FBRS)

Achieving Through Believing

क्रमांक / No. .....

दिनांक / Date: .....

Message

In my capacity as the Chairperson, I am delighted to welcome enthusiastic participants from all over the world to the 61st Annual International Conference of Association of Microbiologists of India (AMI) and 5th Indian Network for Soil contamination Research to be held from 3rd to 5th February, 2021.

Through this message, I congratulate the entire team from The Energy and Resources Institute (TERI), University of Delhi and Indian Agriculture Research Institute (IARI) for bringing out this delightful Abstract Book for the Conference under the aegis of Association of Microbiologists of India (AMI) and Indian Network for Soil Contamination and Research (INSCR). We are optimistic that this abstract book will provide an inspiring insight to contemporary research and emerging technology.

The event is carefully structured to include topics on social relevance and scientific accomplishments significant in these times. The event provides a common platform to young researchers, eminent scientists and educators to deliberate, innovate and find meaningful applications in the field of Microbiology. I am certain that it will be an enriching experience for the participants to gain from research findings shared by the internationally renowned microbiologists. The central themes for the oral and poster presentation of research papers cover the current aspects of Microbiome and One Health, Environmental & Agricultural Microbiology, Industrial Microbial Biotechnology, Advances in Microbial Systematics, Viruses & Vaccines, Translating Innovative Ideas to Enterprise, and Microbial Pathogenesis and AMR. Special effort has been made to promote microbial literacy by reaching out to children and society through the special themed Science and Society.

I appreciate and congratulate the Organizing Committee for their tremendous efforts in the organization of AMI-2021. Concluding, I wish a great success for the International Conference "Microbial World: Recent Developments in Health, Agriculture and Environmental Sciences."

Prof. R.C. Kuhad
Vice-Chancellor

ईमेल/Email: vc@cuh.ac.in; वेबसाइट/Website: www.cuh.ac.in

PATRON

P. C. Joshi

A very warm welcome to the 2021 Annual International Conference of Association of Microbiologists of India (AMI) , which is 61 st of its series and Indian Network for Soil contamination Research (5 th of its series). It gives me immense pleasure in writing this foreword for the Abstract Book of the Conference being jointly organized this year by The Energy and Resources Institute (TERI), University of Delhi and Indian Agriculture Research Institute (IARI) under the aegis of Association of Microbiologists of India (AMI) and Indian Network for Soil Contamination and Research (INSCR) during 3rd to 5th February 2021. This event is targeted towards researchers, professionals, educators and students to share innovative ideas, issues, recent trends and future directions in the field of Microbiology.

I am pleased to note that researchers from various Institutes/ Universities from different parts of the country and abroad are presenting their research papers on current aspects of Microbiome and One Health, Environmental & Agricultural Microbiology, Industrial

Microbial Biotechnology, Advances in Microbial Systematics, Viruses & Vaccines, Translating Innovative Ideas to Enterprise, and Microbial Pathogenesis and AMR. I am sure that this conference would greatly benefit researchers, students and faculty alike. Young scientists and researchers will find the contents of the Abstract Book helpful to set roadmaps for their future endeavours. We hope this collection of abstracts and invited talks will provide the listeners an insight in recent trends and research directions in emerging technology areas.

AMI-2021 is the result of tremendous efforts of the Organizing Committee. The committee took care of all aspects of the conference organization, preparing call for papers, evaluation of submitted papers, inviting guests. The Organizing Committee has done a great job and I wish them a great success for the International Conference “Microbial World: Recent Developments in Health, Agriculture and Environmental Sciences”.

P. C. Joshi
Patron

PATRON

Rakesh Bhatnagar

प्रो० राकेश भटनागर
कुलपति
Prof. Rakesh Bhatnagar Ph.D.
FNA, FASc, FNASc
Vice-Chancellor

काशी हिन्दू विश्वविद्यालय
Banaras Hindu University
(Established by Parliament by Notification No. 225 of 1916)
Varanasi – 221005 (INDIA)
Phone : 91-542-2368938, 2368339
Fax : 91-542-2369100, 2369951
E-mail :vc@bhu.ac.in
Website : www.bhu.ac.in

11th January 2021

Message

Greeting to everyone!!!!!

The best science can be done when we open ourselves for collaborations and this year's International conference, jointly organised by The Energy and Resources Institute, University of Delhi, IARI and INSA is one such example. I am delighted to welcome you all to the **61st Annual International Conference** of **Association of Microbiologists of India (AMI)** and **Indian Network for Soil Contamination and Research (INSCR)** titled **"Microbial World: Recent Developments in Health, Agriculture and Environmental Sciences"**, starting from 3rd to 5th February, 2021. I congratulate the organising committee for their laudable efforts to make this herculean task of bringing a large number of International and National Speakers at one platform. This conference is unique in the way as it provides opportunity to students of all age groups to participate and interact with the eminent experts in Microbiology from all over the world.

With seven thought-provoking themes engaging audience for complete three days, the conference focuses on the current concern for the pandemic caused by SARS-CoV-2. Other sessions that will be covered in the conference include microbial systematics, microbiome, environmental, viruses and vaccines, agricultural and industrial microbiology, pathogenesis, Translating Innovative Ideas to Enterprise thereby silhouetting all the crucial topics. The conference also focuses on a special session on Childcentric Microbiology.

Apart from this, organizers have taken utmost care that this conference should prove be a skill-enhancing platform for students with two pre-conference workshops, one focussing on training students for scientific writing and the other for skilling students in bioinformatics. Not only this, there is yet another special session on **"Young Scientist Colloquium"** to reward young minds for their research.

With this, I wish good luck to all the International and National speakers, resource persons, organisers, researchers, faculty from different institutions, students and all other participants form making this event a great success. Hope you all enjoy the five days' event and augment your knowledge in the world of microbes.

(Rakesh Bhatnagar)

PATRON

Appa Rao Podile

Message

Prof. Appa Rao Podile

Patron

"When learning is purposeful, creativity blossoms. When creativity blossoms, thinking emanates. When thinking emanates, knowledge is fully lit. When knowledge is lit, economy flourishes"- Dr. A.P.J. Abdul Kalam

Warm Greetings to All!!!!!

It gives me immense pleasure to welcome you all to the **61st Annual International Conference** of the Association of Microbiologists of India (AMI) and Indian Network for Soil Contamination and Research (INSCR) on **"Microbial World: Recent Developments in Health, Agriculture and Environmental Sciences"**, which is being jointly organized by TERI, University of Delhi and IARI from 3rd – 5th February 2021.

I am glad to note that there are 7 interesting themes in this three-day conference encompassing diverse aspects of microbiology with a special session on viruses and vaccines emphasizing SARS-CoV-2. The theme is very timely and strongly supports the need of the hour to combat the ongoing COVID-19 pandemic.

I hope that this conference would be a great platform to bring together eminent scientists and researchers in the field worldwide and provide an impetus to young minds to delve further into studying Microbiology and conducting innovative research in the future. Sharing their knowledge through presentations and fruitful discussions on the recent advances in microbiological sciences will generate new ideas and collaborations.

The conference also aims to promote microbiology literacy in the society and engage school students. This is a commendable effort by the organizing committee. I am confident that attending this conference will be a rewarding and enriching experience for all the participants.

I wish the conference a grand success!

APPA RAO PODILE
कुलपति / Vice-Chancellor
हैदराबाद विश्वविद्यालय
University of Hyderabad
हैदराबाद / Hyderabad-500 046, भारत / India

PATRON

A.K. Singh

भा.कृ.अ.प. – भारतीय कृषि अनुसंधान संस्थान, नई दिल्ली–110012 (भारत)
ICAR - INDIAN AGRICULTURAL RESEARCH INSTITUTE
(A DEEMED TO BE UNIVERSITY UNDER SECTION 3 OF UGC ACT, 1956)
NEW DELHI - 110012 (INDIA)

डॉ. अशोक कुमार सिंह
निदेशक
Dr. Ashok Kumar Singh
Director

Phones : 011-2584 2367, 2584 3375
Fax : 011-2584 6420
E-mail : director@iari.res.in
Personal : aks_gene@yahoo.com
Website : www.iari.res.in

Message

I am pleased to extend a very cordial welcome to all of you on the 61st Annual International Conference of Association of Microbiologists of India (AMI) and Indian Network for Soil Contamination Research (INSCR) titled "**Microbial World: Recent Developments in Health, Agriculture and Environmental Sciences**". This year is the first time this International Conference is online being jointly organised by University of Delhi, The Energy and Resources Institute, IARI and INSA.

I am delightful to share that the scientific program is well structured into **seven themes covering all aspects of microbiology, biotechnology and its diverse applications**. We are honoured to have more than 100 distinguished speakers from all over the world to share and exchange their latest research, experiences and ideas. Along with this, special sessions for society and faculty are included to propagate microbiological research.

I am glad to inform you that the conference is preceded by two **pre-conference workshops** on scientific writing and communication and genomics and metagenomic analyses. The excellent program and activities of the conference are the results of diligent effort from the organizing committee members and organizers. I thank all the organizers for their dedication to make an outstanding technical program for the conference and the pre-conference workshops.

I wish all the best to the participants and organizers for the conference. I sincerely hope that you will enjoy this digital five-day event.

(A.K. SINGH)

CO-PATRON

Vibha Dhawan

Web www.teriin.org

teri The Energy and Resources Institute

Darbari Seth Block
I H C Complex
Lodhi Road
New Delhi – 110 003

Tel. 2468 2100 or 7110 2100
E-mail mailbox@teri.res.in
Fax 2468 2144 or 2468 2145
India +91 • Delhi (0) 11

Regional centres within India

North-Eastern Regional Centre
Guwahati
Tel. (361) 233 4790
E-mail terine@teri.res.in
Fax (361) 233 4869

Southern Regional Centre
Bangalore
Tel. (80) 2535 6590 (5 lines)
E-mail terisrc@teri.res.in
Fax (80) 2535 6589

Goa
Tel. (832) 245 9306 or 245 9328
E-mail terisrc@teri.res.in
Fax (832) 245 9338

Western Regional Centre
Mumbai
Tel. (22) 2758 0021 or 4024 1615
E-mail terimumbai@teri.res.in
Fax (22) 2758 0022

Himalayan Centre
Mukteshwar
Tel. (5942) 286 433
E-mail praveen.sharma@teri.res.in
Fax (5942) 286 460/433

TERI **Japan**
Tokyo
Tel. (+81 3) 3519 8970
E-mail teri@iges.or.jp
Fax +81 33 5195 1084

Letter from Co-Patron

On behalf of the organizing committee, it gives me great pleasure to extend a warm welcome to all presenters and participants to the 61st Annual Conference of Association of Microbiologists of India and 5th Annual Conference of Indian Network for Soil contamination Research titled **"Microbial World: Recent Developments in Health, Agriculture and Environmental Sciences"** jointly organized by The Energy and Resources Institute (TERI), University of Delhi and Indian Agriculture Research Institute (IARI) under the aegis of Association of Microbiologists of India (AMI) and Indian Network for Soil Contamination and Research (INSCR) from **3rd to 5th February 2021**. This conference is a premier conference concerning topics of current aspects of Microbiome and One Health, Environmental & Agricultural Microbiology, Industrial Microbial Biotechnology, Advances in Microbial Systematics, Viruses & Vaccines (Special emphasis on SARS-CoV-2), Translating Innovative Ideas to Enterprise, Microbial Pathogenesis and Antibiotic Microbial Resistance. The conference provides an international forum for students, researchers, and scientists to meet on a virtual platform and exchange ideas on the latest developments and future direction of these systems. Two pre-conference workshops on Computational Biology and Art of Scientific Writing and communication are expected to be very useful for the budding scientists. Special sessions on Microbes and Human Health, Viruses and Vaccine, Child-Centric Microbiology (Science & Society), Sand-art display, and Yoga sessions are the major highlights. I take this opportunity to wish you all great success of the International Conference of AMI and INSCR.

Vibha Dhawan.
Vibha Dhawan

CO-PATRON

Jitendra P. Khurana

Greetings!

I welcome all the participants to the 61 st annual conference of Association of Microbiologists of India (AMI) and 5 th Annual conference of Indian Network of Soil Contamination Research (INCSR). AMI each year puts in immense efforts to bring together the scientific community for the exchange of ideas through their conferences which often results in fruitful collaborations. This year AMI and INCSR in association with The Energy and Resources Institute (TERI), University of Delhi and Indian Agricultural Research Institute (IARI) are organizing the conference entitled 'Microbial World: Recent Development in Health, Agriculture and Environmental Science' from 3 rd to 5 th February 2021. This conference has been designed keeping in mind that the COVID 19 pandemic has stressed the need to increase microbial literacy amongst all including school students.

This annual event will be a confluence of research fellows, young scientists and distinguished researchers presenting their work. The organizing body will be holding two pre-conference workshops for hands on training for the participants in data mining and scientific writing. The conference has seven themes including current trends in Microbial Pathogenesis, Industrial Microbial Biotechnology, Microbial Systematics and Environmental and Agricultural Biotechnology. There is a special session on 'Child-centric Microbiology (Science & Society)' for students from schools all across the country spanning both rural areas and cities ensuring microbial literacy at grassroot level. Another highlight of this conference is the 'Young Scientist Colloquium' wherein the teaching faculty, students and researchers can present their work through oral presentations.

I am sure this conference will become a learning experience for you.

Prof. J. P. Khurana
Co-Patron

CHAIRPERSON
ORGANISING SECRETORY

Yogendra Singh

PROF. YOGENDRA SINGH
FNA, FNASc, FASc

DEPARTMENT OF ZOOLOGY
UNIVERSITY OF DELHI,
DELHI- 110007, INDIA
Mobile: 9871095673
Email: ysinghdu@gmail.com

Dear colleagues and guests,

On behalf of the organizing committee, it is my great pleasure to welcome you to the 61st Annual conference of the Association of Microbiologists of India (AMI) and the 5th Annual conference of the Indian Network of Soil Contamination Research (INCSR). This year the AMI and the INCSR, in association with The Energy and Resources Institute, University of Delhi and Indian Agricultural Research Institute, are organizing the conference entitled 'Microbial World: Recent Developments in Health, Agriculture and Environmental Science' from 3rd to 5th February 2021. The idea to host the AMI each year is to build a research network highlighting the importance of microbiology. Due to the current COVID-19 situation, we encourage our participants to stay safe and maintain social distancing. As a result, this conference will be the first of many conferences that will be conducted remotely through the use of advanced digital technologies.

The AMI 2021 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 seven themes including Current Trends in Microbial Pathogenesis, Industrial Microbial Biotechnology, Microbial Systematics and Environmental, and Agricultural Biotechnology. A special session will also be held on 'Child-centric Microbiology (Science & 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 three 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.

Thank you,

Yogendra Singh

Yogendra Singh

ORGANIZING SECRETARY

Rup Lal

Web www.teriin.org

teri The Energy and Resources Institute

Darbari Seth Block
I H C Complex
Lodhi Road
New Delhi – 110 003

Tel. 2468 2100 or 7110 2100
E-mail mailbox@teri.res.in
Fax 2468 2144 or 2468 2145
India +91 • Delhi (0) 11

Regional centres within India

North-Eastern Regional Centre
Guwahati
Tel. (361) 233 4790
E-mail terine@teri.res.in
Fax (361) 233 4869

Southern Regional Centre
Bangalore
Tel. (80) 2535 6590 (5 lines)
E-mail terisrc@teri.res.in
Fax (80) 2535 6589

Goa
Tel. (832) 245 9306 or 245 9328
E-mail terisrc@teri.res.in
Fax (832) 245 9338

Western Regional Centre
Mumbai
Tel. (22) 2758 0021 or 4024 1615
E-mail terimumbai@teri.res.in
Fax (22) 2758 0022

Himalayan Centre
Mukteshwar
Tel. (5942) 286 433
E-mail praveen.sharma@teri.res.in
Fax (5942) 286 460/433

T E R I **Japan**
Tokyo
Tel. (+81 3) 3519 8970
E-mail teri@iges.or.jp
Fax +81 33 5195 1084

Prof. Rup Lal
NASI Senior Scientist

Dated: 21.01.2021

Greetings! On behalf of the organizing team of the 61st Annual Conference of Association of Microbiologists of India (AMI) and 5th Annual Conference of Indian Network for Soil Contamination Research (INSCR), it gives me great pleasure in welcoming all the participants to this event. The AMI-INSCR International Conference 2021 titled, "**Microbial World: Recent Developments in Health, Agriculture and Environmental Sciences**" is being organized by The Energy and Resources Institute (TERI), University of Delhi and Indian Agriculture Research Institute (IARI) under the aegis of AMI and INSCR from 3rd to 5th February, 2021.

Due to the unprecedented pandemic the world is engulfed in, the microbial world is in the highlight again and hence there's a need to spread microbial literacy amongst one and all at the grassroot level. It also necessitates the sharing of ideas and knowledge pertaining to microbial research. The annual AMI conference is an initiative that brings together distinguished scientists from all over the world to a common platform and provides opportunity to interact with them.

The sessions in AMI-INSCR International Conference 2021 focus on interesting themes such as Environmental & Agricultural Microbiology, Advances in Systematics, Virology and Vaccines emphasizing on the SARS-CoV-2 virus, Industrial and Microbial Biotechnology, Microbial Pathogenesis and Antimicrobial Resistance and Translating Innovative Ideas to Enterprise. Two workshops focusing on 'Art of Scientific Writing' and 'Computational Biology for Metagenomic Analysis' have also been planned for the participants to provide them with more exposure in the scientific content development and data analysis. The AMI-INSCR Innovative Research sessions and the special session on "Reaching out to the Children and Society" further aim to stimulate 'out of the box' innovative thinking in young scientists, faculty, UG/PG and school students. The unique initiative of including school students will aid in opening their minds to pursue a career in sciences.

I sincerely hope that these days of engagement in AMI-INSCR Conference 2021 will leave all the participants with knowledge, fond memories and renewed enthusiasm.

Rup Lal

Prof. Rup Lal,
Organizing Secretary

भाकृअनुप
ICAR

डा० सुनील पब्बी
प्रधान वैज्ञानिक

Dr. Sunil Pabbi
Principal Scientist

नील हरित शैवाल संरक्षण एवं उपयोग केंद्र
सूक्ष्म जीव विज्ञान संभाग
भा.कृ.अनु.प.-भारतीय कृषि अनुसंधान संस्थान, नई दिल्ली-110012
Centre for Conservation and Utilisation of Blue Green Algae
DIVISION OF MICROBIOLOGY
ICAR-Indian Agricultural Research Institute, New Delhi - 110 012

MESSAGE

Welcome to the 61st Annual International Conference of Association of Microbiologists of India (AMI) and Indian Network for Soil Contamination Research (INSCR) jointly organized by The Energy and Resources Institute (TERI), University of Delhi (DU), ICAR - Indian Agricultural Research Institute (IARI) and Indian National Science Academy (INSA) under the Theme: "**Microbial World: Recent Developments in Health, Agriculture and Environmental Sciences**". It is my honour, together with my colleagues and organizers to welcome you to this conference which is being organized in a virtual mode.

The world is experiencing many global challenges related to food, feed, fuel and clean air to all which require our immediate action and strategic planning. Microbes and microbial biotechnology can ensure a sustainable production of fuels, chemicals and other commodities of human need. Nevertheless, lot of progress and advancement is happening and with interdisciplinary effort, microbiology would achieve new high levels in transforming the world.

On behalf of the AMI and the organizing committee, I welcome all the distinguished scientists, researchers and participants from around the globe to this conference. I look forward to hearing your presentations, achievements, opinions and views in the next three days, which is not only going to inspire us but will also have an impact on our society.

Dr. Sunil Pabbi
Organizing Secretary

Tel. : 011-2584 8431
Fax : 011-2584 3379

E-mail : sunil_micro@iari.res.in
sunil.pabbi@gmail.com

ORGANIZING SECRETARY

Banwari Lal

Web www.teriin.org

teri The Energy and Resources Institute

Darbari Seth Block
I H C Complex
Lodhi Road
New Delhi – 110 003

Tel. 2468 2100 or 7110 2100
E-mail mailbox@teri.res.in
Fax 2468 2144 or 2468 2145
India +91 • Delhi (0) 11

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E-mail praveen.sharma@teri.res.in
Fax (5942) 286 460/433

TERI **Japan**
Tokyo
Tel. (+81 3) 3519 8970
E-mail teri@iges.or.jp
Fax +81 33 5195 1084

Message

Banwari Lal, PhD

Senior Director
Environmental and Industrial Biotechnology Div

Association of Microbiologists of India (AMI) is one of the largest scientific societies, which is almost 83 years old. More than 1500 microbiologists from all over the world are associated with this prestigious society. Almost every student in the area of Microbiology is associated with AMI.

AMI has been organising annual conferences every year and this year it would be the 61st AMI Conference on "Microbial World: Recent Developments in Health, Agriculture and Environmental Sciences" being organised jointly by The Energy and Resources Institute, University of Delhi and IARI under the aegis of Association of Microbiologists of India (AMI) and Indian Network for Soil Contamination and Research (INSCR), scheduled to be held virtually, **from 2nd to 5th February 2021**. More than 1000 eminent scientists and students from all over the world would be participating in the above international conference. This will provide an excellent opportunity to listen to eminent speakers and to get insight on latest development on all aspect of Microbiology.

Since this would be a virtual conference so there is lot of enthusiasm as it would be a great learning experience for all of us.

I wish all the best for successful 61st AMI Conference.

(Banwari Lal)

भारतीय जीवाणुतत्ववेत्त संगठन
Association of Microbiologists of India

AMI. A leading scientific organization of India since 1938

Professor Namita Singh
General Secretary

No. AMI/----------
Dated: ----------

Message

I am pleased to welcome you all to the 61st Annual International conference of The Association of Microbiologists of India (AMI) from 3rd -5th February, 2021. This conference is being organised in collaboration with Indian Network for Soil Contamination Research (INSCR), The Energy and Resources Institute (TERI), University of Delhi (DU), Indian Agricultural Research Institute (IARI) & Indian National Science Academy (INSA).

AMI was established in 1938 and currently has approximately 5000 individuals and 425 corporate members. It is my conjecture that Microbiology is not only a basic subject from academics point of view but also defines the basics of life and economy. **COVID-19 pandemic has proved it.** Therefore, time has come to the objectives of AMI are going to be much wider than what we thought nine decades earlier. I believe that the theme of current conference is wider concept of Microbiology in our daily life. The advancement in application of modern biology will affect human being and society deeply, consequently Microbiology industries would become leading industries in future.

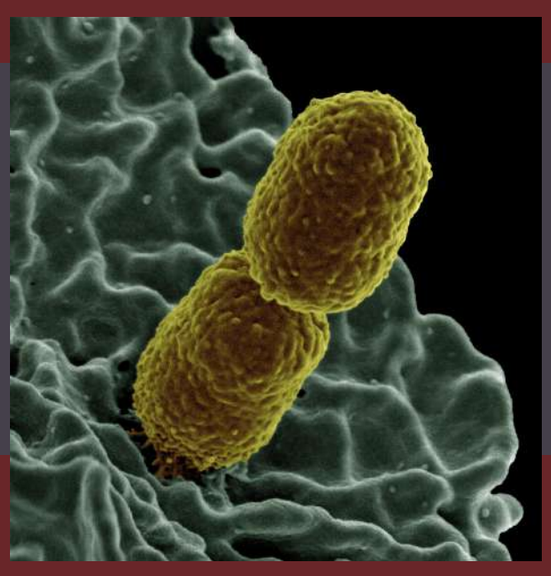
The current pandemic situation throughout the globe has proved that microbial science of common-sense because the basic of microbiology *sanitization, isolation and preservation* is the new way of life now. This is what **Louis Pasteur** (pasteurisation) and **Schroeder Bush** (cotton plugs) did in 18th Century. I believe there is need to take the knowledge of microbiology to the common population and we must make people aware to practice basics of microbiology in day to day life. Covid-19 pandemic has once again taught us a lesson that microbiology as science is beyond any physical or geographical boundaries. Therefore, I pay homage to all the past microbiologist of the world.

As the General Secretary of AMI, and practicing microbiologist I acknowledge the importance of the Microbiologist and the aptly coined conference theme *"Microbial world: Recent developments in health, Agriculture and Environmental Sciences"*. I have also gone through the various scientific programs earlier and I would like to appreciate the hard work done by organising committee to make it very engaging academically and entertaining. I am looking forward to see many happy faces and refreshed minds at the end of this conference theme to the ground reality.

Once again on behalf of AMI and organizing committee I welcome you all and wish you stay safe and comfortable wherever you are. I also wish this conference a success.

JAI HIND (*Long Live India*)

Namita Singh
(General Secretary- AMI)

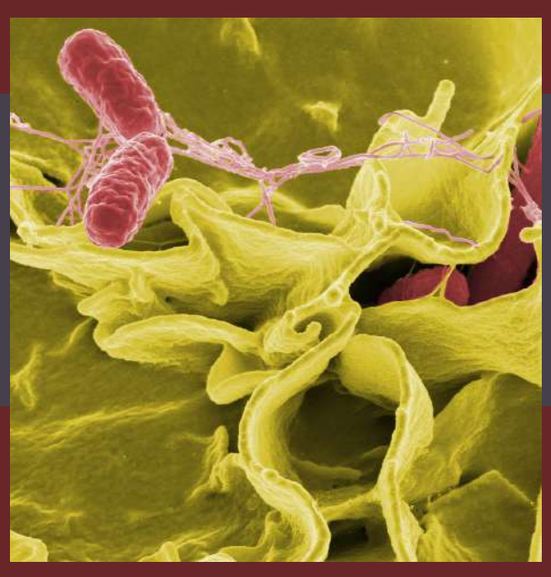


TREASURERS

SUNIL PABBI (TREASURER, AMI)

A. K. DIKSHIT (TREASURER, INSCR)

UTKARSH SOOD (TERI)



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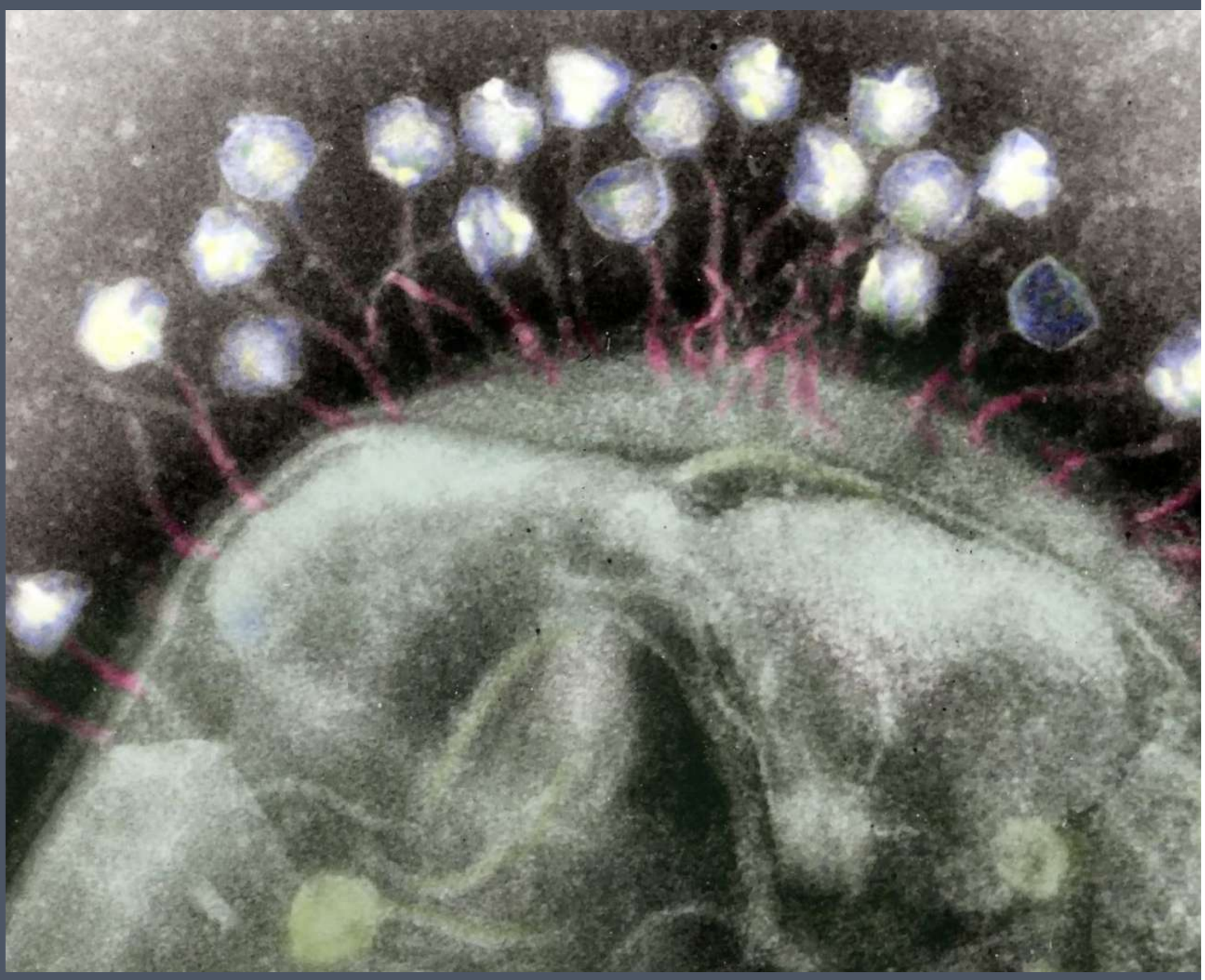
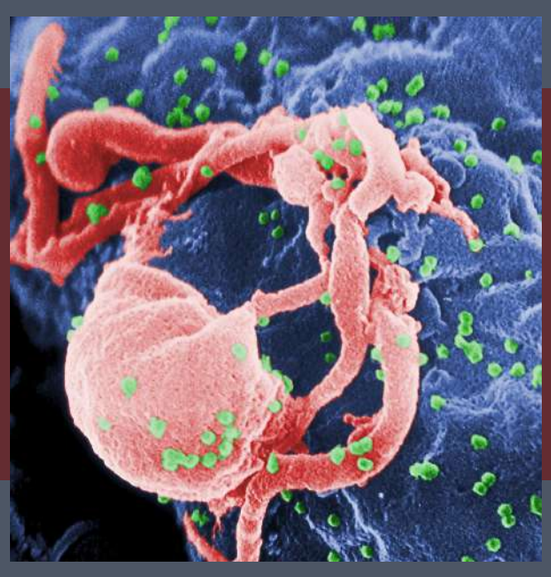
COMMITTEES



A false-color transmission electron micrograph of multiple bacteriophages attached to a bacterial cell wall.



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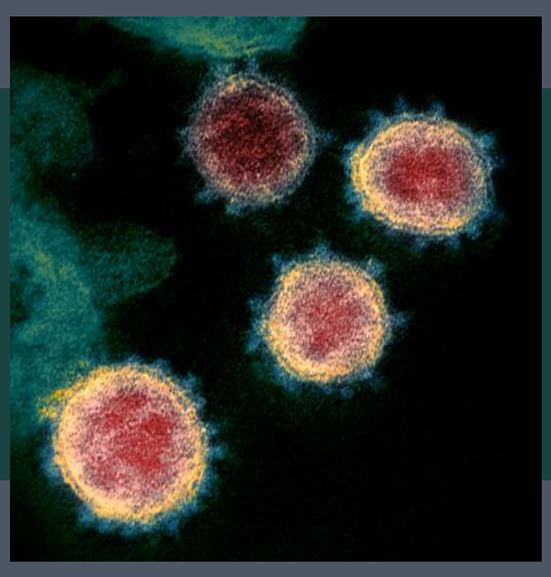

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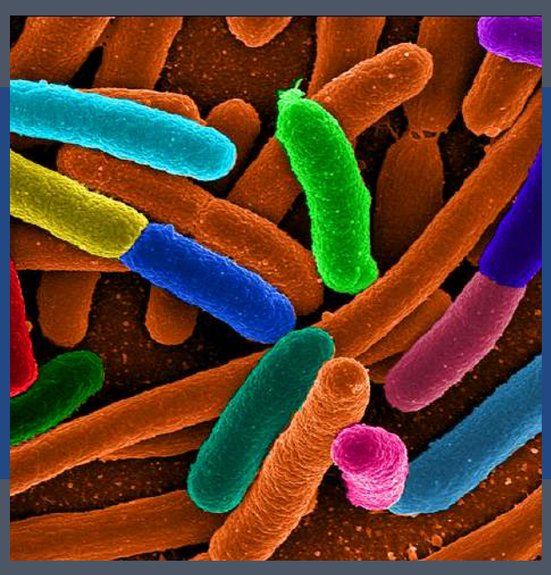

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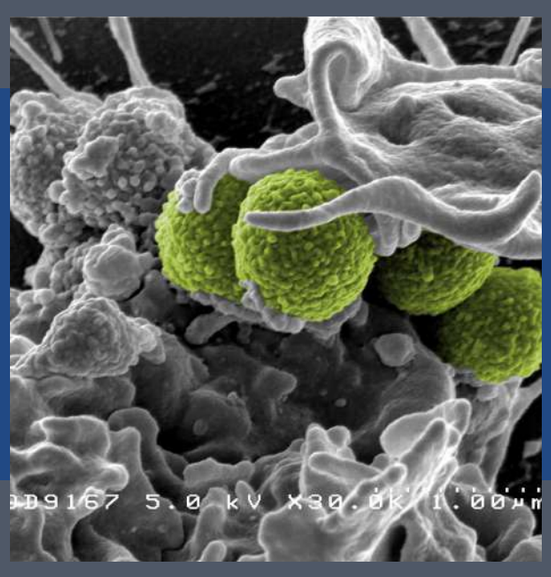

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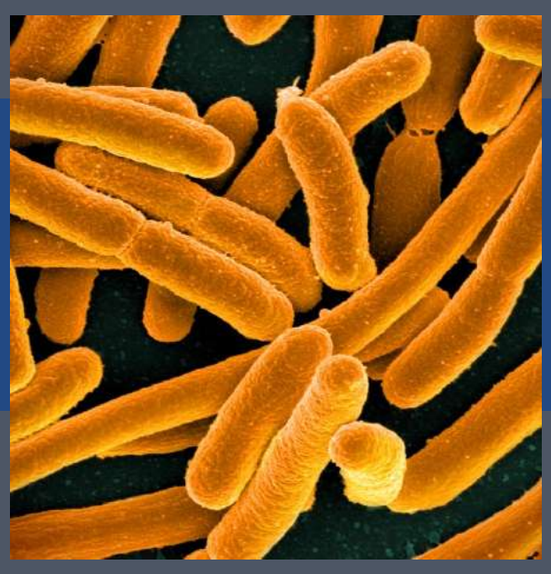

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5 DAYS FULL OF KNOWLEDGE

HANDS ON TO COMPUTATIONAL BIOLOGY FOR (META)GENOMICS ANALYSIS IN COLLABORATION WITH ISME

1ST - 2ND FEB, 2021

Awards

AMI - Alembic Awards

AMI- Louis Pasteur Award

AMI-Prof. B.N Johri Award

AMI - Louis Pasteur Award

AMI-Prof. S.R. Vyas Award

AMI-Young Scientist Awards

Dr. J.V. Bhat Award for Best Paper Published in INJM

AMI- Life time achievement Award

AMI- Best Unit Award

DR DHEERAJ. P. JOSHI

(YOGA & WELLBEING EXPERT)

QUIZ

Special Sessions!

REACHING OUT TO CHILDREN & SOCIETY

- One Food
- See the unseen
- Pet Chemistry
- Global Warming
- Vaccine
- Foldscope
- Discovering Microbes
- Microbes & Action
- Microbiomes

INTERNATIONAL POSTER COMPETITION on "MICROBIOLOGY"

SESSION CHAIR:
KENNETH TIMMIS

SESSION CO-CHAIR:
JITENDRA P. KHURANA

SCIENCE & SOCIETY

Themes

MICROBIOME AND ONE HEALTH

ENVIRONMENTAL & AGRICULTURAL MICROBIOLOGY

INDUSTRIAL MICROBIAL BIOTECHNOLOGY

ADVANCES IN MICROBIAL SYSTEMATICS

VIRUSES & VACCINES (SPECIAL EMPHASIS ON SARS-COV-2)

MICROBIAL PATHOGENESIS AND AMR

TRANSLATING INNOVATIVE IDEAS TO ENTERPRISE

AMI/INSCR INNOVATIVE RESEARCH (FACULTY & STUDENTS/SCHOLARS)

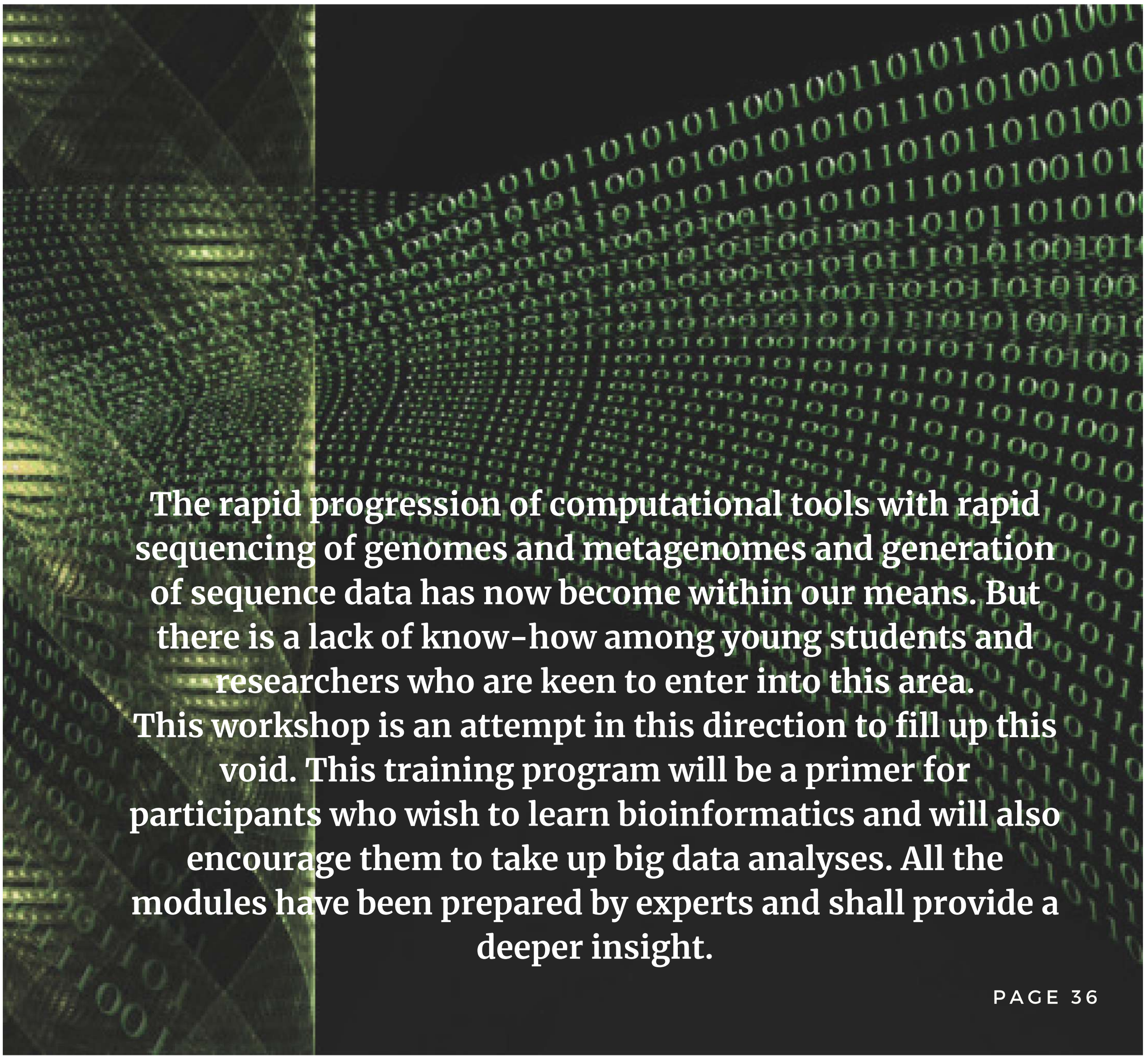
2021

1-2 FEB

PRE-CONFERENCE WORKSHOP

HANDS-ON COMPUTATIONAL BIOLOGY FOR (META)GENOMICS ANALYSIS IN COLLABORATION WITH ISME

ISME



The rapid progression of computational tools with rapid sequencing of genomes and metagenomes and generation of sequence data has now become within our means. But there is a lack of know-how among young students and researchers who are keen to enter into this area.
This workshop is an attempt in this direction to fill up this void. This training program will be a primer for participants who wish to learn bioinformatics and will also encourage them to take up big data analyses. All the modules have been prepared by experts and shall provide a deeper insight.

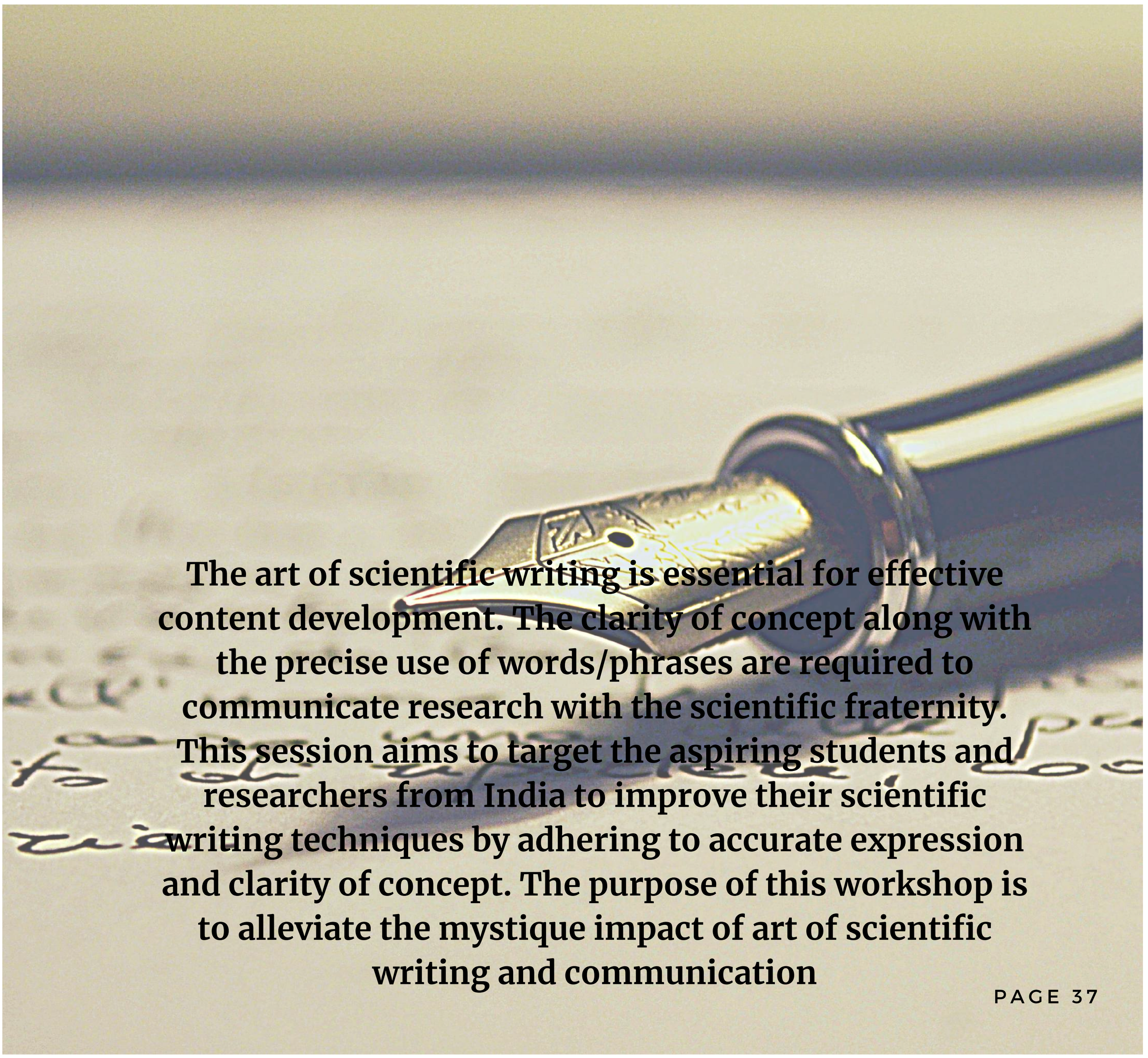
2021

2 FEB

PRE-CONFERENCE WORKSHOP

ART OF SCIENTIFIC WRITING AND COMMUNICATION

AMERICAN SOCIETY FOR MICROBIOLOGY



The art of scientific writing is essential for effective content development. The clarity of concept along with the precise use of words/phrases are required to communicate research with the scientific fraternity. This session aims to target the aspiring students and researchers from India to improve their scientific writing techniques by adhering to accurate expression and clarity of concept. The purpose of this workshop is to alleviate the mystique impact of art of scientific writing and communication

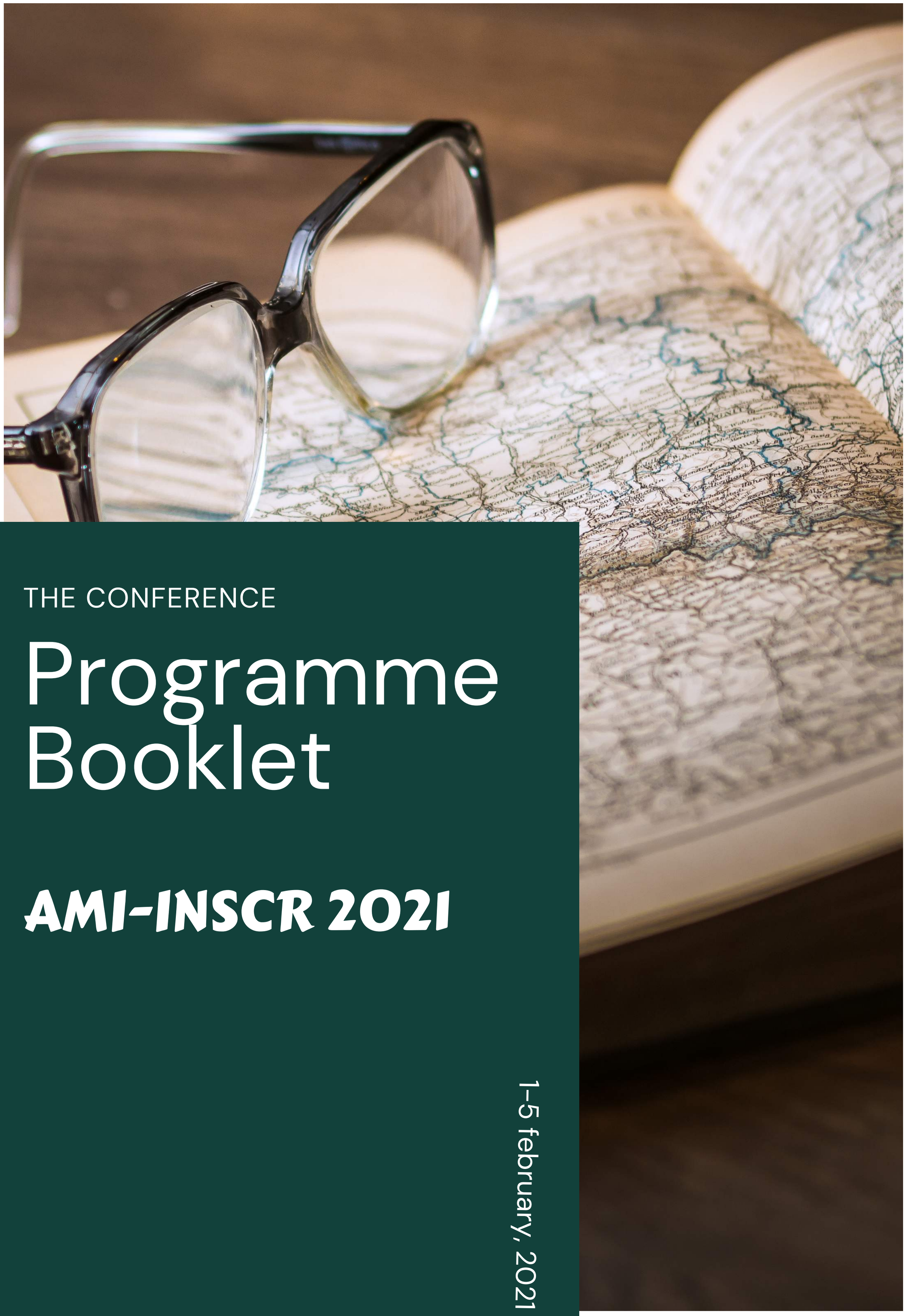
SAND ART!

DR. BADAL BARAI

DID YOU KNOW ?

A SINGLE SAND GRAIN HARBORS UP TO 100,000 MICROORGANISMS FROM THOUSANDS OF SPECIES !!!!

DISCOVER THE WORLD OF MICROBES!



THE CONFERENCE

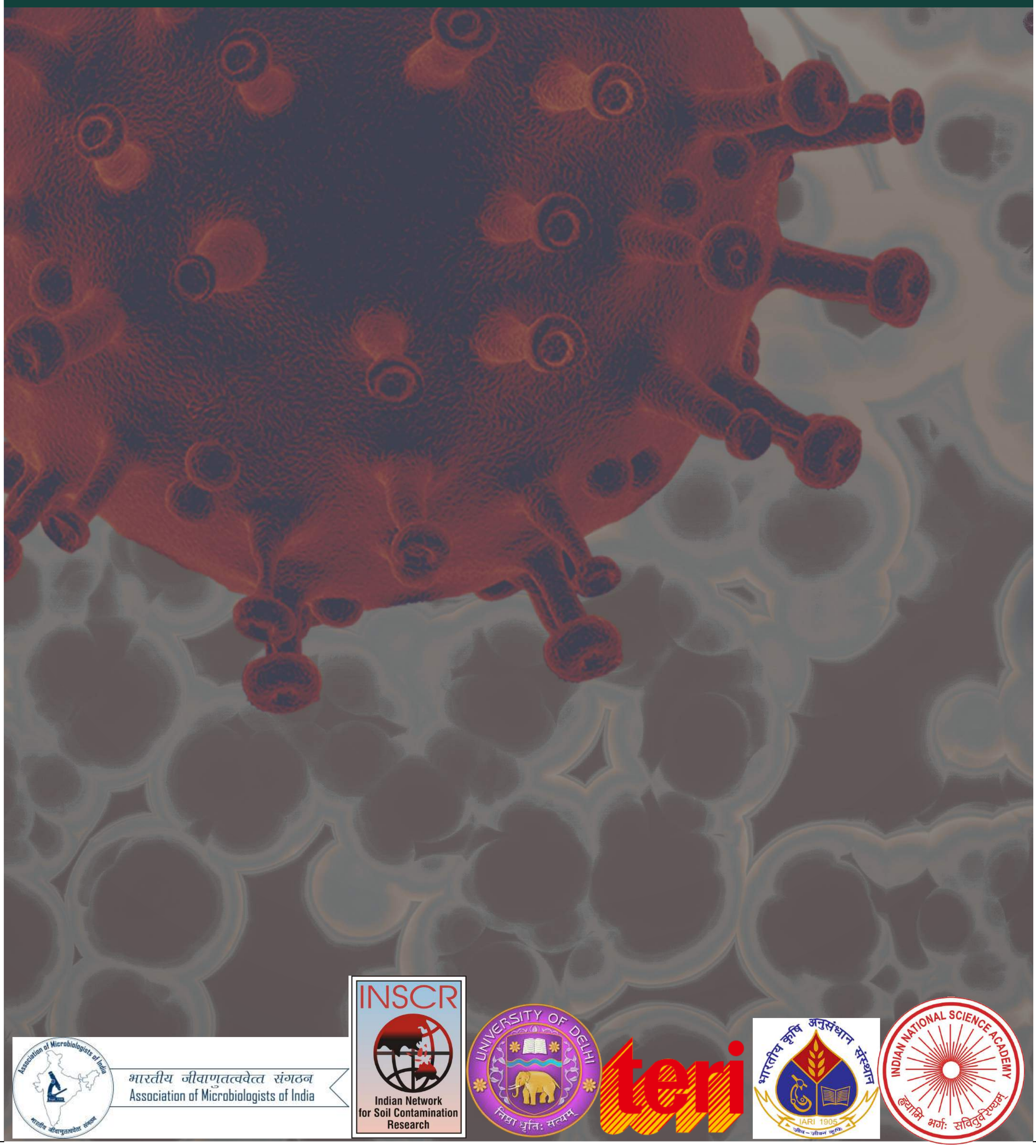
Programme Booklet

AMI-INSCR 2021

1–5 february, 2021

61ST INTERNATIONAL CONFERENCE

Annual International Conference of
The Association of Microbiologists of India (AMI) &
Indian Network for Soil Contamination Research (INSCR)
in association with
The Energy and Resources Institute (TERI),
University of Delhi (DU),
Indian Agricultural Research Institute (IARI) &
Indian National Science Academy (INSA)



भारतीय जीवाणुतत्ववेत्त संगठन
Association of Microbiologists of India

Indian Network for Soil Contamination Research

Pre-conference workshops

on 1-2 february, 2021

HANDS ON TO COMPUTATIONAL BIOLOGY FOR (META)GENOMICS ANALYSIS

1st february, 2021
0900 - 1800

in collaboration with
ISME

2nd february, 2021
0900 – 1100

in collaboration with
ISME

ART OF SCIENTIFIC WRITING & COMMUNICATION

2nd february, 2021
1130 - 1630

in collaboration with
ASM

INJM EDITORIAL BOARD MEETING

2nd february, 2021

1330 - 1430

Only for Members of AMI Central Council and INJM Editorial Board

AMI CC MEETING

2nd february, 2021

1440 - 1530

Only for Members of AMI Central Council and INJM Editorial Board

CONFERENCE

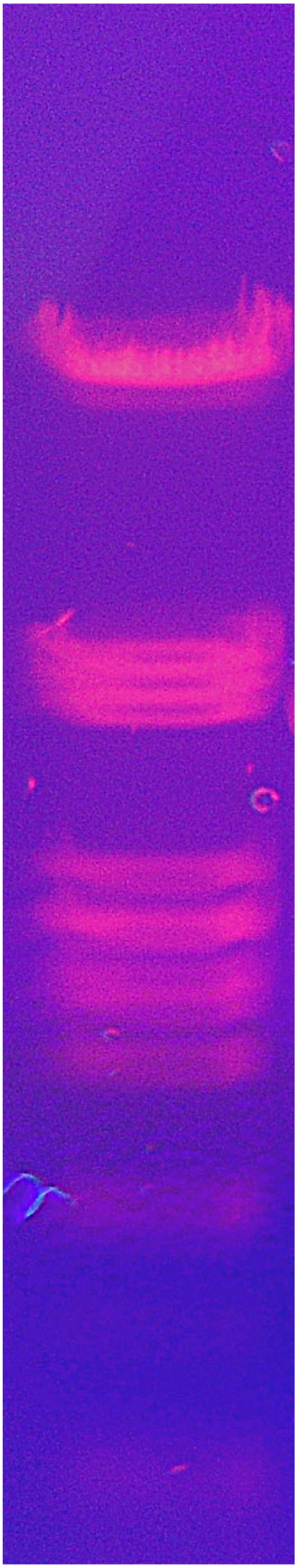
Inauguration

2ND FEB

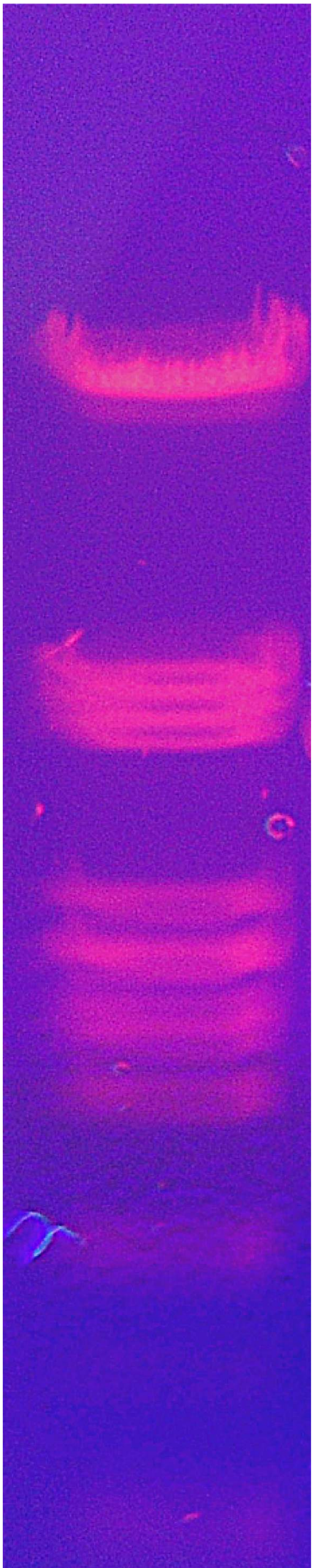
SAND ART

1815 – 1830

INAUGURATION



2 feb, 2021 1735-1740	Welcome Address: **Prof. Rup Lal** (Organizing Secretary, AMI-INSCR-2021)
1740-1745	Introduction to AMI: **Prof. Namita Singh** (General Secretary, AMI)
1745-1755	AMI/INSCR introduction and Presidential Address: **Prof. Yogendra Singh** (President, AMI, General Sec., INSCR)
1755-1805	About FAMSc: **Prof. R. C. Kuhad** (Chairperson, FAMSc)
1805-1815	Remarks: **Prof. Ajay Mathur** (Director General, TERI)
1815-1830	Special Attraction: **Sand Art by Dr. Badal Barai**
1830-1835	AMI Award announcement **Prof. Namita Singh** (General Secretary, AMI)
1835-1850	AMI Albemic Award (2)
1850-1855	AMI Louis Pasture Award
1855-1900	AMI - Prof. B.N. Johri Award
1900-1905	AMI- Prof. S.R. Vyas Award
1905-1930	Young Scientist Award (5)
1930-1940	Dr. J.V. Bhatt Award for Best Paper (2)
1940-2000	AMI- Life Time Achievement Award (2)
2000-2015	AMI- Best Unit Award



2015-2020	**Vote of Thanks** **Prof. Sunil Pabbi** (Organizing Secretary, AMI-INSCR-2021)
2030-2130	**Inaugural Lecture** Chairpersons: Prof. Rup Lal (TERI), Prof. Yogendra Singh (UoD) Speaker: **Prof. Jack Gilbert** (University of California San Diego, USA) Title of the talk: "Microbiology of the Built Environment during a global pandemic"
2130-2135	**Conference Program Concludes for Day 2 & highlights for Day 3**

GUIDE TO THE SESSIONS

1 MICROBIOME AND ONE HEALTH
-3 FEB, 10.35-11.30
CLICK HERE TO JOIN

2 ENVIRONMENTAL AND AGRICULTURAL MICROBIOLOGY
– 3 FEB, 11.45- 19.20
CLICK HERE TO JOIN

3 CHILD-CENTRIC MICROBIOLOGY (PARALLEL TO 2)
– 3 FEB, 11.30-17.30
CLICK HERE TO JOIN

4 INDUSTRIAL MICROBIAL BIOTECHNOLOGY
-4 FEB, 10.10-16.45
CLICK HERE TO JOIN

5 AMI/INSCR INNOVATIVE RESEARCH (FACULTY) (PARALLEL TO 4)
- 4 FEB, 11.20-13.50
CLICK HERE TO JOIN

6 VIRUSES AND VACCINES
– 4 FEB, 16.50-19.00
CLICK HERE TO JOIN

AMI AWARD LECTURES (PARALLEL TO SESSION 6)
-4 FEB, 17.25-18.35
CLICK HERE TO JOIN

7 ADVANCES IN MICROBIAL SYSTEMATICS
5 FEB, 09.30-13.05
CLICK HERE TO JOIN

8 AMI/INSCR INNOVATIVE RESEARCH (STUDENTS & SCHOLARS)
(PARALLEL TO 7)
– 5 FEB, 09.30-16.50
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9 TRANSLATING INNOVATIVE IDEAS TO ENTERPRISE
5 FEB, 13.40-16.50
CLICK HERE TO JOIN

10 MICROBIAL PATHOGENESIS AND AMR
– 5 FEB, 16.55-18.50
CLICK HERE TO JOIN

3 FEBRUARY 2021

DAY 1

Opening

Chairpersons: Prof. Ramesh Chandra Kuhad, Prof. Rup Lal, Prof. Yogendra Singh

DR. RANDEEP GULERIA — 09.00-09.50

Director, AIIMS, Delhi, India

Antimicrobial resistance and One Health (Inaugural Lecture 1)

PROF. EDWARD FRANCIS DELONG — 09.55-10.30

ISME Past president: University of Hawaii, Manoa, USA

Marine microbial dynamics in space and time: a genomic perspective (Inaugural Lecture 2)

DAY 1

Session 1, Microbiome and One Health

PROF. CRAIG CARY — 10.35-11.00

University of Delaware, Delaware, USA and University of Waikato, New Zealand

IN EXTREMIS: Microbial ecology of Antarctica's terrestrial refugia (Keynote Lecture 1)

DR. ANIL KOUL — 11.05-11.30

Johnson and Johnson, Belgium

Science of respiratory infections and new therapeutic approaches (Keynote Lecture 2)

3 FEBRUARY 2021

DAY 1

Session 2, Environmental and Agricultural Microbiology

11.40 - 13.30

Chairpersons: Prof. Appa Rao Podile, Dr. Atya Kapley, Prof. Anil Kumar Puniya
Co-Chair: Dr. Helianthous Verma, Dr. Vivek Negi, Dr. Shashank Kumar Maurya

PROF. RAKESH BHATNAGAR **11.35 –12.05**

Vice-Chancellor, Banaras Hindu University, Varanasi, India

Recombinant Vaccine against Anthrax - From Clone to Clinical Trails (Plenary Lecture 1)

PROF. PRASHANT S. PHALE **12.10-12.30**

Indian Institute of Technology, Mumbai, India

Pseudomonas sp. strain CSV86: An ideal host for bioremediation and metabolic engineering

DR. HEMANT PUROHIT **12.35-12.55**

CSIR-National Environmental Engineering Research Institute, Nagpur, India

Human Gut: A Fed-Batch Bioreactor with varied microbial diversity

DR. NATESAN MANICKAM **13.00–13.15**

CSIR-Indian Institute of Toxicology Research, Lucknow, India

Functional Microbial Diversity for Pollution Abatement: Current Approaches and Future Challenges

BREAK **13.15-13.45**

3 FEBRUARY 2021

DAY 1

Session 2, Environmental and Agricultural Microbiology

13.50 - 15.50

Chairpersons: Dr. Banwari Lal, Prof. D.K. Singh
Co-Chair: Dr. Jaspreet Kaur, Dr. Anjali Saxena

PROF. JAN ROELOF VAN DER MEER — 13.50-14.25

University of Lausanne, Lausanne, Switzerland

The secret life of integrative conjugative elements - agents of open source evolution (Plenary Lecture 2)

DR. HANS - HERMANN RICHNOW — 14.30-14.55

Helmholtz Centre for Environmental Research - UFZ, Leipzig, Germany

Degradation of hexachlorohexane isomers in soil-plant system - implications for phytoremediation (Plenary Lecture 3)

15.00-20.05

Chairpersons: Dr. K. Annapurna, Prof. U. Shivakumar
Co-Chair: Dr. Simran Jit, Dr. Gauri Garg Dhingra

PROF. ANDY BALL — 15.00-15.25

RMIT University, Melbourne, Australia

Current status, challenges and future of bioremediation (Keynote Lecture 3)

PROF. PARAMJIT KHURANA — 15.30-15.50

University of Delhi, South Campus, New Delhi, India

investigating the role of pgprs in alleviating heat stress tolerance in *Triticum aestivum L*

3 FEBRUARY 2021

DAY 1

Session 2, Environmental and Agricultural Microbiology

DR. K. ANNAPURNA **15.55-16.15**

ICAR-Indian Agricultural Resources Institute, New Delhi, India

Microbe to Microbiome: The journey of Rhizobium

DR. VARTIKA MATHUR **16.20-16.40**

Sri Venkateswara College, University of Delhi, Delhi, India

Harnessing the power of microbes in Agriculture

DR. MIKAEL MOTELICA **16.45-17.10**

Université d'Orléans, France

(Keynote Lecture 4)

DR. ANIL SAXENA **17.15-17.35**

ICAR- National Bureau of Agriculturally Important Microorganisms, Mau, India

Quality assurance of biofertilizers: Issues and Concerns

DR. VIKAS YADAV **17.40-18.00**

Jawahar lal Nehru University, Delhi, India

Phosphorus Transport in Mycorrhiza: Journey so far

3 FEBRUARY 2021

DAY 1

Session 2, Environmental and Agricultural Microbiology

PROF. S. DAYANANDA **18.05–18.25**

University of Hyderabad, Hyderabad, India

Novel link between iron acquisition and aromatic carbon catabolism in *Sphingobium fuliginis* ATCC 27551

DR. VIVEKANAND **18.30–18.50**

Malviya National Institute of Technology, Jaipur, India

Biogas production: impact of biological pre-treatment of wheat straw and microbial communities composition

DR. D.L.N RAO **18.55–19.15**

Indian Institute of Soil Science, Bhopal, India

Challenges in Integrating Microbial Diversity-Soil Health Functions

DR. KASHYAP K. DUBEY **19.20–19.40**

Jawahar lal Nehru University, New Delhi, India

Analysis of pellet formation of *Streptomyces toxytricini* to improve lipstatin production

PROF. PRATYOOSH SHUKLA **19.40-20.00**

Banaras Hindu University, Varanasi, India

Futuristic bio-computational approaches towards understanding microbial bioremediation

20.00-20.05

DAY 3 CONCLUSION AND DAY 4 BRIEFING

3 FEBRUARY 2021
(PARALLEL TO SESSION 2)

DAY 1

Session 3, Child/Society-Centric Microbiology

11.35 - 17.30

Chairpersons: Prof. Kenneth Timmis, Prof. J.P. Khurana
Co-Chair: Dr. Shailly Anand, Dr. Vipin Gupta, Dr. Jasvinder Kaur

PROF. RUP LAL **11.35–11.40**

NASI Senior Scientist, TERI, New Delhi, India

Opening Remarks

PROF. KENNETH TIMMIS **11.45–12.25**

Tech. Univ. of Braunschweig, Germany

Microbiology Literacy Initiative

PROF. JACK GILBERT **12.30-13.00**

University of California, San Diego, USA

Human Microbiome: The Importance of Furry Pets in Microbial Health

PROF. D.L.N. RAO **13.05-13.25**

Indian Institute of Soil Science, Bhopal, India

Microbes and Sustainable Agriculture

MR. LANUAKUM IMCHEN **13.30-13.50**

Founder, Cold Mountain, Organic Tea Products, Nagaland, India

Organic Farming in Holistic Approach

BREAK **13.50-15.00**

3 FEBRUARY 2021
(PARALLEL TO SESSION 2)

DAY 1

Session 3, Child/Society-Centric Microbiology

PROF. TERRY MCGENITY **15.05-15.25**

University of Essex, UK

Visualizing the Invisible: Class excursions to Ignite Children's Enthusiasm for Microbes

PROF. RUP LAL **15.30-15.50**

The Energy and Resources Institute, New Delhi, India

Human Microbiome and Health: Communicating Complex Subjects with a Concerned Public and Children

DR. SHAILLY ANAND **15.55-16.15**

Deen Dayan Upadhyaya College, University of Delhi

There is no Plan B for there is no Planet B: Microbiology Literacy is the hope

DR. PRIYA SINGH **16.20-16.40**

Maitreyi College, University of Delhi

Food for Health

MICROBIOLOGY QUIZ **16.40-17.30**

CONCLUDING REMARKS **17.30-17.40**

4TH FEBRUARY 2021

YOGA SESSION

08.00-08.45

Yog Guru: Dr. Dheeraj P. Joshi

Founder, Shivodham International Yog Ashram, Udaipur and Yog Department of JRN Rajasthan Vidyapeeth University, Udaipur, India

DAY 2

Opening

09.00 - 09.35

Chairpersons: Prof. Ajay Mathur, Prof. Vibha Dhawan, Prof. Joel Kostka, Prof. T. Satayanarayan
Co-Chair: Dr. Ankita Dua, Dr. Utkarsh Sood, Dr. Chandni Talwar

PROF. JIZHONG ZHOU

09.00-09.35

University of Oklahoma, Norman, USA

Feedback Responses of Grassland Soil Microbial Communities to Climate Warming
(Plenary Lecture 4)

PROF. JOEL KOSTKA

09.40-10.05

Georgia Institute of Technology, Georgia, USA

A Moveable Feast: The Role of Microbes in the Response to the Deepwater Horizon Oil Spill in the Gulf of Mexico
(Keynote Lecture 5)

4TH FEBRUARY 2021

DAY 2

Session 4: Industrial Microbial Biotechnology

Chairpersons: Prof. Sunil Pabbi, Prof. A. K. Dikshit **10.10 - 11.15**
Co-Chair: Dr. Aeshna Nigam, Nirjara Singhvi

PROF. TAIFO MAHMUD — 10.10-10.35

Oregon State University, Oregon, USA

Genome mining and biosynthetic studies of secondary metabolites in *Streptomyces pactum* (Keynote Lecture 6)

DR. ATYA KAPLEY — 10.40-11.00

CSIR-National Environmental Engineering Research Institute, Nagpur, India

Decentralized Treatment Options for Domestic Wastewater Management

PROF. SUNIL PABBI — 11.00-11.20

ICAR-Indian Agricultural Research Institute, New Delhi, India

Cyanobacterial phycobiliproteins: purification, characterization and a multi factor based optimization for enhanced production

PROF. ANIL TRIPATHI — 11.20-11.45

Banaras Hindu University, Varanasi, India

A network of regulatory cascades of alternative sigma factors controls oxidative and photo- oxidative stress response in *Azospirillum brasilense*

4TH FEBRUARY 2021

DAY 2

Session 4: Industrial Microbial Biotechnology

DR. CHARU DOGRA RAWAT **12.15-12.35**

Ramjas College, University of Delhi, India

Overcoming challenges in microbe-assisted bioremediation - A genomic approach

PROF. BISWAJIT KUNDU **12.40-13.00**

Indian Institute of Technology, New Delhi, India

Intracellular pathogens apply common enzymatic trick to evade host defence mechanism

PROF. DATTA MADAMWAR **13.05-13.25**

Scientific Advisor, Charotar University of Science and Technology, Changa, Anand, Gujarat, India

Characterization and Therapeutic Applications of Phycobiliproteins from Cyanobacteria

DR. SANJUKTA SUBUDHI **13.30-13.50**

The Energy and Resources Institute, New Delhi, India

Next generation biomass as platform feed for production of clean fuel and green chemical

BREAK **13.50-14.30**

4TH FEBRUARY 2021

DAY 2

Session 4: Industrial Microbial Biotechnology

Chairpersons: Dr. Banwari Lal, Prof. Rajendra Prasad
Co-Chair: Dr. Roshan Kumar, Dr. Charu Dogra Rawat

PROF. APPA RAO PODILE **14.30-15.00**

Vice-Chancellor, University of Hyderabad, India

Chitosan patterns matter in inducing plant's response
(Keynote Lecture 8)

PROF. CHRISTOF HOLLIGER **15.05-15.30**

École Polytechnique Fédérale de Lausanne [EPFL], Lausanne, Switzerland

Understanding and managing the aerobic granular sludge microbiome
(Keynote Lecture 9)

INSCR GB MEETING (FOR INSCR MEMBERS) **15.35-16.30**

4TH FEBRUARY 2021

DAY 2

Session 4: Industrial Microbial Biotechnology

Chairpersons: Prof. Anil Tripathi, Prof. Praveen Rishi, Prof. Sanjay Chhibber
Co-Chair: Dr. Priya Singh, Dr. Roshan Kumar

DR. BANWARI LAL **16.30-16.45**

The Energy and Resources Institute, New Delhi, India

Increase oil production from oil wells by prevention of paraffin deposition in oil well tubing

DR. DAVID VAN DE VIJVER **16.50-17.10**

Erasmus University, Rotterdam, The Netherlands

Principles and implications of drug resistance against drugs used for HIV
(Keynote Lecture 10)

4 FEBRUARY 2021
(PARALLEL TO SESSION 4)

DAY 2

Session 5: AMI/INSCR Innovative Research (Faculty)

10.50-14.40

Chairpersons: Dr. Ravi Tuteja, Dr. Sukanya Lal, Dr. Charu Dogra Rawat
Co-Chair: Dr. Mansi Verma

DR. MURUGAIYAN KALAISELVAM — 10.40-10.50

Annamalai University, Tamilnadu (AIF01)

Sustainable utilization of marine wastes for oyster mushroom *Pleurotus florida* (Singer, 1946) production

DR. SHALINI RAJKUMAR — 10.50-11.00

Nirma University, Ahmedabad (AIF02)

Regulation of pqq-dependent glucose dehydrogenase mediated mineral phosphate solubilization by catabolite repression control protein in Acinetobacter sp. SK2

DR. INDERKANT — 11.00-11.10

Deshbandhu College, DU (AIF03)

Gut microbiome, obesity, and colorectal cancer: a tripartite connection

DR. HARISH RAJAK — 11.10-11.20

Guru Ghasidas Vishwavidyalaya, Bilaspur (AIF04)

Antimicrobial properties of novel oxadiazole based analogues

DR. APARNA JITESH TAILOR — 11.20-11.30

Dr. APJ Abdul Kalam Govt. College (AIF05)

A thermoactive alkaline bacterial lipase: optimization, purification and characterization studies

4 FEBRUARY 2021
(PARALLEL TO SESSION 4)

DAY 2

Session 5: AMI/INSCR Innovative Research (Faculty)

DR. MAMTESH SINGH **11.30-11.40**

Gargi College, UoD (AIF06)

Microbial pha production from biowaste aided with petri net modelling for optimized bioprocess development

DR. RAMESH N **11.40-11.50**

Vellore Institute of Technology (AIF07)

Bacteriophage as an alternative antibacterial therapy against pan-drug resistant bacteria

DR. JASVINDER KAUR **11.50-12.00**

Gargi College, UoD (AIF08)

Protocol for in-vitro purification and refolding of hexachlorocyclohexane degrading enzyme haloalkane dehalogenase linB from inclusion bodies

DR. DEBASHIS BANERJEE **12.00-12.10**

Atmiya University, Rajkot (AIF09)

Incidence of growing antibiotic resistant bacterial infections in the city of Rajkot in the recent past

DR. KHEM RAJ **12.10-12.20**

Department of Microbiology, Panjab University (AIF10)

Analysis of specific isoform usage by biofilm lifestyle of *Candida glabrata* through a global transcriptome-wide approach

DR. HELIANTHOUS VERMA **12.20-12.30**

Ramjas College, UoD (AIF11)

Insights into the evolution of drug resistance and potential drug targets of *Mycobacterium tuberculosis* using comparative genomics

4 FEBRUARY 2021
(PARALLEL TO SESSION 4)

DAY 2

Session 5: AMI/INSCR Innovative Research (Faculty)

DR. ROSHAN KUMAR **12.30-12.40**

Magadh University (AIF12)

Global population genomic analysis of *Mycoplasma bovis* isolates reveals transcontinental variations and potential virulence genes throughout all clades

DR. SEEMA SANGWAN **12.40-12.50**

CCS Haryana Agriculture University (AIF13)

Identification of biosurfactant producing *Klebsiella pneumoniae ssp ozaenae* using VITEK 2 automated microbiology system

DR. VIVEK NEGI **12.50-13.00**

Sri Aurobindo College, UoD (AIF14)

Metagenomic Analysis of Pond Sediment to Comprehend Complex Microbial Interactions

DR. ANINA JAMES **13.00-13.10**

Deen Dayal Upadhyaya College, UoD (AIF15)

Aatrazine decontamination by epiphytic root bacteria

DR. SHANU KHANDELVAL **13.10-13.20**

Gujarat University (AIF16)

Diversity and potential bioprospection of certain plant growth-promoting rhizobacteria

DR. G. YAMAL **13.20-13.30**

Kirori Mal College, UoD (AIF17)

Assessment of Ag Nanoparticles in sewage sludge

4 FEBRUARY 2021
(PARALLEL TO SESSION 4)

DAY 2

Session 5: AMI/INSCR Innovative Research (Faculty)

DR. TIKAM CHAND DAKAL **13.30-13.40**

Mohanlal Sukhadia University (AIF18)

Bioinformatics Analyses of SARS-CoV- 2 Spike Protein: Step Towards Designing COVID-19 Therapeutics

DR. JAYSHRI J. BHUKTAR **13.40-13.50**

Dr. BAMU, Aurangabad (AIF19)

Exploring the potential of marine and soil fungi for enzyme production

DR. SATARUPA DEY **13.50-14.00**

Shyampur Siddheswari Mahavidyalay, West Bengal (AIF20)

Physio-biochemical potentials of some alkaliphilic bacterial isolates obtained from bauxite processing residues

DR. GAURAV SHARMA **14.00-14.10**

DST-INSPIRE Faculty Scientist, IBAB, Bengaluru (AIF21)

Exploring the diversity and evolution of chemosensory and flagellar systems amongst Family *Vibrionaceae*

DR. AKHIL AGGRAWAL **14.10-14.20**

Central University of Rajasthan (AIF22)

Unexpected shift in microbial communities leads to enhanced crude Oil recovery

DR. AKSHITA PURI **14.20-14.30**

R.T.M Nagpur University, Nagpur, Maharashtra (AIF23)

Genome metrics analysis for taxonomic delineation of *Paracoccus* spp.

CONCLUDING REMARKS **14.20-14.30**

4 FEBRUARY 2021

DAY 2

Special Session 6
Viruses and Vaccines:
Special emphasis on SARS-CoV2

17.20-18.40

Chairpersons: Prof. Anil Tripathi, Prof. Praveen Rishi, Prof. Sanjay Chhibber
Co-Chair: Dr. Priya Singh, Dr. Roshan Kumar

DR. HARISH PILLAI — 17.25-17.45

CEO, Aster Hospital & Clinics, Bengaluru, India

COVID Pandemic: Learnings and Opportunities - For the healthcare worker, the hospitals and the industry!

DR. SINOSH SKARIYACHAN — 17.50-18.10

St. Pius X College Rajapuram, Kerala, India

Computer Assisted Virtual Screening of Potential Therapeutic Targets and Putative Lead Molecules for SARS CoV-2: Insight for COVID19 lead discovery

DR. MANSI VERMA — 18.15-18.35

Sri Venkateswara College, University of Delhi, India

CpG dinucleotides as potential candidates for zap mediated degradation against SARS-COV-2

DAY 4 CONCLUSION AND DAY 5 BRIEFING — 18.35-18.40

4 FEBRUARY 2021
(PARALLEL TO SESSION 6)

DAY 2

AMI AWARD LECTURES

Chairpersons: Prof. Yogendra Singh, Prof. Surjeet Dudeja, Prof. J.S. Virdi

AMI- ALEMBIC AWARD 2020
DR. SURENDER SINGH **16.35-16.45**

Central University of Haryana, Mahendergarh

Crop residue management- Opportunities and challenges in India

AMI- ALEMBIC AWARD 2020
DR. P. GOPINATH **16.45-16.55**

Indian Institute of Technology, Roorkee

Nanomaterials for antibacterial applications

AMI PROF. B.N. JOHRI AWARD 2020
PROF. U. SIVAKUMAR **16.55-17.05**

Tamil Nadu Agricultural University, Chennai

Biocatalysts and process development for biomass-derived fuels and chemicals

AMI-LOUIS PASTEUR AWARD 2020
DR. INDU VERMA **17.05-17.15**

Postgraduate Institute of Medical Education and Research, Chandigarh

In vivo expressed mycobacterial transcripts: Candidate biomarkers for molecular and immunological diagnosis of tuberculosis

AMI PROF. S. R. VYAS AWAD 2020
PROF. ANIL K. SAXENA **17.15-17.25**

ICAR-NBAIM, Mau, Uttar Pradesh

Microbial Diversity in Indian Soil: Wealth for national prosperity and posterity

4TH FEBRUARY 2021
(PARALLEL TO SESSION 6)

DAY 2

AMI AWARD LECTURES

YOUNG SCIENTIST AWARD IN ENVIRONMENTAL MICROBIOLOGY 2020

DR. VIPIN GUPTA **17.25-17.35**

Comparative Genomics and Integrated Network Approach to study Phylogenic Patterns, Co-mutational Hotspots and Regulatory Interactions in SARS-CoV-2

YOUNG SCIENTIST AWARD IN DAIRY AND FOOD MICROBIOLOGY 2020

DR. SANDEEP KUMAR PANDA **17.35-17.45**

Development of functional foods and beverages from indigenous raw materials

YOUNG SCIENTIST AWARD IN INDUSTRIAL MICROBIOLOGY 2020

DR. SONIKA SONDHI **17.45-17.55**

Bacterial laccases and its potential applications

YOUNG SCIENTIST AWARD IN MEDICAL AND VETERINARY 2020

DR. PUNITA SHARMA **17.55-18.05**

Learning of mosquito-microbiome interactions and tuning innovations in combating Vector borne diseases

YOUNG SCIENTIST AWARD LECTIN MOLECULAR MICROBIOLOGY AND BIOTECHNOLOGY 2020

DR. RAVINDER SINGH **18.05-18.15**

Reverse Vaccinology: Finding vaccine candidates against *Acinetobacter baumannii*

CONCLUDING REMARKS AND DAY 5 BRIEFING **18.15-18.25**

5 FEBRUARY 2021

DAY 3

Opening

Chairpersons: Prof. H.C. Agarwal, Prof. V.C Kalia
Co-Chair: Dr. Shailly Anand, Dr. Jasvinder Kaur

PROF. VICTOR DIRITA **08.25-09.00**

Michigan State University, USA

Growth physiology of enteric pathogens during infection
(Plenary Lecture 5)

DR. CECILIA ALONSO **09.00-09.25**

Centro Universitario de la Region Este, Rocha, Uruguay

Bacterial communities as an indicator of environmental status: from proof of principle to environmental management

DAY 3

Session 7: Advances in Microbial Systematics

09.30-12.50

Chairpersons: Prof. Venkata Ch. Ramana, Prof. Suresh Korpole, Dr. Om Prakash
Co-Chairs: Dr. Charu Tripathi, Dr. Nitish K. Mahato

PROF. VENKATA CH. RAMANA **09.40-10.00**

University of Hyderabad, Hyderabad, India

A need for an extensive and systematic survey of microbiological wealth of India

PROF. SURESH KORPOLE **10.05-10.25**

CSIR-IMTECH, Chandigarh, India

Laterosporulins-Defensin like antimicrobial peptides from *Brevibacillus* species and their applications.

5 FEBRUARY 2021

DAY 3

Session 7: Advances in Microbial Systematics

DR. P. ANIL KUMAR **10.30–10.50**

CSIR-IMTECH, Chandigarh, India

Functional Metagenomics: An advanced approach in Bioremediation (EAM)

DR. OM PRAKASH **11.20–11.40**

National Centre for Cell Science, Pune, India

Recent Trend, Biases and Limitations of Cultivation Based Microbial Diversity Study

BREAK **11.40–11.55**

DR. PUJA YADAV **12.00–12.20**

Central University of Haryana, Haryana, India

Antimicrobial Resistance, Virulence Genes, and Biofilm Formation Capacity Among *Streptococcus agalactiae* Strains Isolated from Indian Population

DR. PRINCY HIRA **12.25–12.35**

Maitreyi College, University of Delhi, New Delhi, India

Genus Mycoplana

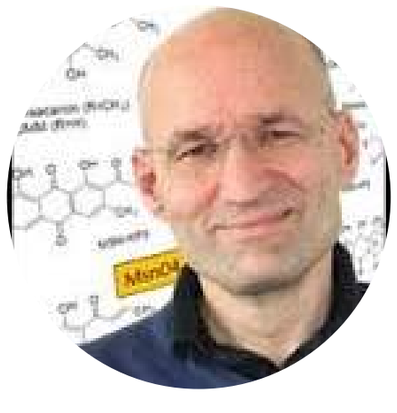
5TH FEBRUARY 2021

DR. NIRJARA SINGHVI **12.40-12.50**

University of Delhi, Delhi, India

Genus Sphingobium

BREAK **12.55-13.30**



Chairpersons: Prof. Rup Lal, Prof. Yogendra Singh

PROF. ANDREAS BECHTHOLD **13.35-14.05**

Albert Ludwig University, Freiburg, Germany

BldA and cyclic di-GMP: Natural product regulators special (Plenary Lecture 6)

Session 9: Translating Innovative Ideas to Enterprise

Chairperson: Dr. Amulya Panda, Dr. Mrutyunjay Suar
Co-Chair: Dr. Mona Singh, Dr. Princy Hira

DR. MRUTYUNJAY SUAR **14.10-14.30**

DG, R&D, KIIT University, Odisha, India

Session Briefing

DR. MANISH DIWAN **14.35-14.55**

Head-SPED, BIRAC, DBT, GoI

BIRAC: Building Biotechnology Innovation ecosystem in India

DR. SHRIRAM RAGHAVAN **15.00-15.20**

Vice President, Jananom, Coimbatore, India

Programmed Live Biotherapeutics

5TH FEBRUARY 2021

DAY 3

Session 9: Translating Innovative Ideas to Enterprise

DR. NAMRATA MISRA **15.25-15.45**

Head-Bioinnovation, KIITTBI-Odisha, India

Role of Incubators: Accelerating Innovations

DR. VISHAKHA RAINA **15.50-16.10**

KIIT-Bhubaneswar, Odisha, India

Microbial Enzymes: Making Safe Food

DR. SHAON RAY CHAUDHURI **16.15-16.35**

Tripura University, Tripura, India

Microbial Technology for Clean Environment

DR. VIPIN GUPTA **16.35-16.45**

PhixGen Pvt. Ltd., Gurugram, India

My Journey as Entrepreneur: Academia to Industry and Research

DR. UTKARSH SOOD **16.45-16.55**

TERI, New Delhi, India and PhixGen Pvt. Ltd., Gurugram, India

Three years of Phixgen Private Limited: Culmination of Academics, Research and Business

5TH FEBRUARY 2021

DAY 3

Session 10: Microbial Pathogenesis and AMR

16.55-17.15

Chairs: Dr. Anil Koul, Prof. Namita Singh
Co-chairs: Dr. Utkarsh Sood, Dr. Vipin Gupta

PROF. YOGENDRA SINGH **16.55-17.15**

University of Delhi, Delhi, India

Serine/threonine kinase PrkC regulates chain length in *Bacillus anthracis*

PROF. V. C. KALIA **17.20-17.40**

Konkuk University, South Korea

Novel Drugs to Target Psycho-Pathogenic Bacteria

PROF. PARVEEN RISHI **17.45-18.05**

Panjab University, Chandigarh, India

Metals as drivers for emerging antibiotic resistance and its clinical validation

PROF. VIBHA TONDON **18.10-18.30**

Jawaharlal Nehru University, New Delhi, India

A Multi-Scale Approach to Combat the Mechanisms of Antimicrobial Resistance through ABTI19b a Known Bacterial topoisomerase IA Inhibitor

DR. RICHA MISHRA **18.35-18.50**

Sri Venkateswara College, University of Delhi, India

Understanding the 'Gut-Lung Axis' in Tuberculosis and its implications

5 FEBRUARY 2021
(PARALLEL TO SESSION 7)

DAY 3/HALL B

Session 8: AMI/INSCR Innovative Research (Students & Scholars)

HALL B **09.30-12.50**

Chairpersons: Prof. Craig Cary, Dr. Sanjukta Subudhi
Co-Chairs: Dr. Ankita Dua, Dr. Anjali Saxena

SACHIN KHURANA 09.30-09.40

(OMOH001)

Protein O- fucosyltransferase 2 -mediated O-glycosylation of MIC2 is dispensable for *Toxoplasma gondii* tachyzoite infection

LEENA 09.40-09.50

(OMOH002)

Cutaneous microbiome in preterm infants

SIDHHI, SAURAV, ANGNANI, KARTHIK 09.50-10.00

(OMOH003)

An assessment of antimicrobial efficacy of liquid soap and alcohol based hand sanitizer on regular hand microbiome

VISHAL SHARMA 10.00-10.10

(OMOH004)

Impairment of the gut metabolites in tuberculosis infection

SUBHASREE V 10.10-10.20

(OMOH005)

Local ecological parameters fostering vaginal dysbiosis causing patho ″logical conditions in women"

S SRIPOORNA 10.20-10.30

(OMOH006)

In-silico identification and characterization of cadmium, copper metalloproteins and cysteine-rich proteins involved in cell defense in the freshwater ciliate

5 FEBRUARY 2021
(PARALLEL TO SESSION 7)

DAY 3/HALL B

Session 8: AMI/INSCR Innovative Research (Students & Scholars)

ATHIRA M MENON **10.30-10.40**

(OIMB001)

Insight into the Structural and Functional Aspects of Osmo/Halo- Responsive Proteins in Yeast

PRITI MAHLA **10.40-10.50**

(OIMB002)

Xylanase Production by Fungi Using Post Methanated Distillery Spent Wash

PAYAL AGHERA **10.50-11.00**

(OIMB003)

Bio-Butanol Production on Post Methanated Waste Water by Batch Fermentation

SANJEET MEHARIYA **11.00-11.10**

(OIMB004)

Cultivation of Micro-Algae for Extraction Of Valuable Products: An Advancement In Algal-Refinery

AMI D. VARIA **11.10-11.20**

(OIMB005)

Diversity & Characterization of Moderately Halophilic bacteria producing alkaline protease

PRASSAN CHOUDHARY **11.20-11.30**

(OIMB006)

Characterization and immobilization of lipase produced from *Pseudomonas plecoglossicida* S7

5 FEBRUARY 2021
(PARALLEL TO SESSION 7)

DAY 3/HALL B

Session 8: AMI/INSCR Innovative Research (Students & Scholars)

DIYA ROY — 11.30-11.40

(OIMB007)

Purification, characterization and functionality analysis of high purity analytical grade C-Phycocyanin from non- heterocystous cyanobacterium *Phormidium* sp. CCC 316 isolated from Rajasthan, India

SWEETA SONI — 11.40-11.50

(OIMB008)

Optimization Of Polyhydroxybutyrate (PHB) Production By Bacillus Endophyticus MTCC 13038

PANKAJ SHARMA — 11.50-12.00

(OIMB009)

Yeast *Meyerozyma guilliermondii* YK22 mediated biosurfactant production using low cost industrial waste and assessment of its extraction methodologies

ROHIT KHANDELWAL — 12.00-12.10

(OIMB010)

Characterization of two promoters from *Zymomonas mobilis* and their functionality in *E.coli*

KISHOR SURESHBHAI PATIL — 12.10-12.20

(OIMB011)

Investigation of kraft lignin degradation by *Bacillus aryabhattai* sp. K13 isolated from compost

SUJATA MAKKAR — 12.20-12.30

(OIMB012)

Effect of shiitake (*lentinus edodes*) mushroom on anti- inflammatory response in carageenan induced rats

5 FEBRUARY 2021
(PARALLEL TO SESSION 7)

DAY 3/HALL B

Session 8: AMI/INSCR Innovative Research (Students & Scholars)

DIPANJANA BANERJEE **12.30-12.40**

(OIMB013)

Biofermentative production of d-lactic acid from whey permeate from ceesh manufacturing industry: a polymer for bioplastic production

BHNAUPRIYA DHABHAI **12.40-12.50**

(OVVS001)

Evaluation of Some Plant Derived Natural Ingredients against SARS-CoV-2: an *In-Silico* Approach

BREAK **12.55-13.30**

14.15-16.00

Chairpersons: Prof. Cecilia Alonso, Dr. D.K. Jha, Dr. Vartika Mathur
Co-Chairs: Dr. Nikki, Dr. Poonam Singh

AMRITA KAUR **14.15-14.25**

(OMP001)

Salmonella Strain Specificity Determines Post- Typhoid Central Nervous System Complications: Intervention By *Lactiplantibacillus Plantarum* At Gut-Brain Axis

RICHA HANS **14.25-14.35**

(OMP002)

Direct-differential slide agglutination assay for brucella detection using antibody conjugated with functionalized gold nanoparticles

PRANJAL KUMAR YADAV **14.35-14.45**

(OMP003)

Development of SYBR green based real time PCR assay for molecular diagnosis of *Burkholderia pseudomalle*

5 FEBRUARY 2021
(PARALLEL TO SESSION 7)

DAY 3/HALL B

Session 8: AMI/INSCR Innovative Research (Students & Scholars)

SUJATA YADAV **14.45-14.55**

(OMP004)

Endophytic actinobacteria associated with *Bryophyllum pinnatum* (lam.) Oken: isolation and assessment of their antimicrobial activity

GEETIKA WAG **14.55-15.50**

(OMP005)

Endophytic rare *Actinoalloteichus cyanogriseus* sir5 (mk793584) from medicinal weed S*phaeranthus indicus linnaeus*: antimicrobial efficacy against drug resistant human pathogens

RENU JAGDISH **15.05-15.15**

(OMP006)

Antimicrobial and anti- biofilm activity of green synthesized ZnO nanoparticles against ESBL producing and biofilm forming uropathogens

PERWEZ BAKHT **15.15-15.25**

(OMP007)

Novel validated carbapenemase inhibitors active against clinical kpc-2 producing strains

RASHMI NIRANJAN **15.25-15.35**

(OMP008)

Modulation of streptococcus mutants biofilm growth by *Lactobacillus rhamnosus*

ANOOP SINGH **15.35-15.45**

(OMP009)

Role of horizontal gene transfer and IS6110 transposition in the evolution of CRISPR-Cas system in *Mycobacterium tuberculosis*

5 FEBRUARY 2021
(PARALLEL TO SESSION 7)

DAY 3/HALL B

Session 8: AMI/INSCR Innovative Research (Students & Scholars)

SURBHI AGARWAL **15.45-15.55**

(OMP010)

Antimicrobial resistance in endosymbionts: another viewpoint

ANVESH GANTA **15.55-16.05**

(OMP011)

Rutin Capped copper nanoparticles exert potent antibiofilm effect against *Klebsiella pneumonia* and curtail planktonic growth in zebrafish mode

CONCLUDING REMARKS **16.05-16.15**

HALL C **09.30-12.50**

Chairpersons: Prof. Pratyoosh Shukla, Prof. T. Satyanarayan
Co-Chairs: Dr. Vishakha Raina, Dr. Shailly Anand

RUCHI SRIVASTAVA **09.30-09.40**

(OEAM001)

Species delineation and genomic similarity among *Exiguobacterium* strains: A pan- genome analysis

SAI HIVARKAR **09.40-09.50**

(OEAM002)

Cultivable diversity of thermophilic anaerobic lignocellulolytic bacteria from Indian hot-springs

5 FEBRUARY 2021
(PARALLEL TO SESSION 7)

DAY 3/HALL C

Session 8: AMI/INSCR Innovative Research (Students & Scholars)

PRIYANKA MANUBHAI **09.50-10.00**

(OEAM003)

Isolation, characterization and identification of pesticide tolerating bacteria from agriculture soil

POOJA YADAV **10.00-10.10**

(OEAM004)

Promotion of microbe- mediated practices and organic amendments at ground level via front line demonstrations (fld)

GARIMA RAI **10.10-10.20**

(OEAM005)

Microbial fortification enhances plant growth and antioxidant defence system in rice (*oryza sativa* l.)

JAGRITI SHUKLA **10.20-10.30**

(OEAM006)

Endophytic fungus *Serendipita indica* colonization in root reduces arsenic mobilization from root-shoot-fruit in the tomato plant

RUPALI MISHRA **10.30-10.40**

(OEAM007)

Bacterial transformation and chemotaxis of heavy metals

SUDIPTA DAS **10.40-10.50**

(OEAM008)

Deciphering genetic and functional diversity of chasmophyte (wild chenopodium) associated bacteria

5 FEBRUARY 2021
(PARALLEL TO SESSION 7)

DAY 3/HALL C

Session 8: AMI/INSCR Innovative Research (Students & Scholars)

KUMAR M **10.50-11.00**

(OEAM009)

Effect of sulfur oxidizers on mustard yield and oil content

GAGANA S **11.00-11.10**

(OEAM010)

Study on removal of heavy metal from industrial effluent using microorganisms

RISHIT KUMAR ATUL KUMAR SONI **11.10-11.20**

(OEAM011)

To study keratinase producing microorganisms from keratinic soil and analyzing their significance for production of keratinase and feed grade amino acids

ALOK KUMAR SINGH **11.20-11.30**

(OEAM012)

Fungal diversity analysis of soil samples from Nagaland and their role in soil health

TILAHUN RABUMA **11.30-11.40**

(OEAM013)

Bacterial transformation deciphering the regulatory role of miRNAs in *C. annuum* L. during *P. capsici* infectionand chemotaxis of heavy metals

MADHULIKA SINGH **11.40-11.50**

(OEAM014)

Physiological and Biochemical perspectives of HD- 2967 wheat cultivar during microbial interaction against salinity stress

5 FEBRUARY 2021
(PARALLEL TO SESSION 7)

DAY 3/HALL C

Session 8: AMI/INSCR Innovative Research (Students & Scholars)

PRAVEEN KUMAR TIWARI — 11.50-12.00

(OEAM015)

Genome of extremely salt resistant bacterium *Exiguobacterium profundum* PHM 11 viewed from the perspective of comparative genomics

VIVEK KUMAR GAUR — 12.00-12.10

(OEAM016)

Microbial derived biosurfactants for their application in environmental bioremediation and as disinfectants

MOHD ASHRAF DAR — 12.10-12.20

(OEAM017)

An overview of residual contamination and bacterial degradation of organophosphate pesticides and investigation of pesticide usage patterns and farmers perception on pesticide use

LATA JAIN — 12.20-12.30

(OEAM018)

Isolation and characterization of bacteriophages against *Xanthomonas oryzae pv. oryzae* as a potent bio-control for bacterial leaf blight of rice

SHALOO VERMA — 12.30-12.40

(OEAM019)

Endophyte mediated modulation of nutrient transporters and root architecture improves Fe and Zn uptake in maize

APARNA KOPPARAPU — 12.40-12.50

(OEAM020)

Simplification of soil microbiological techniques to promote technology translation in agriculture and allied sectors

5 FEBRUARY 2021
(PARALLEL TO SESSION 7)

DAY 3/HALL C

Session 8: AMI/INSCR Innovative Research (Students & Scholars)

BREAK **12.55–13.30**

14.15–16.00

Chairpersons: Dr. Naveen Gupta, Dr. P. Anil Kumar
Co-Chairs: Dr. Sinosh Skariyachan, Dr. Richa Mishra

HARPREET KAUR **14.15-14.25**

(OEAM021)

Cost effective substrates for production of biosurfactant using S*taphylococcus lentus* and exploration of extraction methods

V MAGESHWARAN **14.25-14.35**

(OEAM022)

An accelerated method for in situ decomposition of agricultural wastes: A need of the hour

VIDHI KALOLA **14.35-14.45**

(OEAM023)

Characterization and purification of extracellular polymeric substances (EPS) purified by *Halomonas sp*. DK4: Biosorptional properties of EPS coated magnetic magnetite nanoparticle for rapid treatment of real chrome electroplating wastewater

KAMLA MALIK **14.45-14.55**

(OEAM024)

Bioconversion process for compost production from agricultural residue

SHIKHA GUPTA **14.55-15.05**

(OEAM025)

Evaluation of *Pseudomonas* sp. for its multifarious plant growth promoting potential, antifungal activity and salinity alleviation in tomato (*Solanum lycopersicum*) plants

5 FEBRUARY 2021
(PARALLEL TO SESSION 7)

DAY 3/HALL C

Session 8: AMI/INSCR Innovative Research (Students & Scholars)

MONIKA RANI **15.05-15.15**

(OEAM026)

Isolation, screening, and characterization of saponin producing endophytic fungi from roots of *Asparagus racemosus*

JEEVA SUSAN ABRAHAM **15.15-15.25**

(OAMS001)

A study on ciliate diversity of Delhi using traditional microscopic and modern molecular methods

HARPREET KAUR **15.25-15.35**

(OAMS002)

Species delimitation using integrative taxonomy: case study of *Stylonychia notophora* sensu Sapra and Dass 1970

MOHAMMAD RIYAZ **15.35-15.45**

(OMP012)

Planktonic and sessile microbial growth hindered by herbal extracts and their nanoparticle

ARCHANA L **15.45-15.55**

(OMP013)

Phage therapy as an alternative treatment for MRSA infection

RAJA SINGH **15.55-16.05**

(OMP014)

Development of BBZ as Potent, Broad Spectrum Antibacterial Agent Active against Clinical MDR Strains

CONCLUDING REMARKS **16.05-16.15**

5 FEBRUARY

VALEDICTORY

CHIEF GUEST

DR. RANDEEP GULERIA
DIRECTOR, AIIMS, NEW DELHI, INDIA

GUEST OF HONOUR

PROF. VICTOR DIRITA
MICHIGAN STATE UNIVERSITY, USA

DIGNITARIES

PROF. R. C. KUHAD
CHAIRPERSON, AMSC

PROF. D. K. SINGH
PRESIDENT AMI 2021-22

PROF. PRAVEEN RISHI
PRESIDENT ELECT-AMI (2022-23)

PROF. V.C. KALIA
EDITOR-IN-CHIEF, INJM

5 FEBRUARY

VALEDICTORY

PROGRAMME

18.55-19.05	**PROF. RUP LAL** ORGANIZING SECRETARY, AMI-INSCR-2021 & **PROF. YOGENDRA SINGH** WELCOME
19.05-19.10	**PROF. NAMITA SINGH** (GS, AMI) REMARKS
19.10-19.20	PRIZE DISTRIBUTION
19.20-19.25	**DR. BANWARI LAL** (ORGANIZING SECRETARY, AMI-INSCR 2021) CONCLUDING REMARKS
19.25-19.30	**PROF. SUNIL PABBI** (ORGANIZING SECRETARY, AMI-INSCR 2021) VOTE OF THANKS

ABSTRACT BOOK

ANNUAL INTERNATIONAL CONFERENCE

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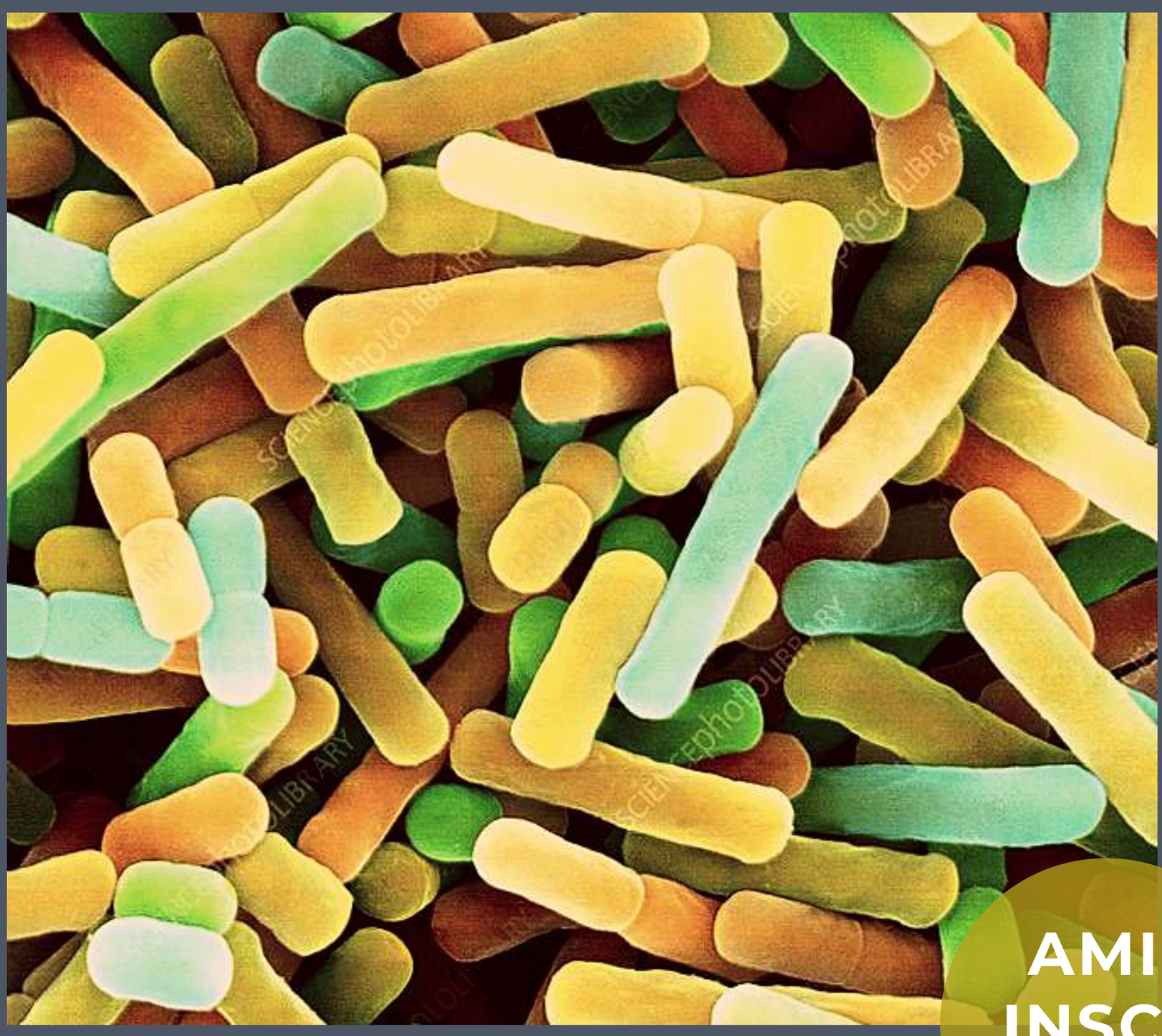
LACTOBACILLUS BULGARICUS



AMI-INSCR 2021

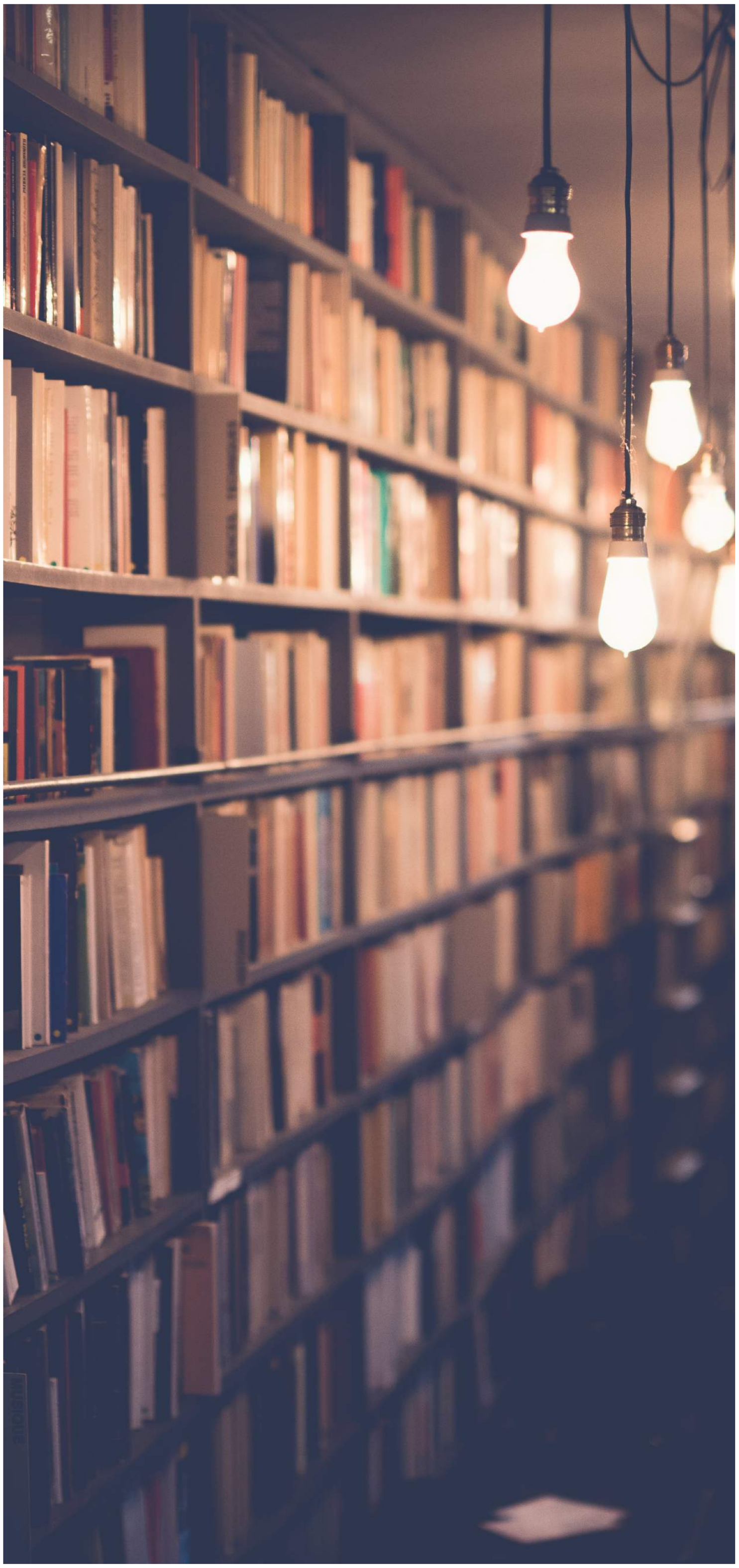
Microbial World: Recent Developments in Health, Agriculture and Environmental Sciences

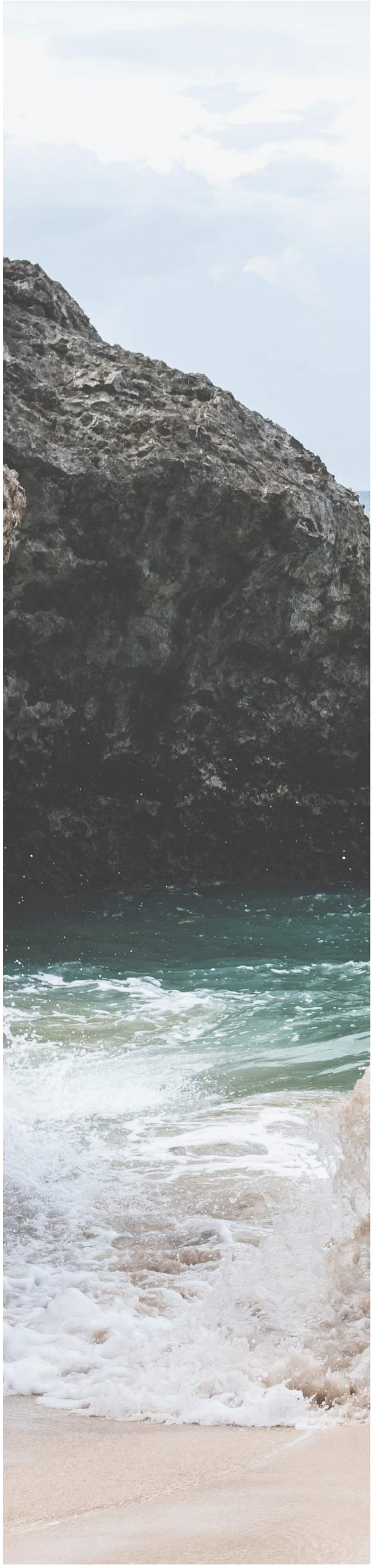
WORKSHOPS
1-2 FEBRUARY 2021

03-05 FEBRUARY 2021

INVITED SPEAKERS - ABSTRACTS

The only true wisdom is in knowing you know nothing





ABSTRACT

FEB 03, 09.55-10.30

MARINE MICROBIAL DYNAMICS IN SPACE AND TIME: A GENOMIC PERSPECTIVE (INAUGURAL LECTURE 2)

*Edward F. DeLong**
Professor, Daniel K. Inouye Center for Microbial Oceanography: Research and Education (C-MORE), University of Hawaii, Manoa, Honolulu, HI
Email edelong@hawaii.edu

Microbes regulate the cycling of energy and matter in the marine environment, yet the details of how they interact with one another, respond to environmental change, and how their activities vary in space and time, are not well understood. Genomic methods and allied technologies are now providing new perspectives on the distribution of microbial taxa, genes, and processes in the marine environment. One of the larger challenges remaining is defining the dynamics and interactions of microbial taxa, gene and process distributions on appropriate spatial and temporal scales. How do the activities and interactions of specific planktonic microbial populations vary over the course of minutes, hours, days and weeks? Over what spatial scales? Do microbial genomes have predictable properties at different depths in the sea, and how have these properties evolved? How do microbial processes influence sinking particles in the ocean environment, and the flux of carbon and energy to the deep-sea? By leveraging robotic sampling technologies coupled to community-wide genomic and gene expression analyses we are beginning to address some of these questions. Results using such approaches show that in surface waters, individual populations, as well as very different bacterial and archaeal species, display remarkably similar, time-variable patterns of synchronous gene expression over extended periods of time. These new results suggest that specific environmental cues may elicit cross-species coordination of gene expression among diverse microbial groups, that has potential to enable multispecies coupling of metabolic activities. Furthermore, new data suggests that the specific nutrient conditions in the water column may evolutionarily shape the composition of microbial genomes and proteomes in predictable ways. The coupling of in situ genomic data with new oceanographic sampling approaches discussed, is advancing our understanding of the inner workings of complex planktonic microbial ecosystems in the wild.

ABSTRACT

FEB 03, 10.35- 11.00

IN EXTREMIS: MICROBIAL ECOLOGY OF ANTARCTICA'S TERRESTRIAL REFUGIA (KEYNOTE LECTURE 1)

*Craig Cary**
University of Waikato, New Zealand
*Email *caryc@waikato.ac.nz*

After almost 60 years of dedicated terrestrial microbiological research in Antarctica we are only now beginning to understand the uniqueness and complexity of these fragile ultraoligotrophic ecosystems. Use of modern genetic tools has revealed far more diverse and functionally complex communities that appear structured predominantly by abiotic parameters but where biotic interactions still play a role. In the dry arid desert systems the interplay of microclimate and geochemistry overlaid onto landscape history constitute the dominating environmental factors that drive the composition and structure of these cryptic communities. Recent studies have revealed that the biotic component is incredibly responsive to subtle changes in the environment resulting in a dramatic shift in community structure and a significant decline in biodiversity in just a few years. Such responsiveness suggests that, if better understood, these cold dry soil communities can serve as early warning sentinels to climate change in Antarctica. In contrast, the rare geothermal systems in Antarctica support a diverse microbiota and may have served as essential refugia for terrestrial organisms before and during periodic glacial maxima. As the most remote geothermal environments on the planet, they also provide a rare opportunity to address questions around microbial biogeography and the interactions between globally distributed and endemic microbes. Despite their biological importance, these extremely remote geothermal locations remain vastly understudied.

ABSTRACT

FEB 03, 11.35-12.05

RECOMBINANT VACCINE AGAINST ANTHRAX: FROM CLONE TO CLINICAL TRIALS (PLENARY LECTURE 1)

*Rakesh Bhatnagar**
Vice-Chancellor, Banaras Hindu University, Varanasi, India
*Email *vc@bhu.ac.in, *rakeshbhatnagar@jnu.ac.in*

The nature of bio-terrorism resulting from an anthrax attack is such that an aggressor is likely to strike at a time and place calculated to induce maximum terror through mass casualties. In the absence of any specific intelligence, in terms of medical surveillance and integrated real-time detection systems, the unpredictable nature of such events compels the development of medical countermeasures, which will enable the authorities to treat the exposed individuals. Early treatment is essential, before the disease reaches a point at which antibiotics are no longer effective owing to the accumulation of a lethal level of toxins, even though the organism is sensitive to the agent. The currently recommended post exposure treatment is a combination of an antibiotic (ciprofloxacin) and a licensed human vaccine AVA (highly toxic with side effects).We have PCR-cloned and overexpressed the anthrax protective antigen gene. Bioprocess optimization was done to improve the yields of the genetically engineered protective antigen. The total yield of the genetically engineered vaccine obtained was 25 g from a 5-liter bioreactor, which is equivalent to 1 million shots. The genetically engineered protein was found to be functionally and biologically identical to its Bacillus anthracis antigen. Toxicity studies conducted on this protein indicated that the protein is devoid of any toxicity and can be safely used for the development of a safe and effective genetically engineered vaccine against anthrax. Phase II clinical trials are being done as per guidelines of Drug Controller of India and US FDA. Technology for making genetically engineered vaccine against anthrax has already been transferred to Panacea Biotech Ltd., New Delhi, India a pharmaceutical company already in the business of making polio and Hepatitis B vaccines.

ABSTRACT

FEB 03, 12.10-12.30

PSEUDOMONAS SP. STRAIN CSV86: AN IDEAL HOST FOR BIOREMEDIATION AND METABOLIC ENGINEERING

*Prashant S. Phale**
Dept. Of Biosciences and Bioengg, IIT-Bombay, Mumbai, India
*Email *pphale@iitb.ac.in*

Anthropogenic activities have led to release of a significant quantity of aromatics into the biosphere. Consequently, microbes have adapted to their presence by evolving degradation pathways. Bioremediation involves the application of microbes to clean-up pollutants from the environment. Certain characteristics like efficient degradation, metabolic versatility, biosurfactant production, chemotaxis, oxidative stress tolerance and stability of degradation phenotype influence the choice of strain for in-situ bioremediation applications. Further, metabolic engineering can enhance the metabolic versatility and degradation efficiency of natural isolates by expression of necessary enzymes. Pseudomonas sp. strain CSV86, a soil isolate, degrades a broad range of aromatics and preferentially utilises them over glucose. Further, this strain co-metabolises aromatics with organic acids. This carbon source utilisation hierarchy is unique amongst Pseudomonads and makes this strain an ideal candidate forin situ bioremediation. Further, the aromatic degradation property of this strain is stable and localised on the chromosome. The genes involved in the glucose transport and utilisation have been shown to be repressed at a transcriptional as well as protein level in presence of aromatics. Further, the naphthalene degradation pathway in this strain shares similarity to the Carbaryl degradation pathway of various organisms. The expression of the enzymes, carbaryl hydrolase and 1-naphthol 2-hydroxylase in strain CSV86 can therefore broaden its metabolic diversity to degrade Carbaryl.

ABSTRACT

FEB 03, 13.00-13.15

FUNCTIONAL MICROBIAL DIVERSITY FOR POLLUTION ABATEMENT: CURRENT APPROACHES AND FUTURE CHALLENGES

*Natesan Manickam**
Environmental Biotechnology Laboratory, CSIR-Indian Institute of Toxicology Research, Vishvigyan Bhavan, 31 Mahatma Gandhi Marg, Lucknow, Uttar Pradesh, 226001, India
*Email *nmanickam@iitr.res.in*

Enumeration of specific bacteria is invaluable for the biodegradation of persistent pollutants as it provides a better understanding of the studying individual strains to get significance usually done using isolated bacteria. To overcome this, large number of bacteria were also isolated employing polymerase chain reaction PCR and molecular hybridizations based on previously reported genetic and biochemical information. Recently, for a comprehensive analysis quantitative analysis metagenome based workflow is also widely being used. For the biodegradation of varieties of aromatic compounds, we have isolated and characterized pure cultures from various ecological niches. Successfully, bacteria belonging to gram+ve, and gram-ve group were isolated by us for biodegradation of persistent pesticides, solvents and polyaromatic hydrocarbons. Five major Indian River water microbiome was comprehensively analysed for biodegradation, antimicrobial resistance, and metal resistance and to obtain novel insights on transposans and bacteriophages from 19 different locations. We have analysed a number samples for microbiome from pesticide contaminated soils. Our data showed that the microbiome was significantly dominated by Proteobacteria, Actinobacteria, Firmicutes, Bacteroidetes and Acidobacteria. Large number of functional genes based on KEGG pathway database revealed occurrence of both substrate specific upper pathway genes and common lower pathway genes. The biodegradative genes were involved in degradation of nitrotoluene, benzoate, chloroalkane and chloroalkene, polycyclic aromatic hydrocarbon, chlorocyclohexane and chlorobenzene. Similary, when compared the microbiome and functional genes derived from river water samples, it was observed that a specific bacterial abundance due to anthropogenic activities and impact of chemical contaminations. Therefore, possibly, combining both the culture dependent and independent approaches may provide insights that are required to realize the complete potential of microbial wealth that may be useful for our better future.
Keywords: Biodegradation, Metagenome, Antimicrobial Resistance, Bacteriophage

ABSTRACT

FEB 03, 13.50-14.25

THE SECRET LIFE OF INTEGRATIVE CONJUGATIVE ELEMENTS - AGENTS OF OPEN SOURCE EVOLUTION (PLENARY LECTURE 2)

Jan Roelof van der Meer, Nicolas Carraro, Roxane Moritz, Andrea Daveri*
University of Lausanne, Switzerland
*Email *janroelof.vandermeer@unil.ch*

Horizontal gene transfer is arguably one of the most important mechanisms for bacterial evolution, leading to the single-step rapid distribution of dozens to hundreds of genes with potential adaptive benefit, such as resistance to antibiotic or other toxic compounds, or productive catabolism of complex carbon substrates. While the importance of horizontal gene transfer is widely appreciated, it is less acknowledged that the mechanisms and process of horizontal gene transfer constitute an ecological and cellular balance between fitness optimisation of a selfish DNA and its bacterial host. On the basis of studies of an integrative and conjugative element (ICEclc) in Pseudomonas I will illustrate here the manifold and subtle regulatory, cellular and mechanistic details of an ongoing adaptation, which tends to select for maximum lateral distribution of the ICE while minimising host effects. I will show how the ICE manipulates and transforms the host cell to effective ICE-DNA transfer machines, but is only able to do so in a small proportion of cells in the population, at the cost of producing host cells that are no longer able to divide. As such, we find that the evolutionary mechanism of horizontal gene transfer itself is subject to selection and adaptation, even at the smallest scale of the individual cell.

ABSTRACT FEB 03, 15.00-15.25

CURRENT STATUS, CHALLENGES AND FUTURE OF BIOREMEDIATION (KEYNOTE LECTURE 3)

*Andy Ball**
School of Science, Department of Biosciences and Food Technology, RMIT University, Melbourne, Australia
*Email *andy.ball@rmit.edu.au*

Our environment is threatened by thousands of contaminants, mainly as a result of human activities and industrialization. These include both inorganic (e.g. heavy metals) and organic compounds (e.g. polycyclic aromatic hydrocarbons, chlorinated hydrocarbons and herbicides). It has been shown that many of these hazardous chemicals cause health problem such as cancer in living organisms. Therefore, removing them from environments and soils represents a key challenge from both ecosystem and human health perspectives. Among the approaches used to remove these pollutants, microbial remediation or bioremediation represents a promising technology that is cost-effective, environmentally friendly and less disruptive than alternative technologies. Bioremediation involves microbes that are present in or added to the contaminated environment which are capable of degrading contaminants, or reducing them to less toxic forms. There are a number of bioremediation techniques, including natural attenuation, bioaugmentation, biostimulation, phytoremediation/rhizoremediation and necro phytoremediation. Many factors, such as soil texture, pH, temperature, levels of oxygen, nutrients and the microbial status of the soils, influence the rate and extent of bioremediation along with the type and bioavailability of the contaminants. Here, we highlight the current status of bioremediation, examining the development of techniques used to assess and optimize the degradation of the contaminants.

ABSTRACT FEB 03, 15.30-15.50

INVESTIGATING THE ROLE OF PGPRS IN ALLEVIATING HEAT STRESS TOLERANCE IN TRITICUM AESTIVUM L

Paramjit Khurana1, Shaloo Meena1, Roshan Kumar2, Vipin Gupta3, Utkarsh Sood4, Rup Lal4*
1Department of Plant Molecular Biology, University of Delhi South Campus, New Delhi-110021, India
2P.G. Department of Zoology, Magadh University, Bodh Gaya-824234, India
3Phixgen Pvt. Ltd. Gurugram, India-122001
4The Energy and Research Institute (TERI), Lodhi Road, New Delhi-110003, India
*Email *param@genomeindia.org*

Plant-microbe interactions are of great significance under stressful environmental conditions by favorably altering the host physiology and metabolism. Plant-Growth-Promoting Rhizobacteria (PGPR) are the beneficial bacteria that are associated with the plant roots and enhance plant growth, productivity and immunity. PGPRs are conducive and benefit the plants directly by promoting their growth under extreme environmental conditions. There microbes are beneficial to plants and enhance processes such as stimulation of root growth, rhizoremediation, biofertilization and plant stress response control. These microbes are also known to synthesize certain enzymes and phytohormones to promote the plant growth. PGPR may provide a biological alternative to fix atmospheric nitrogen to increase the crop yield. In the present study, we have undertaken the transcriptome analysis of wheat plants after Paenibacillus spp. inoculation and studied its beneficial role under heat stress. Differential gene expression analysis was undertaken in root and shoot tissues to differentiate the expression of genes in uninoculated and inoculated plants under control and heat stress conditions. Differentially expressed genes were categorized according to their functions. Further validation was undertaken by expression of genes by real time PCR analysis. Results obtained are discussed in light of recent literature and its practical relevance.

ABSTRACT

FEB 03, 15.55-16.15

MICROBE TO MICROBIOME: THE JOURNEY OF RHIZOBIUM

K. Annapurna and K. Swarnalakshmi*
Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi-110012, India
*Email *annapurna96@yahoo.co.in*

Legume plants are notable from a microbial perspective because they form specialized, N-fixing organs, called nodules, through intimate association with bacterial symbionts of the orders Rhizobiales and Burkholderiales. Biological N-fixation by legumes plays a significant role in the global N cycle, with estimates of N fixed per year on a global scale ranging from 39 to 70 Gg. Owing to the agricultural and ecological importance of N-fixation, this plant-microbe symbiosis has been the subject of intense research for several decades. As a result, much is known about the genes and chemical signals and molecular mechanisms that underpin this symbiosis. While nodulation has traditionally been studied as a two-member system, it has more recently become clear that root nodules harbor an accessory microbiome. A recent study has shown that the different rhizocompartments of Medicago sativa (i.e., the rhizosphere, root endosphere, and nodules) were successively limited in microbial diversity, with the nodule containing the simplest community. Over the last decade, non-Rhizobiales members of nodule microbiomes have previously been detected in root nodule tissue. However, it is unclear if these bacteria are present across the lifetime of individual nodules. Multiple studies have used 16S amplicon sequencing to profile root nodule communities, including those of Medicago sativa, Lotus japonicus, and Glycine max. Across these studies, the major phyla that were consistently observed as nodule associated included Actinobacteria, Proteobacteria, and Firmicutes. Our study presents the consolidated work on the diversity of nodule microbiome.

ABSTRACT

FEB 03, 11.05- 11.30

HARNESSING THE POWER OF MICROBES IN AGRICULTURE

*Vartika Mathur**
Department of Zoology, Sri Venkateswara College, Benito Juarez Marg, New Delhi-110021
*Email *vmathur@svc.ac.in*

The importance of microbes in agriculture is undeniable. Following the establishment of harmful effects of chemical fertilizers and pesticides on the health of man and animals, as well as the environment, scientists and farmers turned towards harnessing the power of microbes for agriculture. Utilizing their services for growth and protection of plants as microbial fertilizers and pesticides, respectively, is gaining popularity. However, unlike their chemical counterparts, the potential of microbes varies with the plant species, soil chemistry and microbiota as well as surrounding environmental conditions. In effect, commercial microbial fertilizers and pesticides may not be as efficient as expected in the prescribed quantity for every plant or soil condition. In contrast, some microbes may even induce secondary metabolites in plants through 'vaccination' and thus protect them from herbivores and pathogens. Thus, future research to understand the exact behaviour and potential of microbes in the plant rhizosphere and phyllosphere would prove beneficial for informed decision making while utilizing them in agriculture.

ABSTRACT FEB 03, 17.15-17.35

QUALITY ASSURANCE OF BIOFERTILIZERS IN INDIA: ISSUES AND CONCERNS

*Anil Kumar Saxena**
Director, ICAR-National Bureau of Agriculturally Important Microorganisms Kushmaur, Mau- 275103, India
*Email *director.nbaim@icar.gov.in*

In India the biofertilizer industry has developed over years and many significant changes have taken place. The shift from carrier based to liquid formulations, inclusion of microbial consortium in the Fertilizer Control Order (FCO), increase in the number of biofertilizer strains from initial five (Rhizobium, Azotobacter, Azospirillum, PSB and AM fungi) have led to the surge in the production of biofertilizers. The success of any biofertilizer product is directly linked to its quality. A bioinoculant industry is successful if it has a sustained demand for its products from the stakeholders. This sustained demand and ultimately the success of industry is again linked to the quality of biofertilizers it produces. In general, the inoculant quality is determined by recording the viable cell count in the product which in turn indicates its inoculating potential. Population counts in terms of colony forming units (cfu) are so vital in determining the quality of microbial products and their success in the field that different countries have developed their own quality control system. In India, Bureau of Indian Standards (BIS) published the Indian standard specifications initially for Rhizobium and Azotobacter inoculants and later on included Azospirillum, PSB and Mycorrhizal biofertilizers. In 2006 biofertilizers and organic fertilizers were included under section 3 of the Essential Commodities Act, 1955 (10 of 1955), in Fertilizer (Control) Order, 1985. There are various spurious products of biofertilizers in the market, reason being either the inherent problem in quality control parameters according to BIS or the non-availability of proper scrutinizing protocols. The inherent problem in BIS specification is that the specification speaks only of proper population as viable count, moisture content, pH and shelf life of the products. There are no specifications fixed for the claims from the firms for particular product, to check the true to type nature of the species used for formulating the products. The quality assurance by the concerned agencies is also confined to the presence of the right type of microorganisms in active form and in desired numbers. The presence of desired traits like amount of nitrogen fixed or P solubilized are not routinely checked. To overcome these problems in quality control there should be a stringent regulatory mechanism from the Government. The supply of culture needs to be regulated and appropriate, duly validated microbial cultures should be supplied. Some of the concerns in production of biofertilizers will be covered during the presentation.

ABSTRACT FEB 03, 17.40-18.00

PHOSPHORUS TRANSPORT IN MYCORRHIZA: JOURNEY SO FAR

Vikas Yadav, Atul Kumar Johri*
School of Life Sciences, Jawaharlal Nehru University, New Delhi-110067, India
*Email *vikasjnu@gmail.com*

The poor availability of Phosphorus (P) affects the plant growth and development adversely and consequently limits the crop yield and ecosystem productivity. To cope with phosphorus limitations, plants have evolved several strategies for the solubilization and enhancing phosphorus uptake. Among these strategies, the most ancient arbuscular mycorrhizal (AM) symbioses are one of the most successful and widespread strategies to maximize access of plants to available phosphorus. These biotrophic AM fungi colonize the root cortex of most plant species and develop an extra radical mycelium network outside the rhizosphere beyond the nutrient depletion zone of the soil surrounding plant roots. This hyphal network is specialized in the acquisition of low mobility nutrients from soil, particularly phosphorus. During the last 25 years or so, molecular biology techniques coupled to novel physiological approaches have provided fascinating contributions to our understanding of the mechanisms of symbiotic phosphorus transport. Several mycorrhiza-specific plant phosphate transporters, which are required not only for symbiotic phosphorus transfer but also for maintenance of the symbiosis, have been identified. Gathering in-depth scientific information on mycorrhizal phosphorus transport will not only improve the phosphorus uptake efficiency in agroecological systems but also will guide us towards addressing future research challenges.

ABSTRACT FEB 03, 18.30-18.50

BIOGAS PRODUCTION: IMPACT OF BIOLOGICAL PRETREATMENT OF WHEAT STRAW AND MICROBIAL COMMUNITIES COMPOSITION

*Vivekanand Vivekanand**
Centre for Energy and Environment, Malaviya National Institute of Technology, Jaipur, Rajasthan 302017, India
*Email *vivekanand.cee@mnit.ac.in*

Necessity of pretreatment emerged aiming to reduce the recalcitrance of biomass and exposing the cellulose fibres for enzymatic hydrolysis. For biological pretreatment of wheat straw (WS), fungal strains, Chaetomium globosporum and Curvularia lunata were employed which were isolated from soil (thermophilic regions of Bikaner, Rajasthan, India). Further, the study also attempted to bioaugment the process of biogas production by employing chitinolytic bacteria to degrade the fungal mycelia left in pretreated WS and utilize it as a carbon source for biogas production. Bacillus subtilis was isolated as chitinolytic bacteria from fish scales and prawns collected from Ramganj, Jaipur, Rajasthan, India. Among the isolated fungal strains, C. globosporum was identified as the most potent strain for biological pretreatment with highest laccase activity followed by C. lunata. Effect of three factors (temperature, pretreatment time, moisture content) was investigated at three severity levels on output response of biological pretreatment in terms of releasing reducing sugar. Optimized pretreatment conditions for C. globosporum were obtained as: 36°C, 31 days pretreatment time and 81% moisture content. For C. lunata, the optimized conditions were: 32°C, 23 days pretreatment time and 65% moisture content. Significant differences in the structural morphologies, functional group distribution and crystallinity was observed between untreated and pretreated samples. The composition analysis revealed the highest lignin removal (45%) after pretreatment of WS with C. globosporum. The pretreated straw was subjected to anaerobic digestion in batch scale followed by upscaling to continuous stirred tank reactors. Estimation of biomethane production potential in batch scale revealed highest increase of 31% increase in biogas yield for WS after optimized pretreatment. The addition of chitinolytic bacteria further increased biogas yield (41%). The upscaling of bioaugmentation process for pretreated WS in continuous stirred tank reactors also revealed higher biogas and methane yield compared to untreated straw. In presence of bioaugmentation with chitinolytic bacteria, the WS pretreated with C. globosporum resulted in 16% higher biogas yield in continuous stirred tank reactor compared to untreated wheat straw. The abundance of methanogens was observed to be higher in continuous stirred tank reactors running with pretreated WS during microbial community analysis. The identified bacteria belonged mostly to Firmicutes, Bacteroidetes, Proteobacteria phyla. While the most abundant methanogens were observed to be Methanosaeta and Methanosarcina.

ABSTRACT FEB 03, 18.55-19.15

CHALLENGES IN INTEGRATING MICROBIAL DIVERSITY-SOIL HEALTH FUNCTIONS

*D. L. N. Rao**
Ex-ICAR-Indian Institute of Soil Science, Nabi Bagh, Bhopal, Madhya Pradesh, India
*Email *dlnrao.icar@gmail.com*

Much of the cultivated soils globally are afflicted by one or the other kind of stresses that adversely impact soil and plant productivity. Soil health improvement is thus an urgent imperative to reverse the ill effects. Soil is an integrated system; the physical and chemical properties are shaped by biological activity, and biological activity is enhanced or limited by chemical and physical condition. A “healthy” soil is one, in which there is a large, diverse, and active population of various organisms and the physical, chemical and biological processes are functioning efficiently. While the effects of soil physical and chemical degradation are obvious, the effects of biological degradation are insidious, for example, how does the loss of specific biomolecules constituting soil organic matter impact specific microbial species/communities involved in their formation and/or dependent on them for nutrition. Similarly, how does the destruction of microhabitats inside soil aggregates affect specific soil microorganisms and ecological speciation. Due to a great functional redundancy of microbes, the quest for a single universal microbial indicator of soil health or of “key-stone” species is a big challenge. Soil microbiome analysis provides a better indication of the direction and magnitude of soil health improvement, earlier and better than other indicators. Several studies show that healthy soils have high numbers of Actinobacteria while robust functional indicators include soil respiration and β-glucosidase activity. Any single index has limitations, and integrated indices like rate of formation of organic matter by soil microorganisms (labile carbon, microbial quotient) and its turnover (metabolic quotient) have proved to be more reliable indicators of the eco-physiological condition of soil microbes. Various examples from our work in India and elsewhere will be discussed.

ABSTRACT FEB 03, 19.20-19.40

ANALYSIS OF PELLET FORMATION OF STREPTOMYCES TOXYTRICINI TO IMPROVE LIPSTATIN PRODUCTION

Kashyap Kumar Dubey
School of Biotechnology, Jawaharlal Nehru University, New Delhi, India
*Email *kashyapdubey@mail.jnu.ac.in*

Streptomycetes are the best-known sources for the production of secondary metabolites with medicinal properties against various diseases along with obesity. However, the members of the Streptomyces genus possess a complex lifecycle with the mycelial formation and lead to the propagation via sporulation. Lipstatin, a natural inhibitor of pancreatic lipase, synthesized by Streptomyces toxytricini as a secondary metabolite. The mycelial formation is the major problem in the industrial application of this strain. The branched vegetative mycelial network forms the pellet which in turn leads to mass transfer problems and slow growth, i.e. indirectly lowers the production of lipstatin. Various strain improvement strategies have been applied for the better growth of Streptomyces toxytricini to enhance the production of lipstatin from 900 mg/l to 2.3 g/l at shake flask level.
Keywords: Streptomyces, Lipstatin, Obesity, Mycelium, Pellet.

ABSTRACT FEB 03, 19.45-20.05

FUTURISTIC BIO-COMPUTATIONAL APPROACHES TOWARDS UNDERSTANDING MICROBIAL BIOREMEDIATION

*Pratyoosh Shukla**
School of Biotechnology, Institute of Science, Banaras Hindu University, Varanasi-221005, India
*Email *pratyoosh.shukla@gmail.com*

The bio-computational approaches including tools of systems biology have created lots of new avenues for carrying out innovative research and it has wider applications in microbial biotechnology. The efficient bioremediation of environmental pollutants is very significant towards sustainable perspectives and the tools of systems biology may be helpful in various ways. This field is gaining attention as these tools can be quite noteworthy in discovery of new genes and understanding the metabolic pathways involved in bioremediation. Here we will describe the diverse aspects towards their applications in developing the synthetic microbial consortium and a futuristic idea of co-cultivation of microbes for bioremediation. The present study comprises an extensive survey of heavy metal bioaccumulation using both wet lab and bio-computational approaches collectively. In the present work, we have deciphered the Lead bioaccumulation by Bacillus cereus BPS-9 which was isolated from an industrial waste contaminated site. This Bacillus cereus BPS-9 strain showed a more significant MIC value (2400 ppm) than already reported strains. In addition to this, the superoxide dismutase and dehydrogenase assay of Bacillus cereus BPS-9 under lead stress conditions were studied. The results obtained by functional analysis through SEED viewer established the presence of genes encoding heavy metal resistant proteins and transporters for the efflux of heavy metals viz., Lead, Nickel, Mercury, Cadmium, Chromium, Copper, and Zinc. These futuristic techniques in combination with tools of metabolic engineering may decipher the importance of knock-in and knock-out of key genes for attaining effectual bioremediation.

ABSTRACT FEB 04, 10.10-10.35

GENOME MINING AND BIOSYNTHETIC STUDIES OF SECONDARY METABOLITES IN STREPTOMYCES PACTUM (KEYNOTE LECTURE 6)

*Taifo Mahmud**
Department of Pharmaceutical Sciences, Oregon State University, Corvallis, OR 97331, U.S.A.
*Email *taifo.mahmud@oregonstate.edu*

Soil bacteria (actinomycetes), especially those from the genus Streptomyces, are known to be a prolific source of bioactive secondary metabolites. They produce a wide variety of natural products including polyketides, peptides, terpenes, glycosides, and aminocyclitols. Genome sequences of many Streptomyces revealed the presence of two dozen or more biosynthetic gene clusters in their genomes; however, in most cases only a few are actively expressed to produce detectable amounts of secondary metabolites under typical laboratory conditions. The soil bacterium Streptomyces pactum ATCC 27456 produces a number of structurally intriguing and highly bioactive compounds with distinct mechanisms of action. Among them is pactamycin, a broad-spectrum aminocyclitol-derived antitumor antibiotic. The strain also produces NFAT-133, an aromatic polyketide compound with immunosuppressive, antidiabetic, and anti-trypanosomal activities; conglobatin, a C2-symmetrical macrodiolide antitumor compound; and piericidins, a group of polyketide natural products with strong electron transport inhibitory activity. Genome sequencing and bioinformatic studies of S. pactum ATCC 27456 revealed their biosynthetic gene clusters, and genetic engineering and chemoenzymatic approaches led to the identification and the production of their analogues.

ABSTRACT FEB 03, 10.40-11.00

RENEU: DECENTRALIZED TREATMENT OPTIONS FOR DOMESTIC WASTEWATER MANAGEMENT

*Atya Kapley**
Senior Principal Scientist, CSIR-NEERI, Nagpur 440020, India
*Email *a_kapley@neeri.res.in*

Diminishing freshwater reserves and growing population create a host of problems that disturb ecosystem balance. Hence, practice of wastewater reuse is imperative wherein wastewater needs to be relooked at, as a resource. In urban India, that resource is approximately 70,000 MLD from Class I and Class II cities alone. Unfortunately, the majority of this domestic wastewater flows untreated, polluting the nearest river or water body. The challenges in treating such wastewater are a combination of scientific and economic hurdles. RENEU is a technology developed by CSIR-NEERI to tackle both challenges. It uses a combination of engineering and biological tools to treat the water as it flows in open drains. The design incorporates the features of an STP like sedimentation, anoxic and aerobic digestion with a specialized bacterial consortia to enhance biological degradation. Excessive nutrients that cause eutrophication like nitrogen and phosphates are removed by incorporating phytoremediation. Metagenomic tools are used to follow microbial diversity vis-à-vis their performance. RENEU was recently awarded the CSIR-Technology Award 2020.

ABSTRACT FEB 04, 11.00-11.20

CYANOBACTERIAL PHYCOBILIPROTEINS: PURIFICATION, CHARACTERIZATION AND A MULTI FACTOR BASED OPTIMIZATION FOR ENHANCED PRODUCTION

*Sunil Pabbi**
Centre for Conservation and Utilisation of Blue Green Algae, Division of Microbiology, ICAR - Indian Agricultural Research Institute, New Delhi-110012, India
*Email *sunil.pabbi@gmail.com*

Cyanobacterial phycobiliprotein (C-PBPs) pigments have extensive application in the food, cosmetic and pharmaceutical industry. Purified native PBPs viz. phycocyanin (PC), allophycocyanin (APC), phycoerythrin (PE) and their subunits fluoresce strongly and have been widely used as external labels for cell sorting and analysis and are convenient markers in gel electrophoresis, isoelectric focussing and gel exclusion chromatography. However, the potential of these high value pigments have yet not been fully realized, mainly because of cumbersome purification strategies to achieve high purity and inefficient production systems. A protocol for extraction and purification of phycobiliproteins from selected cyanobacteria has been developed resulting in purification of above 4 with good recovery. The purified phycobiliproteins were characterized using SDS-PAGE, HPLC and MALDI-TOF MS. The relative expression of cpc B gene coding for β subunit of phycocyanin under different physico-chemical conditions showed varied regulation irrespective of the source organism. PC production as well as cpc B gene expression increased under mild salt stress (10mm NaCl). In order to enhance PBPs production in selected cyanobacteria, conventional response surface method followed by GA-fuzzy logic methodology has been applied which resulted in higher coefficient of determination (R2) with 408.5 mg/L PBPs production as compared to 390.20 mg/L obtained by RSM model confirming the superiority of GA-fuzzy logic methodology. Upscaling of PBPs was successfully carried out in a photobioreactor under controlled conditions and raceways lodged in a glass house using alternative medium source to increase the biomass productivity vis-a-vis enhancement of PBPs production in an economical way.

ABSTRACT FEB 03, 11.20-11.45

A NETWORK OF REGULATORY CASCADES OF ALTERNATIVE SIGMA FACTORS CONTROLS OXIDATIVE AND PHOTO-OXIDATIVE STRESS RESPONSE IN AZOSPIRILLUM BRASILENSE

Anil K Tripathi, Ashutosh K. Rai, Ashutosh P. Dubey, Sudhir Singh, Amit Srivastava*
School of Biotechnology, Institute of Science, Banaras Hindu University, Varanasi-221005, India
*Email *tripathianil@rediffmail.com*

Azospirillum brasilense is a non-photosynthetic, plant-growth-promoting rhizobacterium which colonizes the rhizosphere, where it has to cope with environment fluctuations and consequent stresses. The genome of A. brasilense codes for 1 housekeeping and 22 alternative sigma factors consisting of 10 RpoE, 5 RpoH, 1 RpoN, and 6 FecI sigma factors. Out of the 10 RpoE sigma factors, RpoE1 and RpoE2 are involved in coping with photooxidative as well as oxidative stress. Carotenoids constitute an important component of defense against photooxidative stress. The carotenoid synthesis in A. brasilense is controlled by a pair of extracytoplasmic function sigma factors (RpoEs) and their cognate zinc-binding anti-sigma factors (ChrRs). The genome of A. brasilense harbors two copies of the gene encoding geranylgeranyl pyrophosphate synthase (CrtE), the first critical step in the carotenoid biosynthetic pathway in bacteria. Using a two-plasmid system in E. coli, we have shown that the crtE2 gene of A. brasilense Sp7 is regulated by two cascades of sigma factors: one consisting of RpoE1 and RpoH2 and the other consisting of RpoE2 and RpoH1. We have shown that the regulation of carotenoid biosynthetic pathway involves a network of multiple cascades of alternative sigma factors. During the colonization of the rhizosphere, A. brasilense has to cope with ROS released by roots as a host defense response. For coping with oxidative stress, A. brasilense genome harbors 2 paralogs of genes encoding 2 OxyR transcription regulators and 3 paralogs for catalases. Out of the 5 RpoH paralogs found in A. brasilense genome, only RpoH1 is responsible for coping with heat stress. But, RpoH3 and RpoH5 regulate oxidative stress response by controlling the expression of catalases. Out of the three catalases in A. brasilense, those corresponding to katN and katAII are regulated by RpoH3 and RpoH5, respectively. Expression of the gene encoding an inducible catalase (katAII) is regulated by a cascade of RpoE1→RpoH5 and OxyR2. The OxyR1, however, is involved in the negative regulation of alkyl hydroperoxide reducatse (AhpC). We have developed a scheme of regulatory network that is involved in the regulation of expression of enzymes involved in responding to photooxidative and oxidative stress response in A. brasilense Sp7.

ABSTRACT

FEB 04, 12.15-12.35

OVERCOMING CHALLENGES OF MICROBE-ASSISTED BIOREMEDIATION – A GENOMIC APPROACH

Charu Dogra Rawat1, Sonika Phian1, Helianthous Verma1, Durgesh Narain Singh2, Yogendra Singh2 and Rup Lal3
1Molecular Biology and Genomics Research Laboratory, Ramjas College, University of Delhi, Delhi 110007, India
2Department of Zoology, University of Delhi, Delhi 110007, India
3The Energy and Resources Institute, Lodhi Road, New Delhi 110003, India
*Email *cdrawat@ramjas.du.ac.in*

Bioremediation involves the usage of living forms like microbes, bacteria, fungi and plants for detoxification or mineralization of noxious pollutants that induce structural, physiological, neurological and reproductive disorders/deformities in biotic forms including humans. Bioaugmentation (addition of microbes) and biostimulation (addition of nutrients to stimulate indigenous microbes) are two majorly employed microbial assisted remediation methods. However, factors such as dynamic environment, toxicity and bioavailability of the contaminants, monitoring and survival of microbe degraders are some of the challenges that impede the degradation process. Cell immobilization, acclimatization, genetic modifications, rhizoremediation are strategies used to aid in microbial sustainability in the field conditions, bioventing, biosparging, use of surfactants and nanoparticles hasten the microbial degradation while use of biomarkers and stable isotope probing (SIP) aid in assessing the remediation process. Use of advanced technologies like “omics” (genomics, proteomics, metabolomics) and synthetic and system biology approaches (mining genes from databases and genome editing) have opened the way for better understood, alternative and more effective microbe-assisted remediation. We have employed genomics approach for devising a PCR-based method to monitor the bioinoculant Sphingobium indicum B90A, which is a well-known degrader of Hexachlorocyclohexane (HCH), in the bioaugmentation field trials at HCH contaminated dumpsite. I will discuss the development, testing and validation of the strategy that aids in overcoming the challenge of monitoring bioinoculant in the field during microbe-assisted remediation.

ABSTRACT

FEB 04, 12.40-13.00

INTRACELLULAR PATHOGENS APPLY COMMON ENZYMATIC TRICK TO EVADE HOST DEFENCE MECHANISM

*Bishwajit Kundu**
Kusuma school of Biological sciences, Indian Institute of Technology, Delhi, India
*Email *bkundu@bioschool.iitd.ac.in, **kundudr@yahoo.com*

Intracellular pathogens such as Mycobacterium tuberculosis (Mtb), Leishmania donovani (Ld) and Neisseria gonorrhoeae (Ng) proceed through infection stages by interacting with various host immune cells before establishing as a proliferating recurrent pathogen. Analyses of key metabolic pathways and/or receptors have provided clues which resulted in the discovery of frontline antibiotics. These include drugs like isoniazid, rifampicin, ethambutol for Mtb, miltefosine, amphotericin B for Ld and ceftriaxone, azithromycin for Ng.However, emergence of multiple drug resistance and extreme drug resistance pathogens have alarmed the health sector forcing the scientific community to look for alternate molecular pathways. In this quest we found that a key metabolic enzyme l-asparaginase is commonly found in all the above -mentioned intracellular pathogens. These intracellular pathogens experience a low pH environment which is detrimental for their survival inside the host. We hypothesise that ammonia released by the action of the l-asparaginase may act to neutralise the low pH onslaught implemented by the host as a defence response. Prior insights gained on structure and function of l-asparaginases in our lab raised our inquisitiveness about its role in the survival of these pathogens. We analysed the active site architecture of the l-asparaginases from respective organisms and elucidated their detailed mode of action. Based on these we obtained potential binder/compounds against each enzyme through docking and molecular dynamic simulations. In each case the selected compounds showed effective inhibition of L-asparaginases thereby preventing the growth of cultured pathogens. Therefore, we propose l-asparaginases as noble metabolic targets against these intracellular pathogens.

ABSTRACT FEB 04, 13.05-13.25

CHARACTERIZATION AND THERAPEUTIC APPLICATIONS OF PHYCOBILIPROTEINS FROM CYANOBACTERIA

*Datta Madamwar**
Charotar University of Science & Technology, Changa 388 421, Dist. Anand, Gujarat, India
*Email *datta_madamwar@yahoo.com*

Phycobiliproteins (PBPs) are water-soluble light harvesting proteins found in cyanobacteria and red algae. They facilitate efficient capturing and controlled-transfer of sunlight energy downhill towards photosystem by holding the water insoluble chromophores very precisely in aqueous cell environment. Crystal structures of various sub-classes (phycoerythrin, phycocyanin and allophycocyanin) of phycobiliproteins from fresh water and marine cyanobacteria have been solved using X-ray crystallography in order to understand the underlying light harvesting principle. The crystal structure of unique single peptide phycoerythrin (PDB ID: 3MWN), produced under prolonged starvation condition have been solved, which depicts no role of first 31st N-terminal amino acids in structure assembly and functionality of phycoerythrin. The geometry and arrangement of chromophores and the energy transfer pathway in marine phycoerythrin (showing distinct sequence features) have been recognized through the solution of its high-resolution crystal structure (PDB ID: 5AQD, 5FAB). Crystal structure of scarily found phycobiliprotein, allophycocyanin (which makes the core of cyanobacterial light harvesting complex) is solved (PDB ID: 4RMP). This structure described the importance of some 'amino acid substitutions' in marine cyanobacteria providing the extra hydrophobic environment to the chromophore. Moreover, some therapeutically important properties (including antioxidant, anti-aging and anti-Alzheimeric activity) of phycobiliproteins that have been noticed in eukaryotic cell line and Caenorhabditis elegans model, is validated using homology-based protein structure modelling and protein-proteins docking.

ABSTRACT FEB 04, 13.50-14.10

BEING CREATIVE: NEED OF THE HOUR SIMPLE WAYS TO TAKE RESEARCH FROM CLASSROOM TO LAB TO SOCIETY

*Naveen Gupta**
Department of Microbiology, Panjab University, Chandigarh, India
*Email *ng.puchd@pu.ac.in*

Imagination is more important than knowledge. For knowledge is limited to all we know and understand. While imagination embraces the entire world and all there ever will be to know and understand. Creativity can be god gifted in some people. However, creativity in science can also be cultivated to do meaningful science. Some of the important footsteps to increase the creative potential in science are to be 'happy but not satisfied', being alert, habit of wider thinking, asking questions, brainstorming, feedback from others and most importantly enjoying the work to do. By doing science in a creative way we can take science from classroom to laboratory to society.In modern cities, the majority of the sewage water is treated in sewage treatment plants (STP) but even after treatment it is mainly disposed off in the natural water recourses. However tertiary treated sewage water (TT Water) can be used for a number of alternate purposes such as irrigation, construction, service stations, recreational purposes like replenishment of lakes etc. However there are problems associated with the use of treated water for these purposes such asImproper treatment and irregular monitoring of the efficiency of STP'SPresence of excess nutrients such as phosphates and nitrates which lead to eutrophicationGrowth of sulphate reducing bacteria (SRB) which leads to foul smell.By working in collaboration with the Department of Environment Chandigarh all these problems were addressed.For one year STP's of Chandigarh were monitored regularly and it was concluded that it is not the type of technology it is management of the STP's which determines the quality of treated water, with given recommendations the quality of treated water was improved.To explore the possibility of using TT water for the management of Sukhna Lake Chandigarh quality of TT water was compared with water of Sukhna Lake. It was found to be fit in all aspects except excess of nutrients. An inherent technology was standardized using denitrifying and phosphate solubilizing bacteria; which completely removed these nutrients from TT water. Chandigarh administration has taken a note of the work and is exploring the use of sewage water with this process for saving the Sukhna lake Chandigarh.TT water is being used for irrigation in Chandigarh but the foul smell in it is the major problem. A process was standardized to reduce the growth of SRB's by aeration and addition of acceptable chemicals which led to the complete removal of smell form TT water. Municipal Corporation has taken up the process and is going to apply it for solving the problem of foul smell.Therefore microbial processes can be used to convert waste water into assets and solve various problems related to society at large.

ABSTRACT

FEB 04, 14.35-15.05

CHITOSAN PATTERNS MATTER IN INDUCING PLANT'S RESPONSE (KEYNOTE LECTURE 8)

*Appa Rao Podile**
Department of Plant Sciences, School of Life Sciences, University of Hyderabad, Hyderabad – 500 046, Telangana, India
*Email *podilerao@gmail.com*

Chitin is the major constituent of the fungal cell walls and the exoskeleton of the crustaceans. The deacetylated forms of chitin, referred to as chitosans, either in oligomeric form or in polymeric form, can be found with different patterns of acetylation. We have been working in collaboration with Prof. Bruno Moerchbacher for over a decade. We have together and independently cloned and expressed several microbial chitinases and chitosanases which have been extensively used to understand the structure-function relation of the chitosans. This lecture would cover as to how microbial enzymes have facilitated synthesis of defined patterns of acetylated chitosan oligomers that were difficult to synthesize using chemical processes.

ABSTRACT

FEB 04, 15.05-15.30

UNDERSTANDING AND MANAGING THE AEROBIC GRANULAR SLUDGE MICROBIOME (KEYNOTE LECTURE 9)

*Christof Holliger**
Laboratory for Environmental Biotechnology, Ecole Polytechnique Fédérale de Lausanne (EPFL), CH-1015 Lausanne, Switzerland
*Email *christof.holliger@epfl.ch*

Aerobic granular sludge is more and more often implemented in biological wastewater treatment since it allows constructing smaller and energy-efficient wastewater treatment plants. It is implemented in so-called sequencing batch reactor systems which allows to remove carbon, nitrogen, and phosphorous in one single reactor. In laboratory reactors we got to understand why start-up with activated sludge as inoculum took months until getting granules with target metabolic activities and based on that information optimized the start-up allowing creating nutrient-removing granules within less than a month. We also optimized nitrogen removal and created a complex synthetic wastewater selecting for a very similar microbial community as real municipal wastewater which allows to work with a system that optimally mimics real-world situation at laboratory scale. Future work attempts to identify the triggers for granulation and transforming suspended floccular biomass into dense granular biofilm aggregates.

ABSTRACT FEB 04, 16.30-16.45

INCREASE OIL PRODUCTION FROM OIL WELLS BY PREVENTION OF PARAFFIN DEPOSITION IN OIL WELL TUBING

Banwari Lal, Subhasis Das, K Nanthakumar, Mukesh Yadav, Veeranna A Channashettar, Manish Dwivedi, Mrigangka M Barooah*
The Energy and Resources Institute (TERI), Darbari Seth Block, IHC, Lodhi Road, New Delhi – 110 003, India
*Email *banwaril@teri.res.in*

Paraffins are organic compounds and a natural component of crude oil. They consist of various forms and combinations of aliphatic hydrocarbons and asphaltenes and they form complex paraffins and thus their melting point and cloud point are very high. Paraffinic crude oil flows freely at high temperatures through oil wells and pipes and conduits carrying oil; however at below 30°C temperature the paraffin begins to precipitate out and deposit on the inner wall of the oil well tubing through which it is flowing. These deposits keep getting thicker and more complex due to deposition of asphaltenes clay and corrosion products keep adding onto them. As the blockage keeps increasing there is a simultaneous pressure drop in the oil well bore. Eventually there is a complete blockage and crude oil stop flowing through the bore well pipe. Conventional techniques of paraffin control are expensive and plagued with other associated problems. Chemicals and solvents are used to dissolve the paraffin deposition but are also expensive, environmentally hazardous and toxic. Periodic mechanical scrapping is currently being employed but that also requires a frequent shut down of the well and hence production losses. Circulation of hot oil/air/water has also been tried with marginal success. Prevention of paraffins deposition in oil wells tubing by using microbes offers a cost effective approach. To solve this problem, a thermophilic microaerophilic paraffin degrading consortium was developed along with compatible biocatalysts capable of reducing the pour point of the paraffinic crude oil. Paraffin degrading bacterial consortium along with biocatalyst was tested under laboratory conditions and has been successfully used commercially in oil wells of ONGC & Oil India Ltd. Till date OTBL has executed 300 jobs in different ONGC Assets and also in Oil India Ltd. All the Assets are highly satisfied with the performance of PDB jobs. All these jobs have been executed with HOC & CTU cleaning methodology. HOC & CTU are utilized for cleaning the inner surface of well tubing by hot oil (HOC) through CTU (GL wells) or by HOC (SRP wells). The cleaning of oil well tubings through HOC/CTU is highly effective as compared to cleaning through Steaming system. After the cleaning of the oil well tubings, microbial slurry is placed in the tubing just around the wellbore. Subsequently the well is closed for 5 days for developing a biofilm by bacteria which does not allow the wax to get deposited on to the inner surface of the tubing. After 5 days incubation well is allowed to flow. The results showed that paraffin deposition in oil well tubing was prevented from 3 month to one year depending on the type of wax in crude oil.

ABSTRACT FEB 04, 16.50-17.10

VIROLOGY OF HIV DRUG RESISTANCE (KEYNOTE LECTURE 10)

*David van de Vijver**
Department of the Erasmus Medical Center, Erasmus University, Rotterdam, The Netherlands
Email d.vandevijver@erasmusmc.nl

The continuous development of novel antiretroviral drugs has resulted in significant improvements in treatment of HIV. Due to these improvements, individuals living with HIV can have a near-normal life span when they adhere to antiretroviral drug treatment. In addition, it has been shown that antiretroviral drugs can be used for prevention of HIV transmission as 1) individuals living with HIV that are virally suppressed due to antiretroviral drug treatment cannot transmit the virus to others and 2) the use of Preexposure prophylaxis (PrEP) can prevent HIV in individuals at high risk of infection. Unfortunately, drug resistance can be a challenge in the use of antiretroviral drugs for treatment and prevention of HIV. The aim of my presentation is to give an overview of the virological mechanisms explaining the emergence of HIV drug resistance. In particular, I will present the data from our work on a unique drug resistance pattern for the integrase strand transfer inhibitor dolutegravir and on resistance towards PrEP.

ABSTRACT

FEB 04, 17.25-17.45

COMPUTER ASSISTED VIRTUAL SCREENING OF POTENTIAL THERAPEUTIC TARGETS AND PUTATIVE LEAD MOLECULES FOR SARS COV-2: INSIGHT FOR COVID19 LEAD DISCOVERY

*Dr. Harish Pillai**
CEO - Aster Hospitals & Clinics, India
*Email *drharish.p@asterdmhealthcare.com*

The COVID-19 pandemic was a Black Swan event that took the world by surprise, the effects of which we are still experiencing till this day. This pandemic has been an eye-opener and offers us a great opportunity to reflect on our current way of working and make the necessary modifications in our processes to be better prepared for any future eventualities. The healthcare industry is out to make the required changes in all aspects, beginning from basic principles of hospitals design; planning, and all the way to staff and patient management.

ABSTRACT

FEB 04, 17.50-18.10

COMPUTER ASSISTED VIRTUAL SCREENING OF POTENTIAL THERAPEUTIC TARGETS AND PUTATIVE LEAD MOLECULES FOR SARS COV-2: INSIGHT FOR COVID19 LEAD DISCOVERY

*Sinosh Skariyachan**
Dept. of Microbiology, St. Pius X College, Rajapuram, Kasaragod, Kannur University, Kerala, India
*Email *sinoshskariya@gmail.com*

Though significant attempts and efforts are in progress to develop drugs and vaccines against COVID-19, limited therapeutic candidates are currently available. Thus, it is essential to undertake COVID-19 research and to identify probable therapeutic strategies in which computational modelling of putative drug targets and virtual screening of lead molecules provide profound insights for the drug screening against SARS-CoV-2. The drug-likeliness and pharmacokinetic features of more than hundreds natural molecules were predicted, four lead molecules with ideal drug likeliness and pharmacokinetic properties were selected and docked against fifteen targets, some of them are modelled, and their binding energies were compared with the binding energy of the interaction between Chloroquine and Hydroxychloroquine to their usual targets. The stabilities of selected docked complexes were confirmed by MD simulation and energy calculations. Four natural molecules demonstrated profound binding to most of the prioritized targets, especially, Hyoscyamine and Tamaridone to spike glycoprotein and Rotiorinol-C and Scutifoliamide-A to replicase polyprotein-1ab main protease of SARS-CoV-2 showed better binding, conformational and dynamic stability compared to the binding of Chloroquine and its usual target glutathione-S-transferase. Similarly, binding potential of six FDA drugs towards the selected targets of SARS-CoV-2 and propose the structural and molecular basis of the interaction by molecular docking and dynamic simulation. Among the selected drugs, Ritonavir and Lopinavir showed better binding towards the prioritized targets with minimum binding energy (kcal/mol), cluster-RMS, number of interacting residues, and stabilizing forces when compared with the binding of Chloroquine, Favipiravir, and Hydroxychloroquine, later drugs demonstrated better binding when compared to the binding with their usual targets. Remdesvir showed better binding to the prioritized targets in comparison with the binding of Chloroquine, Favipiravir, and Hydroxychloroquine, but showed lesser binding potential when compared to the interaction between Ritonavir and Lopinavir and the prioritized targets. The structural and molecular basis of interactions suggest that the selected natural molecules and FDA drugs can be targeted against the multiple targets of SARS-CoV-2, and the present computational models provide insights for future experimental investigations, and develop putative molecular targets and lead molecules against SARS-CoV-2.

CPG DINUCLEOTIDES AS POTENTIAL CANDIDATES FOR ZAP MEDIATED DEGRADATION AGAINST SARS-COV-2

*Mansi Verma**
Sri Venkateswara College, University of Delhi (South Campus), New Delhi 110021, India
*Email *mansiverma20@gmail.com*

RNA viruses are always a threat to mankind due to their high mutation rates and tendency to modulate their GC contents as per their host GC %. Recently we have witnessed one such virus creating havoc worldwide i.e., SARS-CoV-2. The CG rich regions in RNA viral genomes are the sites of identification for Zinc Antiviral protein (ZAP), an antiviral restriction factor present within the host system. ZAP contributes towards innate immunity in response to viral invasion. In the present work, we have analysed CpG islands among 6,700 genomes of Coronaviruses which presently hubs four genera. Betacoronavirus genus is one of the important genus as it exploits humans as its host and includes SARS-CoV, MERS-CoV, and SARS CoV-2. We aimed to explore the CpG islands to decipher the genomic diversification and the pathogenicity of Coronaviruses in various hosts including mammals and birds. We found that species having humans as their host have lower GC contents as compared to bats and other mammals as host. Species infecting Homo sapiens have an average of 38.1% GC content, whereas the one infecting bats were found to have an average of 40.97 % GC content. SARS-CoV-2 infecting humans (with GC content 46.1) were found to have GC value as 38.01% while other strains of SARS infecting humans possess higher GC value upto 40.87%. This lower GC value of SARS-CoV-2 could be the reason for its more pathogenic nature as compared to other betacoronaviruses. Many CpG islands were found across coronaviruses, with some unique patterns observed in each genus. Specifically, SARS-CoV-2 genomes were found to show conservancy for CpG dinucleotide rich regions in Nsp1 and N proteins reflecting their role in pathogenesis and can be targeted by Zinc Finger Antiviral Proteins or exploited to design CpG-recoded vaccines.

ABSTRACT

FEB 05, 09.00-09.25

BACTERIAL COMMUNITIES AS AN INDICATOR OF ENVIRONMENTAL STATUS: FROM PROOF OF PRINCIPLE TO ENVIRONMENTAL MANAGEMENT (KEYNOTE LECTURE 11)

*Cecilia Alonso**
Centro Universitario de la Region Este, Rocha, Uruguay
*Email *calonso@cure.edu.uy*

Monitoring the environmental impact of human activities is critical to preserve the existence, functioning, and ultimately, the associated services provided by ecosystems. Thus, there is interest in finding indicators of environmental status that, while reflecting the ecosystem complexity, remain relatively simple and easy to assess at large spatial and temporal monitoring scales. Microbial communities comprise the greatest share of biological diversity on Earth and have been shown to rapidly adjust their composition and/or functions in response to changing environments. Even though microorganisms have long been used to assess faecal pollution by targeting a restricted array of culturable microorganisms, the comparatively difficult methodology to approach in situ microbial diversity and ecology undoubtedly has played a role in discouraging a broader use by conservation biologists and environmental practitioners. A key attribute of the nowadays widely employed high-throughput sequencing methodology is the opportunity for deeply evaluating microbial taxonomic and functional diversity in large numbers of samples. This allows working with microbial communities applying similar approaches to the ones initially developed for macro-organisms. Among those approaches lie the tools for the identification of bioindicators of environmental quality. In this talk, a proof of concept will be presented on the identification of bacterial indicators and their use as predictors of different environmental categories, further exploring their application in the context of chemical emergent contamination risk assessment of aquatic ecosystems.

ABSTRACT

FEB 05, 09.40-10.00

A NEED FOR AN EXTENSIVE AND SYSTEMATIC SURVEY OF MICROBIOLOGICAL WEALTH OF INDIA

Venkata Ramana, 1 and Sasikala, 2
1Department of Plant Sciences, University of Hyderabad, Hyderabad 500045, India
2Centre for Environment, IST, JNT University Hyderabad 500085, India
Email chvrsl@uohyd.emet.in

Time and again we emphasize the need for an extensive and systematic survey of microbiological wealth of our country. India is one of the seventeen megadiverse countries of the world, hosting four biodiversity hotspots. However, there are no records of assets and liabilities of our country's microbiological wealth and thus there is an urgent need to initiate a systematic survey to record and conserve Indian microbiome. The task is not as simple as it is said, but requires an extensive deliberation among microbiologists with the involvement of Botanists (BSI), Zoologists (ZSI), Geologists (GSI) and Social scientists. In this talk, I share my personal experience of studying bacterial diversity of the country, through an extensive travelling across the length and breadth of our country in search of "The prokaryotes".

ABSTRACT FEB 05, 10.05-10.25

LATEROSPORULINS – DEFENSIN LIKE AMPS FROM BREVIBACILLUS SP. AND THEIR APPLICATIONS

Suresh Korpole, Shelley Sardul Singh, Deepika Sharma, Piyush Baindara, Krishan Gopal*
MTCC & Gene bank, CSIR-Institute of Microbial Technology, Sector-39 A, Chandigarh-160036, India
*Email *suresh@imtech.res.in*

Defensins constitute a class of broad spectrum cationic cysteine rich antimicrobial peptides that are essential components of the innate immune system. Defensins have been reported from all eukaryotic life forms, but not from prokaryotes. Recently, our lab has reported a bacterial origin structural homolog of human defensins from Brevibacillus sp. strain GI9 named as laterosporulin (LS). The crystal structure of LS showed a closed all-β conformation attained by formation of three intramolecular disulfide bonds. LS effectively killed both active and non-multiplying cells of Gram-positive and Gram-negative bacterial cells. Next, we characterized a laterosporulin variant LS10, from Brevibacillus sp. SKDU10. LS10 inhibited the growth of pathogenic bacteria like Mycobacterium tuberculosis Rv strain. LS10 also displayed cytotoxicity against cancer lines MCF-7, HEK293T, HT1080, HeLa and H1299. Further, we also isolated another laterosporulin variant LS3, from Brevibacillus sp. SKR3, which possessed potent antimicrobial activity against MRSA and VRE. All the laterosporulins were non hemolytic in nature. Despite having high structural similarity, there is a significant difference between microbicidal potency of laterosporulin variants. Surface electrostatic potential studies reveal difference in distribution of positive charges that is hypothesized to impart different activity spectrum. Additionally, lipoeptides from Brevibacillus strains GI9, SKDU10, SKR3, SVDS-15 and AF8 were found to inhibit various pathogenic resistant Candida strains. Lipopeptides did not show any phytotoxic effect in seed germination experiments. The emulgel formulation of lipopeptides showed antimicrobial activity in vitro and did not show any irritation effects in animal studies using BALB/c mice. Studies are being done to explore food, pharmaceutical and biotechnological applications of the discussed compounds.

ABSTRACT FEB 05, 10.30-10.50

FUNCTIONAL METAGENOMICS: AN ADVANCED APPROACH IN BIOREMEDIATION

Anil Kumar Pinnaka, Gunjan Vasudeva, Chandni Sidhu, Vipul Solanki, Krishan Gopal*
CSIR-Institute of Microbial Technology, Chandigarh-160036, India
*Email *apinnaka@imtech.res.in*

The increase in industrial revolution and development has raised the synthetic pollutants and hazardous xenobiotic compounds in the environment, causing severe health concerns. Oxygenases are the crucial enzymes in the aerobic degradation of recalcitrant aromatic compounds. They catalyze their ring cleavage and thus transform these compounds into a non-toxic form. Oxygenases are broadly classified into two categories, i.e., monooxygenases (catalyzes the addition of one oxygen atom) and dioxygenases (catalyzes the addition of two oxygen atoms). Functional metagenomics is an efficient technique to uncover the potential enzymes useful for bioremediation. In this case, we used a functional metagenomics approach to construct fosmid libraries containing ~40Kb fragment of environmental DNA. We did the activity-based screening for the catechol dioxygenase using catechol as a substrate. Positive clones were selected for further production, purification, and characterization of the enzymes. In this study, we found four novel enzymes, i.e., 2,3- dihydroxy biphenyl 1,2-dioxygenase (Bphc-SD3), Catechol 2,3- dioxygenase (C230-RW1), Metapyrocatechase (RW4-MPC), Chlorocatechol 2,3 dioxygenase (RW1-4CC) with excellent efficiency to degrade catechol compounds. Our findings suggest these enzymes can efficiently degrade 2,3 Dihydroxybiphenyl, Catechol, 3-methyl catechol, 4-chlorocatechol, 3-chlorocatechol. One of these enzymes, Bphc-SD3, a novel octameric protein, was fully characterized for its degradation efficiency and also exploited for its biosensing properties to detect catechol compounds. The catalytic efficiency of these enzymes helped us to detect the pollutants using electrochemical methods. The studies of enzymes open the opportunity for directed evolution further to enhance their catalytic efficiency and stability in extreme conditions.

ABSTRACT

FEB 05, 10.55-11.15

GUT BACTERIAL DIVERSITY IN THE TWO FAMILIES (THOMISIDAE AND OXYOPIDAE) OF SPIDERS FROM INDIA

Vikas Kumar, Inderjeet Tyagi, Kaomud Tyagi and Kailash Chandra*
Centre for DNA Taxonomy, Molecular Systematics Division, Zoological Survey of India, Kolkata, West Bengal, India
*Email *vikaszsi77@gmail.com*

Spiders are one of the most diverse Arachnids, widely distributed globally, which are important for ecological balance through their prey–predator associations. The gut bacteria of spiders have a major role in their survival through various physiological processes. Hence, it is pivotal to explore the gut bacterial diversity of wild spiders to have an insight of their host bacterial relationship. In the present work, we studied the diversity and structure of bacterial diversity of seven species of spiders belonging to the family Thomisidae and Oxyopidae. The 16S rRNA Amplicon Sequencing data (v3-v4 region) analysis revealed 5039 OTUs, out of which 16% forms the core bacterial composition between these two spider families. The analysis with DADA2 pipeline and QIIME2 (ver. 2019.10) software using SILVA database revealed the presence of 16 bacterial phyla. The Proteobacteria and Firmicutes were dominant in the spider family Thomisidae and Oxyopidae respectively. The bacterial genera Acinetobacter, Staphylococcus, Corynebacterium, Cutibacterium, and Pseudomonas were found as the core bacterial communities in the spider gut. The bacterial genus Paraclostridium was observed for the first time in spider species, Peucetia viridans. Our data analysis revealed that the bacterial community similarity was more within family Thomisidae as compared to Oxyopidae. PICRUSt2 analysis for the functional metabolic pathway revealed nine active pathways for fatty acid metabolism, organic compound degradation, sugar metabolism, and vitamin E biosynthesis (tocopherols). The scatter plot analysis indicated that the predicted pathways are more active in Thomisidae than Oxyopidae. The present study is a preliminary investigation to explore the gut bacterial diversity in spiders. The more comprehensive studies using more number of species in diverse spider families will foster a clear understanding on the structure, diversity of bacteria and their interaction to the host spider species.

ABSTRACT

FEB 05, 11.20-11.40

RECENT TREND, BIASES AND LIMITATIONS OF CULTIVATION BASED DIVERSITY STUDIES OF MICROBES

Om Prakash1, Mrinalini Parmar 2, Manali Vaijanapurkar1, 3*
1National Centre for Microbial Resource (NCMR), National Centre for Cell Science (NCCS), Pune, India
2Dept.of Biotechnology, Goa University, Goa, India
3Symbiosis School of Biological Sciences, Pune, India
*Email *prakas1974@gmail.com*

In current study we tried to observe the recent trend, biases and limitations of cultivation based microbial diversity study on the basis of papers published on description of novel microbial taxa in past six years in the International Journal of Systematic and Evolutionary Microbiology (IJSEM), the official publication of the International Committee on Systematics of Prokaryotes and the Bacteriology and Applied Microbiology Division of the International Union of Microbiological Societies. All the published papers were retrieved, sorted and analyzed based on the objectives of the study. Objective of the study includes: What is the current rate of novel taxa description? Which country's contribution is more and what are the over- and underrepresented phyla in culturable diversity? What are the current limitations? Data indicated that 600-700 novel taxa are published each year in IJSEM which is only a minor fraction of available microbial diversity. China, Korea, Germany, United Kingdom, India and USA are leading contributors in cultivation based diversity analysis, while contributions of other nations are not substantial or negligible. Despite the recent improvement in culturomics tools the dominance of Proteobacteria, Bacteroidetes and Actinobacteria are still maintained in cultivation based diversity study while representation of Archaea, obligate anaerobes, microaerophile, Synergistic, Symbionts, Aerotolerant and other fastidious microbes are poor. Single strain based taxonomic description prevails over multistrain based study and emphasis on objective based cultivation for biotechnological and environmental significance is not appreciated.

ABSTRACT

FEB 05, 12.00-12.20

ANTIMICROBIAL RESISTANCE, VIRULENCE GENES, AND BIOFILM FORMATION CAPACITY AMONG STREPTOCOCCUS AGALACTIAE STRAINS ISOLATED FROM INDIAN POPULATION

Shalini Verma1, Puja Yadav2***
1Central University of Haryana, Mahendergarh, India
2Jawaharlal Nehru University, Delhi, India
*Email *shaliniverma7993@gmail.com, **pujayadav@cuh.ac.in*

Streptococcus agalactiae (Group B streptococci, GBS) is a gram positive, catalase negative bacteria that causes mainly infections in neonates and adult immunocompromised patients. Similar to other streptococci, GBS has the ability to develop biofilms that facilitate colonization and survival in the host. Biofilms as a bacterial survival strategy allow evasion of host immunity and protection against antibiotic therapy which make these infections much harder to treat. Hence, the aim of this study was to characterize antibiotic resistance, virulence genes, and biofilm formation of GBS clinical strains isolated from different patients. Total of 250 samples were collected from both men and women of different ages (10–83 years) from different body sites during the study period of 2 years. All 250 samples were primarily screened based on their phenotype and biochemical tests. 30 of GBS strains finally confirmed by latex agglutination test and molecular typing by using GBS specific primers. The antibiotic resistance of each isolate was detected according to the Kirby-Bauer disk diffusion method. Previous studies have shown that an increase in the rate of infection and biofilm producing ability of GBS isolates, exhibit resistance to antibiotics. Therefore, biofilm forming ability of collected GBS samples was evaluated by qualitative method (Congo Red assay) and quantitative method (Crystal Violet assay). These data suggested that all GBS isolates were capable to have strong and moderate biofilm forming ability. Previously it has been reported that antibiotics resistance is achieved by the biofilm development and both have an association with each other. Hence, to find out if there is any correlation between the amount of biofilm production and antibiotic resistance or not, statistical analysis was performed by using spearman's rank correlation test.Involvement of virulence-associated genes in pathogenicity by increasing the biofilm formation suggest positive correlation between the presence of virulence gene (s) and amount of biofilm production. Therefore, we investigated the presence or absence of virulence genes in all GBS isolates by PCR. In conclusion, the present study provides information about the association of GBS serotype, virulence factors, antibiotic susceptibility and biofilm formation.

ABSTRACT

FEB 05, 13.35-14.05

BLDA AND CYCLIC DI-GMP: NATURAL PRODUCT REGULATORS SPECIAL (PLENARY LECTURE 6)

*Andreas Bechthold**
Institute for Pharmaceutical Sciences, Albert-Ludwigs-University of Freiburg, Freiburg, Germany
*Email *andreas.bechthold@pharmazie.uni- freiburg.de*

Since more than one year we have been facing a Corona pandemic. Since more than 20 years we are also facing an antibiotic resistant crisis. Each year around 1 million people die because of resistant bugs and there is a huge demand for novel antibiotics. Streptomyces are very talented gram-positive bacteria known to produce valuable antibiotics. Interestingly, the number of natural product gene clusters in the genome of Streptomyces is higher than the number of products produced by the strains. The challenge is to activate gene clusters which are silent under normal lab conditions to find novel antibiotics.Natural product biosynthesis is controlled on the level of transcription and on the level of translation.In Streptomyces c-di-GMP is involved in regulating transcription, and the tRNA BldA controls the translation process. In my talk I would like to answer the question whether c-di-GMP and BldA can be used to wake up genes clusters in Streptomyces.

THREE YEARS OF PHIXGEN PRIVATE LIMITED: CULMINATION OF ACADEMICS, RESEARCH AND BUSINESS

*Utkarsh Sood**
Research Associate (Consultant), The Energy and Resources Institute, New Delhi. Director and Co-Founder, PhiXGen Private Limited, Gurugram, India
*Email *utkarsh.sood@gmail.com*

PhiXGen Private Limited came into existence on 30th January 2018 with an idea to develop an institution that can work in the field of academics, research, and business. Under the mentorship of our Ph.D. supervisor, Prof. Rup Lal, we constituted a startup to implement the expertise and leads that we found during our Ph.D. The research branch of PhiXGen is actively working on two projects one awarded by BIRAC, Department of Biotechnology, Government of India, where we are trying to scale-up the production of novel antibiotic analog and the second project deals with studying and documenting the microbial diversity of the entire stretch of river Ganges funded by National Mission for Clean Ganga (NMCG), New Delhi. The commercial and academics branch of PhiXGen deals with the sequencing and analysis of biological sequences. The research done, experiences gathered and achievements in the journey of three years will be shared with the audience.

ABSTRACT FEB 05, 16.55-17.15

SERINE/THREONINE KINASE PRKC REGULATES CHAIN LENGTH IN BACILLUS ANTHRACIS

*Yogendra Singh**
Department of Zoology, University of Delhi, Delhi 110007, India
*Email *ysinghdu@gmail.com*

Bacillus anthracis (B. anthracis) is the etiological agent of anthrax and primarily affects livestock and wildlife worldwide. The pathophysiological consequences of anthrax are primarily attributed to toxins, and capsule and a relative new factor - bacterial chain length. Bacillus anthracis grows in long chains consisting of rod-shape cells which causes blockade in host pulmonary capillaries and thus helps in its escape from phagocytic cells. We identified PrkC, a ser/thr protein kinase of B. anthracis, as a bacterial chain length determinant by using a null mutant strain of prkC (BAS ΔprkC). We observed shorter bacillus chains, reduced cell wall thickness and multi-septa phenotype in the mutant strain. We also found an upregulation in bacillus chain length determinant proteins - BslO, a septal murein hydrolase actively involved in the bacillus de-chaining process, and Sap (surface layer protein), required for BslO localization. These results suggest that PrkC regulates chaining phenotype in Bacillus anthracis.

ABSTRACT FEB 05, 17.20-17.40

NOVEL DRUGS TO TARGET PSYCHO-PATHOGENIC BACTERIA

*Vipin Chandra Kalia**
Department of Chemical Engineering, Konkuk University, Seoul 05029, Republic of Korea
*Email *vckaliaku@gmail.com*

Microbes have a highly evolved genetic and metabolic system to counter environmental stress. The major threat to human beings is from bacterial pathogens. These pathogens behave like “sociopaths” – who mount a violent attack and leave the host quickly but completely crippled or as “psychopaths” – who are “cold-hearted”, make a very calculative move and stay inside the host. Their repertoire of unique genomic arsenal enables them to invade and infect eukaryotic hosts. Antibiotics, which are intended to kill bacteria, get a strong challenge from the pathogen. Consequently, bacteria activate their efflux pumps leading to rapid expulsion of antibiotics or undergo genetic modifications leading to emergence of drug-resistance. Regular, repeated and even indiscriminate use of antibiotics has enabled bacteria to develop multi-drug resistance against almost all antibiotics developed over the last eight decades. Efforts to circumvent bacterial drug resistance have led to the realization that they possess a unique cell density dependent gene expression system. During this phenomenon termed as quorum sensing (QS), bacteria synthesis signal molecules, which above a threshold level activate transcription of virulence factors. Thus, it has been realized that targeting the QS system will prevent pathogenicity without killing the bacteria. This approach is likely to exert negligible selective pressure on bacteria, which will not be provoked to develop drug resistance. In addition, it has been shown that QS inhibitors (QSIs) enable bacterial killing at much lower doses of antibiotics than required otherwise. Bacteria, legumes, and medicinal plants have been shown to produce QSIs to act as antipathogens. This approach can be extended to protect crop plants and fishes, prevent biofouling of membranes used for producing potable water, shipping industry, etc.

ABSTRACT

FEB 05, 17.45-18.05

METALS AS ADDITIONAL DRIVERS FOR EMERGING ANTIBIOTIC RESISTANCE AND ITS CLINICAL VALIDATION

*Praveen Rishi**
Microbiology, Panjab University, Chandigarh, Panjab, India
*Email *rishiparveen@pu.ac.in*

Heavy metals are widespread in sewage as a consequence of ungoverned industrial and anthropological activities. Salmonella enterica serovar Typhi (the causative agent of typhoid fever) is known to persist for longer durations in sewage sludge of sewage treatment plants, where it encounters the heavy metal selective pressure. The pathogen penetrates into the food chain and water through agricultural practices, thereafter entering the human host through contaminated food and water. Significantly enhanced expression of genes involved in co-selection/ co-inheritance of metal and antibiotic resistance has been reported in various pathogens. Thus, there are concerns regarding the potential of metal contamination in maintaining a pool of antibiotic resistance genes in both environmental as well as clinical settings. In this context, the study carried out by us to substantiate this association in serovar Ty2 and clinical Salmonella Typhi isolates interestingly indicated a co-relation between cadmium and antibiotic resistance, which led to an increase in MIC values suggesting that the sensitive isolates became resistant and resistant became more resistant as per their MICs. Further transgenerational cadmium accumulation indicated the multitudinous survival efforts that were made by the cadmium exposed cells, thereby indicating a necessity to devise a fresh regulatory framework for management and disposal of industrial as well as household waste, which act as reservoir of antimicrobial resistance genes. This metal induced antibiotic resistance could be enfeebled using a NMP, an efflux pump inhibitor in combination with antibiotic, which was validated using clinical strains. Thus, it is being strongly felt that a wider analysis of the concept in more clinical strains and in other potential pathogens will help in addressing the present day challenge of antibiotic resistance arising due to metal exposure of the pathogen in the environment/ industrial effluent. The combination of EPI(s)-antibiotics may be exploited in future as one of the strategies for combating metal induced antibiotic resistance.

ABSTRACT

FEB 05, 18.10-18.30

BACTERIAL QUORUM-QUENCHING WITH TRICLOSAN CONTROLS SLIME FORMATION IN PAPER MILLS

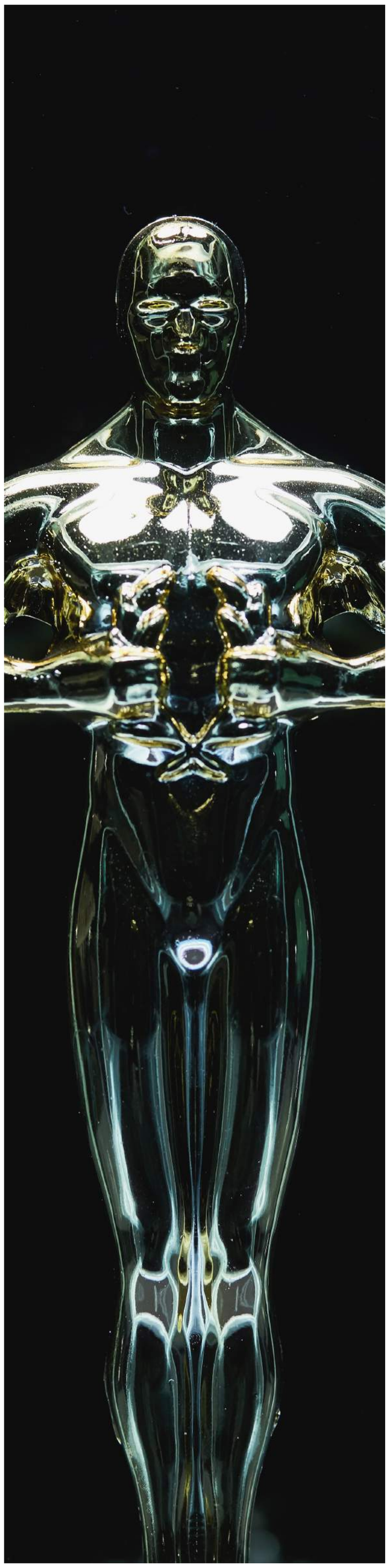
*Prince Sharma**
Department of Microbiology, Panjab University, Chandigarh, India
*Email *princess@pu.ac.in*

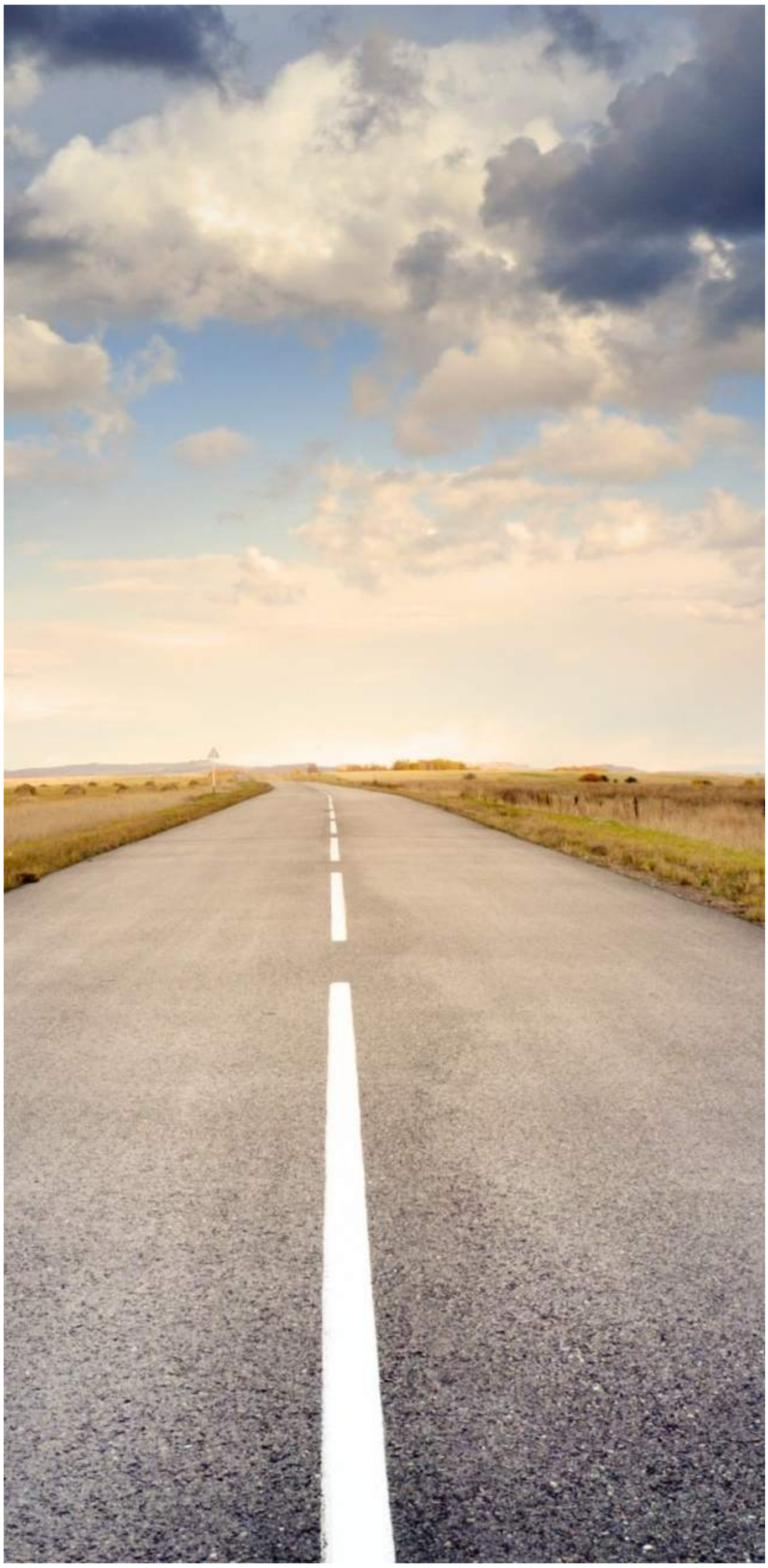
Slime deposition on paper by bacteria is a major problem confronted by paper-mills, resulting in retraining the efficacy of the final product and huge economic losses. Conventional methods used for the eradication of slime involve the use of combinations of chemical biocides which lead to effluent toxicity. Bacterial quorum-quenching with natural and synthetic eco-friendly compounds can be used as an alternative method for inhibiting the slime formation. Autoinducer-2 (AI-2, furanosyl borates) mediated quorum sensing is a universal communication system in bacteria. In this study, bacteria from paper-mill slime samples were isolated and identified for biofilm (slime) forming potential and AI-2 activity. Several natural and synthetic compounds were selected as quorum quenchers by docking with AI-2 producer -LuxS protein. Compounds with highest docking score were tested for inhibition of biofilm formation by the consortium of all bacterial isolates, and triclosan was found to be the best as it significantly reduced the expression of luxS and inhibited the formation of consortium biofilm, as shown by FE-SEM studies, to 50% (BI-50) at a concentration of 23.43µg/ml and completely (acted as biocide) at 30µg/ml when tested in the R and D set-up of paper mill.

UNDERSTANDING THE GUT-LUNG AXIS IN TUBERCULOSIS AND ITS IMPLICATIONS

*Richa Misra**
Department of Zoology, Sri Venkateswara College, University of Delhi, Delhi, India
*Email *richamisra@svc.ac.in*

Tuberculosis (TB), caused by Mycobacterium tuberculosis (Mtb), shows two different disease manifestations in the human body. While the deadly pulmonary TB remains one of the biggest killers worldwide, the extra-pulmonary TB manifestations that include infection at all the other body sites is also increasingly becoming a concern, especially in India. Diagnosis, management and eradication of TB remains a major challenge worldwide and many aspects about the infection process in hosts still remain elusive. High-throughput sequencing technologies have helped unravel the importance of gut microbiome (GM) in human immune response, nutrition and metabolism. Dysbiois of GM has been implicated in several disease processes and new concepts such as “gut-brain axis” and “gut-lung axis” have come to light with recent advances. Since TB is closely associated with decline in immunity, we studied the GM alteration in pulmonary TB patients by 16S rRNA gene and whole-genome shotgun sequencing. Significant GM dysbiosis was observed in TB patients as compared to their healthy household contacts. Analysis showed enrichment of butyrate and propionate producers in TB patients and reduced biosynthesis of vitamins and amino acids. The results suggested that Mtb might utilize the anti-inflammatory milieu of hosts generated by the microbial dysbiosis. Exploration of the gut microbial DNA also revealed presence of Mtb DNA in stool of patients, which was studied further with help of molecular diagnosis techniques. Our results showed the ability of PCR to detect Mtb DNA in stool samples from TB patients and the potential use of stool as a sample to facilitate routine screening of high-risk cases.





AMI AWARDS- ABSTRACTS

The road to success and the road to failure are almost exactly the same

ABSTRACT

FEB 04, 16.45-16.55

AMI- ALEMBIC AWARD 2020:
DR. P. GOPINATH

Indian Institute of Technology Roorkee

"Nanomaterials for antibacterial applications"

The need for novel nanomaterials with antibacterial activity arises due to antibiotic resistance developed by most of the bacteria. We have developed several antibacterial nanomaterials and studied their antibacterial mechanism using Staphylococcus aureus as a Gram-positive model and antibiotic resistance Green Fluorescent Protein (GFP) expressing Escherichia coli as a Gram-negative model system. Our research group is also working in areas to address some of the most pressing issues that our society faces, like water and air pollution. Waterborne diseases are common in India due to the lack of access to clean water that leads to the intake of water containing bacteria and arsenic in several states of India. We have developed a portable nanofibrous membrane filter by the electrospinning method. This membrane removes bacteria present in the water using the traditional gravity flow filtration. This can be used as a filter as well as an adsorbent for the removal of bacteria and toxic heavy metals in water. We found that the developed membrane could be able to remove 10 lakhs bacteria within 60 minutes through filtration and possess an adsorption efficiency of ~89 % for heavy metals like arsenic. We have also fabricated antibacterial nanofilters that can be worn as a nose mask, and that can effectively block particles in the air of size 0.2 µ or more in air. The most encouraging aspect of these developed materials is that it is possible to take these developed technologies to industries.

ABSTRACT

FEB 04, 16.55-17.05

AMI-LOUIS PASTURE AWARD 2020:
DR. INDU VERMA

Postgraduate Institute of Medical Education and Research, Chandigarh

"In vivo expressed mycobacterial transcripts: Candidate biomarkers for molecular and immunological diagnosis of tuberculosis"

Tuberculosis is still a major health problem particularly due to diagnostic challenges. To achieve the ambitious target of “End TB” strategy, novel diagnostics are required. There is need for the identification of biomarkers that are specifically expressed by pathogen/host abundantly during the disease condition. Work from our lab has led to identification of Mycobacterium tuberculosis (Mtb) genes expressed at the site of infection both during pulmonary TB (PTB) and extra-pulmonary TB (EPTB). Whole genome microarray of the mycobacterial transcriptome in biological specimens from PTB and Pleural TB demonstrated a set of genes that are upregulated only in TB patients and not in the disease control. Based on these transcripts, a RNA based molecular assay led to detection of sputum smear positive and sputum smear negative patients with sensitivities ranging from 87-100% and 50-67% respectively with high specificities. In patients with pleural TB, mycobacterial transcripts were identified from the pleural biopsies and a molecular diagnostic test has been developed and validated in pleural TB suspects. Further, using the combination of in silico tools and high throughput novel technique of peptide array, immunodominant epitopes of the mycobacterial proteins encoded by in vivo expressed transcripts have been identified for the development of rapid antigen/antibody detection immunoassays. Our study highlights the importance of biomarkers being expressed under in vivo conditions at the site of infection in clinical specimens of TB patients as promising candidates for the development of both molecular as well as immunological tests for the diagnosis of tuberculosis.

ABSTRACT

FEB 04, 17.05-17.15

AMI PROF. B.N. JOHRI AWARD 2020:
PROF. U. SIVAKUMAR

Tamil Nadu Agricultural University, Chennai

"Biocatalysts and process development for biomass-derived fuels and chemicals"

The forefront mosts constraints impeding the lignocellulose biomass conversion are robust, scalable technologies for a smooth transition from laboratory to commercial scale, including biocatalysts for biomass hydrolysis, biomass deconstruction technologies, and fermentation strategies that work on a biorefinery approach. Biocatalysts with such wide diversity and novel catalytic properties are required for the bio-based conversion leading to fuels and chemicals. In this context, multifunctional Glycosyl Hydrolases that possess thermo-and pH stable cellulases from extreme environments have shown their potential under conditions that are appropriate for bioconversion processes in industries. These enzymes performing the processes at higher temperatures are showing reduced risk of microbial contamination, lower viscosity, improved transfer rates, and improved solubility of substrates, reduce the viscosity of the reaction mixture allowing the use of higher solids loadings, decreasing water demand. Enzymes that possess delignification and depolymerization properties for conversion of lignin to high-value platform chemicals are gaining importance. Laccase from archaea, Haloferax volcani and fungal source of Hexagonia hirta MSF2 were successful. The laccase-based delignification process was developed for deconstruction of corn cob, wood biomass, and sugarcane bagasse. Furthermore, a hydrodynamic cavitation reactor coupled with laccase pretreatment showed enhanced (47%) delignification efficiency in corn cob biomass. A combination of enzyme and catalyst mediated depolymerization of corn cob and birch wood biomass has revealed high-value Low weight monomeric (LWM) green chemicals such as eugenol, cinnamic acids, guiacol, etc. biomassFurthermore, thermophilic bacteria such as Bacillus tequilensis, Bacillus subtilis, Bacillus licheniformis, and other Bacillus spp. were biprospected from hot springs of Manikaran (~95 °C), Kalath (~50°C) and Vasist (~65 °C), The Himalayas, India by in situ enrichment method. The thermotolerant cellulases and xylanases identified tolerated up to 80 oC and pH 7. The endoglucanase exhibited maximum relative activity of 108.2 and 112.4% in the presence of calcium and potassium ions. Under the submerged condition, a thermophilic bacterial strain B.aerius CMCPS1 from paddy straw compost showed maximum filter paper activity (FPA) and endoglucanase activity of 4.36 IU mL−1 and 2.98 IU mL−1, respectively, at 44 h. The saccharification efficiency of 55% was achieved with CMCPS1 multifunctional cellulases at 50 °C and pH 5.0. Similarly, a thermophilic fungus isolated from elephant dung, Chaetomium thermophilum EDWF1 produced thermotolerant and alkali-tolerant endoglucanases, filter paper units, and beta-glucosidase. Therefore, thermophilic enzymes with multifarious functions is a future demand for sustaining bio-refineries and bio-economy.

ABSTRACT

FEB 04, 17.25-17.35

YOUNG SCIENTIST AWARD IN ENVIRONMENTAL MICROBIOLOGY 2020:
DR. VIPIN GUPTA

phiXgen Pvt.Ltd.,GH-11,Sector 47,Gurugram,122001, Haryana, India

"Comparative Genomics and Integrated Network Approach to study Phylogenic Patterns, Co-mutational Hotspots and Regulatory Interactions in SARS-CoV-2"

SARS-CoV-2 pandemic resulted in 92 million cases in a span of one year. The study focuses on understanding population specific variations attributing to its high rate of infections in specific geographical regions particularly in the USA. Rigorous phylogenomic network analysis of complete SARS-CoV-2 genomes (245) inferred five central clades named a (ancestral), b, c, d and e (subtype e1 & e2). The clade d & e2 were found exclusively comprising of USA. Clades were distinguished by 10 co-mutational combinations in Nsp3, ORF8, Nsp13, S, Nsp12, Nsp2 and Nsp6. Our analysis revealed that only 67.46% of SNP mutations were at amino acid level. T1103P mutation in Nsp3 was predicted to increase protein stability in 238 strains except 6 strains which were marked as ancestral type; whereas co-mutation (P409L & Y446C) in Nsp13 were found in 64 genomes from USA highlighting its 100% co-occurrence. Docking highlighted mutation (D614G) caused reduction in binding of Spike proteins with ACE2, but it also showed better interaction with TMPRSS2 receptor contributing to high transmissibility among USA strains. We also found host proteins, MYO5A, MYO5B, MYO5C had maximum interaction with viral proteins (N, S, M). Thus, blocking the internalization pathway by inhibiting MYO5 proteins which could be an effective target for COVID-19 treatment. The functional annotations of the HPI network were found to be closely associated with hypoxia and thrombotic conditions confirming the vulnerability and severity of infection.

ABSTRACT

FEB 04, 17.35-17.45

YOUNG SCIENTIST AWARD IN DAIRY AND FOOD MICROBIOLOGY 2020: DR. SANDEEP KUMAR PANDA

School of Biotechnology, campus 11, KIIT University, Bhubaneshwar, Odisha, India

"Development of functional foods and beverages from indigenous raw materials"

Innovative foods and beverages with health-promoting potential and preferable organoleptic attributes are the priority of the consumers of the present times. The presentation depicts the development and characterization of red wine and anthocyanin-rich beer from purple sweet potato. The reports of the sensory evaluation of the sweet potato wine and beer have been provided. Also, wine production from bael fruit has been described. The presentation illustrates the production and the dynamics of biochemical parameters and volatile compounds during the course of lactic acid fermentation (using Lactobacillus fermentum) of prickly pears. Application of folate producing Lactobacillus sp. in value addition of millets have been described in the presentation. Fermentation of beet-carrot juice using Lactobacillus brevis and its efficacy in different cell lines as a functional protective food has been elaborated. Food microbiologists need to understand the technological gaps and possible mechanisms to overcome them. Multidisciplinary studies including nanotechnology, chemical technology and cost economics are the important aspects of the commercialization of the novel functional foods and beverages. The talk includes the future projections, novel strategies and plans for collaborations for novel findings and new functional foods and beverages development.

ABSTRACT

FEB 04, 17.45-17.55

YOUNG SCIENTIST AWARD IN INDUSTRIAL MICROBIOLOGY 2020: DR. SONICA SONDHI

Department of Biotechnology, Chandigarh College of Technology, Landran, Mohali-140307, Punjab, India

"Bacterial laccases and its potential applications"

Mosquito- the deadliest animal on the earth is the major hurdle for the National program of malaria elimination by 2030. Scientific studies decoding the Plasmodium biology in context to its relations with the inhabitant microbes in invertebrate host may prove a vital weapon in fighting this disease. For combating the Plasmodium transmission, three main parasite interacting targets organs- midgut, hemolymph and salivary gland play a crucial role. Several studies prove that immediately after blood feeding, a vital tripartite interaction occurs among mosquito-microbe-parasite in the mosquito's gut lumen. Harnessing the power of gut symbionts against parasite transmission is an emerging concept wherein, Wolbachia has proven to be a great success in Aedes mosquito against dengue virus. The studies of microbes like Elizabethkingia and Serratia against the Plasmodium in Anopheles are in nascent stage. The molecular basis of how Plasmodium manages its survival, development, and transmission is not well-known. Using meta-transcriptomic studies, currently we are identifying resident microbes, and exploring their anti-Plasmodium role in Indian vectors. I would share my research experience and discuss how an early suppression of gut microbial population by P. vivax favors its own successful invasion and development in the mosquito A. stephensi.

ABSTRACT

FEB 04, 17.55-18.05

YOUNG SCIENTIST AWARD IN MEDICAL AND VETERINARY MICROBIOLOGY 2020: DR. PUNITA SHARMA

National institute of Malaria Research, Indian council of medical research, Sector-9, Dwarka, New Delhi

"Learning of mosquito-microbiome interactions and tuning innovations in combating Vector borne diseases"

Mosquito- the deadliest animal on the earth is the major hurdle for the National program of malaria elimination by 2030. Scientific studies decoding the Plasmodium biology in context to its relations with the inhabitant microbes in invertebrate host may prove a vital weapon in fighting this disease. For combating the Plasmodium transmission, three main parasite interacting targets organs- midgut, hemolymph and salivary gland play a crucial role. Several studies prove that immediately after blood feeding, a vital tripartite interaction occurs among mosquito-microbe-parasite in the mosquito's gut lumen. Harnessing the power of gut symbionts against parasite transmission is an emerging concept wherein, Wolbachia has proven to be a great success in Aedes mosquito against dengue virus. The studies of microbes like Elizabethkingia and Serratia against the Plasmodium in Anopheles are in nascent stage. The molecular basis of how Plasmodium manages its survival, development, and transmission is not well-known. Using meta-transcriptomic studies, currently we are identifying resident microbes, and exploring their anti-Plasmodium role in Indian vectors. I would share my research experience and discuss how an early suppression of gut microbial population by P. vivax favors its own successful invasion and development in the mosquito A. stephensi.

ABSTRACT

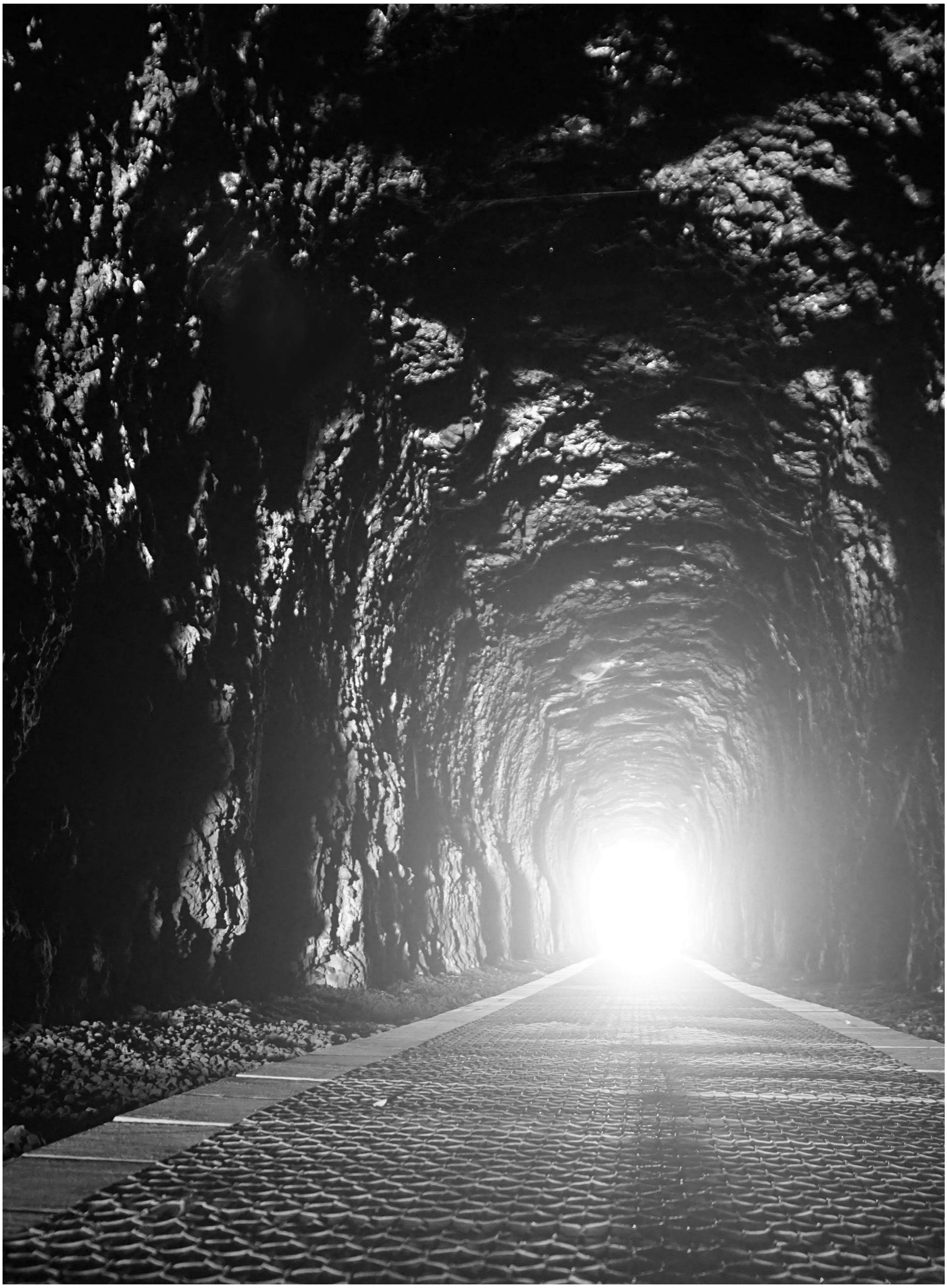
FEB 04, 18.05-18.15

YOUNG SCIENTIST AWARD IN MOLECULAR MICROBIOLOGY AND BIOTECHNOLOGY 2020: DR. RAVINDER SINGH

Department of Experimental Medicine and Biotechnology, PGIMER Chandigarh, India

"Reverse Vaccinology: Finding vaccine candidates against Acinetobacter baumannii"

Acinetobacter baumannii has emerged as a multi drug resistant opportunistic human pathogen causing serious nosocomial infections in immunocompromised patients. Using Reverse Vaccinology approach, the pan-proteome of A. baumannii was analyzed in silico to find potential vaccine candidate proteins on the basis of sub-cellular localization, number of transmembrane helices, adhesion probability, ability to bind MHCs and dissimilarity with human and mouse proteome. Out of 4589 proteins, 51 proteins fulfilled the criteria of good vaccine candidates. Three proteins viz. FilF, BamA and nuclease were cloned in pET28-a, expressed in E.coli BL21 (DE3) and purified. Their immunoprotective efficacies were evaluated in A. baumannii associated murine pneumonia models (intratracheal and intranasal) developed in our lab. Immunization with purified recombinant proteins evoked significant antibody titers in mouse that facilitated the reduction of bacterial load in lungs, levels of pro-inflammatory cytokines were reduced and those of anti-inflammatory IL10 increased significantly. Decreased neutrophil infiltration was observed in immunized mice. Active immunization with FilF and BamA resulted in 50 and 80% survival of A. baumannii challenged mice, whereas passive immunization with BamA resulted in 60% survival. These proteins predicted as potential vaccine candidates by in silico analysis, showed immunoprotective efficacy and can contribute significantly in vaccine development against A. baumannii. To identify more novel vaccine candidates, a pan- and core-genome of MDR A. baumannii clinical isolates was generated using MinION-Oxford Nanopore Technologies. Also, we focus on the use of reverse vaccinology for the development of a broad-spectrum epitope-driven vaccine against more than one nosocomial, resistant pathogens.



AMI/INSCR INNOVATIVE RESEARCH (FACULTY) - ABSTRACTS

When you reach the end of your rope, tie a knot in it and hang on

SUSTAINABLE UTILIZATION OF MARINE WASTES FOR OYSTER MUSHROOM PLEUROTUS FLORIDA (SINGER, 1946) PRODUCTION

Kalaiselvam, M
Centre of Advanced Study in Marine Biology, Faculty of Marine Sciences, Annamalai University
Email Parangipettaikalaifms@gmail.com

Edible mushroom cultivation is a profitable cottage industry, in which oyster mushroom occupies a prominent place in India. A good substrate is a key factor that determines the profitability of the mushroom cultivation. Marine waste were evaluated for the production of oyster mushroom as a means of managing the vast amount of organic waste that are being generated by fast growing seafood industries. In the present study, sustainable utilization of marine resources for the production of oyster mushroom (Pleurotus florida) and the standardized technology was transferred to scheduled caste population in and around Parangipettai, Tamil Nadu, India. The participants have collected marine wastes from the landing centre and processed as per the procedure taught during the lectures as well as demonstration. The experimental work was designed with Completely Randomized Design (CRD) with four treatments (375 g of paddy straw with 125 g of fish waste, shell waste, seaweed and seagrass amended separately) and a control (500 g of paddy straw) with three replications. Continuous hands on training were given for a period of one month to the participants on cultivation of oyster mushroom using marine bio-wastes as supplementary substrate along with paddy straw. During this one month training, the participants understand the technology thoroughly starting from the substrate preparation and processing, spawn handling, mushroom bed preparation, continuous monitoring of the culture environment, harvest, value addition and marketing etc. Further, the nutritive value and biological activities of oyster mushroom cultured on different marine waste was evaluated. Average yield was tested in three flushes of P. florida on four different substrates with control. Among various substrates, maximum yield (498.11 ± 7.80 g) was recorded in fish waste. However, minimum average yield (266.91 ± 4.35 g) was recorded in seaweed. The biological efficiency was recorded in four different substrates along with control. Among these, fish waste exhibited highest biological efficiency (99.62 ± 1.56 %). Very least efficiency was observed in control (53.38333± 0.86784 %). The proximate composition such as moisture, protein, carbohydrate, total lipid, crude fiber, amino acids and vitamins were estimated in P. florida which harvested from five different substrates. The highest moisture content (90.71 %) was recorded in paddy straw and the least value (82.97 %) was recorded in shell waste. The highest content of protein was found in fish waste (23.52 %) and the lowest protein was found in seaweed (17.18 %). The lowest lipid percentage was observed in fish waste (4 %) and the highest lipid percentage was observed in paddy straw (8 %). The lowest percentage (22.09 %) of carbohydrate was observed in seaweed substrate and the highest carbohydrate percentage was observed in fish waste (36.54 %). The maximum percentage of crude fiber was observed in fish waste (14.67 %) and minimum in seaweed (8.75 %). Fish waste substrate was identified to enhance the protein and carbohydrate content in P. florida, so this substrate may be adopted for β-glucan isolation commercially. In vitro study of β-glucan showed moderate cytotoxicity in MCF-7. Further in vivo studies are required to check the cancer and immunomodulatory properties. Four training programmes were successfully conducted to scheduled caste women population under the technology transfer programme with the financial support of Department Science and Technology, Government of India. Micro funding was provided to the two self help groups belong to SC population and they became a small entrepreneur in that area. It is interesting to note that the oyster mushroom production using marine waste as supplementary substrate along with paddy straw not only increase the yield and nutritional quality but it could be an alternative livelihood for scheduled caste population.

Keywords: Mushroom production, marine resources, proximate composition, biomolegules, technology transfer and alternate livelihood

ABSTRACT (AIF02) FEB 04, 10.50-11.00

REGULATION OF PQQ-DEPENDENT GLUCOSE DEHYDROGENASE MEDIATED MINERAL PHOSPHATE SOLUBILIZATION BY CATABOLITE REPRESSION CONTROL PROTEIN IN ACINETOBACTER SP. SK2

*Krishna Bharwad and Shalini Rajkumar**
Institute of Science, Nirma University, Ahmedabad – 382481, Gujarat, India
*Email * shalini.rjk@nirmauni.ac.in,*

Plant growth promoting rhizobacteria isolated from the rhizosphere of Vigna radiata was used which was identified as Acinetobacter sp. SK2. The mechanism of mineral phosphate solubilization (MPS) in SK2 was studied in detail and attempts were made to elucidate the role of mGDH and sGDH. The periplasmic glucose oxidation to gluconate was the main mechanism of MPS. Therefore the mutants for mGDH and sGDH were generated individually. The mutants revealed that mGDH was solely responsible for periplasmic oxidation of glucose to gluconate which lead to MPS and sGDH was not responsible for extracellular secretion of gluconate. Succinate mediated repression of MPS phenotype of Acinetobacter sp. SK2 strain was studied. Gluconate mediated MPS phenotype of SK2 was post-transcriptionally repressed by Crc in presence of succinate. Gluconate production and expression of genes of the glucose oxidation (gdhA and gdhB) was found only in glucose but not in succinate and glucose+succinate grown cells. Crc, global regulator for carbon source utilization, was inactivated using an single cross over recombination system resulting in derepressed MPS phenotype through constitutive expression of the gdhA. Inactivation of Crc resulted in increased activity of the gdhA encoding mGDH enzymes even in glucose+succinate grown cells. An augmented phosphate solubilization up to 44% was attained in glucose+succinate-grown Δcrc strain as compared to wild-type strain. Vigna radiata plants inoculated with wild-type improved both root and shoot length by 1.3-1.4 fold. However, crc deletion strain increased root and shoot length by 1.6 folds, compared to uninoculated controls. While mimicking the soil condition, the crc inactivated PSBs better served as compared to wild-type. A strategy of similar kind may be employed when phosphate solubilization or other PGP traits are influenced by CCR. By these means repression relieved strains can be developed which may further improve plant growth under natural soil conditions also.

ABSTRACT (AIF03) FEB 04, 11.00-11.10

GUT MICROBIOME, OBESITY, AND COLORECTAL CANCER: A TRIPARTITE CONNECTION

Indrakant Kumar Singh1, Pooja Mittal1 and Archana Singh2*
1Molecular Biology Research Lab., Department of Zoology, Deshbandhu College, University of Delhi, Kalkaji, Delhi-110019,
2Department of Botany, Hansraj College, University of Delhi, Delhi-110007, India
*Email *iksingh@db.du.ac.in*

Colorectal cancer (CRC), the third most common cancer type, accounts for 10 percent of the new cancer cases worldwide. The gut microbiome (microbiota) represents the community of all microorganisms inhabiting the gut and lies in proximity to the colorectal epithelium. Various studies have shown the prevalence of gut microbial imbalance/dysbiosis in CRC patients, though the molecular mechanisms involved remain elusive and an emerging area in CRC research. These research findings aim to pave way for use of gut microbiome for CRC treatment. Also, unhealthy food habits/diet from childhood may negatively impact the gut microbiome's composition, further leading to increased risk of CRC in adults. Thus personalized diet may modulate the gut microbiome, with a potential to reduce CRC risk. The further investigation and characterization of tumorigenic bacterial species in the obese microbiome may create an efficient diagnostic tool, biomarker or treatment option in CRC patients. Herein, we aim to provide an overview of the connection between obesity, gut microbiome composition, and CRC risk and also highlight the associated molecular mechanisms.

Keywords: Colorectal, Cancer, Obesity, Gut, Microbiome

ABSTRACT (AIF04)

FEB 04, 11.10-11.20

ANTIMICROBIAL POTENTIAL OF NOVEL 1,3,4-OXADIAZOLE DERIVATIVES

Harish Rajak1, Pradeep Mishra2*
1Institute of Pharmaceutical Sciences, Guru Ghasidas Vishwavidyalaya, Bilaspur-495 009, (CG) India
2Department of Pharmaceutical Sciences, Dr. H. S. Gour University, Sagar-470 003 (MP)
Email Indiaharishdops@yahoo.co.in

The emergence of drug resistance to first line antibiotics and the importance of oxadiazole as antimicrobial agent have prompted us to undertake the synthesis of few novel oxadiazole analogues hitherto unreported for their antimicrobial activities. The structures of the compounds were confirmed by Nitrogen analysis, IR and 13C-NMR spectral data. The antimicrobial properties of the compounds were investigated against bacterial strains i.e. Proteus mirabilis (MTCC-425), Pseudomonas aeruginosa (MTCC-424), Bacillus subtilis (MTCC-639) and Staphylococcus aureus (MTCC-96) and fungal strains i.e. Aspergillus niger (MTCC-1334) and Candida albicans (MTCC-227) using disk diffusion method. Some of the compounds demonstrated marked antibacterial and antifungal activities. Compound 27 was found to possess significant antimicrobial properties against all the tested pathogenic microorganisms. Other active compounds were 3, 8, 11 and 35. Structure activity relationship among the synthesized oxadiazoles has also been studied. Keywords : Oxadiazoles, Antimicrobial activity, Disk diffusion method.

ABSTRACT (AIF05)

FEB 04, 11.20-11.30

A THERMOACTIVE ALKALINE BACTERIAL LIPASE: OPTIMIZATION, PURIFICATION AND CHARACTERIZATION STUDIES

Tailor A. J.1 and Gadhvi R. R.2*
*1*Department of Microbiology, Dr. APJ Abdul Kalam Govt. College, Dadra & Nagar Haveli Ucchha Shikshya Samiti, Dokmardi, Silvassa, DNH. (U. T.) 396230. India.*
2Department of Biotechnology, Veer Narmad South Gujarat University, Surat. Gujarat. Pin. 396125. India.
*Email *ajtailor109@gmail.com*

Lipases obtained from thermo-alkaliphilic bacteria are currently in demand due to their robust nature, and potential applications in various fields. An extracellular lipase producing thermo-alkaliphilic bacterial strain GP-1, isolated from hot water springs, is identified as Brevibacillus borstelensis, based on biochemical and 16S rRNA characterization (GenBank Accession no. MN282927). The present study implicated optimization of media parameters for GP-1 isolate, using Plackett-Burman Design and response surface methodology. Eight variables viz., peptone, yeast extract, KNO3, olive oil, coconut oil, KH2PO4, MgSO4, and CaCl2 were tested using 16 runs design. As per the statistical analysis (Pareto chart), yeast extract, coconut oil and MgSO4 were significant factors. The maximum lipase activity obtained was 211.35 Enzyme Units (EU)/ml. The significant variables were subjected to randomized Central Composite Design optimization using Design Expert (v.12.0.1). The lipolytic activity further increased to 321.85 EU/ml, which was 1.5 times greater. The maximum lipase activity was obtained with 3 % (v/v) coconut oil, 3.5 gm/L yeast extract, and 0.5 gm/L MgSO4. Purification of lipase produced was done by ammonium sulphate precipitation (70%), followed by dialysis and Sephadex G100 chromatographic separation, with about 14 fold purification. Molecular weight was determined using SDS-PAGE and was found to be approximately 25 kDa. Current research accomplished that the strain of Brevibacillus borstelensis GP-1 strain can be a prospective lipase source for large scale production.
Keywords: Lipases, Brevibacillus borstelensis, Response surface methodology, coconut oil, yeast extract

ABSTRACT (AIF06) FEB 04, 11.30-11.40

MICROBIAL PHA PRODUCTION FROM BIOWASTE AIDED WITH PETRI NET MODELLING FOR OPTIMIZED BIOPROCESS DEVELOPMENT

Mamtesh Singh1 and Gajendra Pratap Singh2*
1 Department of Zoology, Gargi College (University of Delhi), Siri Fort Road, Delhi 110049, India.
2 Mathematical Sciences and Interdisciplinary Research Lab (MathSciIntR-Lab), School of Computational and Integrative Sciences, Jawaharlal Nehru University, New Delhi 110067, India
*Email *s.mamtesh@yahoo.com*

Environment pollution and depleting fossil fuels are prime environmental issues. Production of biofuel and biopolymers can help to solve these issues, however, their production process is very costly. To overcome this problem, the use of biowaste for production of bio-products is one of the alternative. In case of polyhydroxyalkanoate (PHA), efforts for reducing its production cost by using biowaste and improving its quality by copolymer production using various culture and feeding strategies have been successfully documented. However, the industrial production of PHA has been still limited. Since the production is at laboratory scale and needs to manifested as scaled-up at production scale. It indicates the need of further strategies apart from biotechnological tools for its optimization and establishment. Model development and system automation using such statistical, mathematical and computational tools can giving new direction to bioprocess development and designing at production scale. This study reports the PHA production from sweet lime and use of Petri Net for modeling the PHA production from the step of biowaste i.e. sweet lime degradation to the step of utilising these biowaste hydrolysed products into PHA production.
Keywords: Polyhydroxyalkanoate, Economic production, scale-up, bioprocess development, Petri Net modeling

ABSTRACT (AIF07) FEB 04, 11.40-11.50

BACTERIOPHAGE AS AN ALTERNATIVE ANTIBACTERIAL THERAPY AGAINST PAN-DRUG RESISTANT BACTERIA

Ramesh Nachimuthu1, Prasanth Manohar2*
1School of Bioscience and Technology, Vellore Institute of Technology (VIT), Vellore, Tamil Nadu, India
2Zhejiang University-University of Edinburgh (ZJU-UoE) Institute, Zhejiang University, School of Medicine, Haining, Zhejiang 314400, P.R. China
Email drpnramesh@gmail.com

The ESKAPE pathogens are the leading cause of nosocomial infections throughout the world. Most are multi-drug-resistant isolates, which is one of the main clinical practice obstacles. Consequently, there is a prompt requirement for the other option and compelling restorative procedure. Bacteriophages are viruses, which have shown a compelling clinical result for treating the infectious pathogens in clinical setups. The aim of this study includes determining the resistance pattern of priority pathogens of Gram-negative bacteria as stated by WHO and isolate therapeutically significant phages against ESKAPE pathogens. The clinical isolates were collected from diagnostic laboratories located at Tamil Nadu. Antibiotic resistance profiling was performed to determine the resistant pattern. Genotypic screening was done against blaNDM-1, blaOXA-48, blaIMP, blaVIM, blaKPC genes. The bacteriophages against these clinical isolates were isolated by enrichment method from water samples collected from Tamil Nadu, India. All the phages were studied for their life cycle, genome analysis, and in vitro phage cocktail activity. Therapeutical efficient bacteriophages were studied namely, Escherichia virus myPSH2311, Klebsiella virus myPSH1235 and Enterobacter virus myPSH1140 were considered for the study. Transmission Electron Microscope suggested that the bacteriophages belonged to, Phieco32virus (Escherichia virus myPSH2311), Podoviridae (Klebsiella virus myPSH1235), and Myoviridae (Enterobacter virus myPSH1140). Whole Genome Sequence analysis was performed on the characterized phage and the data has been deposited in GenBank with the accession numbers MG976803 (Escherichia phage myPSH2311), MG972768 (Klebsiella phage myPSH1235), and MG999954 (Enterobacter phage myPSH1140). This study conclude that bacteriophages can be a good alternative in complicated or life-threatening PDR (Pan Drug-resistant) bacterial infections.

ABSTRACT (AIF08) FEB 04, 11.50-12.00

MICROBIAL PHA PRODUCTION FROM BIOWASTE AIDED WITH PETRI NET MODELLING FOR OPTIMIZED BIOPROCESS DEVELOPMENT

*Jasvinder Kaur1, Anupam Singh2, Amulya K. Panda2 and Rup Lala,3**
*1*Molecular Biology Lab., Department of Zoology, University of Delhi, New Delhi-110007*
2Product Development Cell, National Institute of Immunology, Aruna Asif Ali Marg, New Delhi-110067, India
3The Energy and Resources Institute Darbari Seth Block, IHC Complex, Lodhi Road, New Delhi-110003, India.
Email jasvinder1511@gmail.com

LinB is an important haloalkane dehalogenase involved in the degradation pathway of different isomers of hexachlorocyclohexane (HCH), mainly in catalyzing degradation of the notorious β-HCH. The HCH isomers are known to have neurotoxic, carcinogenic and estrogenic effects. Enzymatic bioremediation for decontamination of β- as well as other HCH isomers can prove to be a potential remediation strategy. For any bioremediation technology that is to be developed, apart from having high turnover number, the candidate enzyme must also be available in sufficient amounts. In this direction, the LinB variants reported in database were tested in laboratory studies. The variant LinBSSO4-3 however could not be obtained in soluble fraction by using standard procedures. The protein LinBSSO4-3 was cloned in pDEST17 vector and codon optimized for better expression in Escherichia coli BL21AI using a strong T7 promoter. However, the over-expression of this protein in ectopic host E. coli, led to aggregation of the protein in form of inclusion bodies, which are insoluble aggregates of misfolded or partially folded proteins. SEM analysis of the inclusion bodies showed them as aggregated spherical particles. The inclusion bodies were isolated using high speed sonication and homogenization. This was followed by solubilization in the strong denaturing agent urea. Refolding into its native state was done by using pulsatile refolding. This was done by slowly decreasing the denaturant concentration in the presence of sucrose. The turnover number of the refolded protein was then determined for different isomers of HCH. The protein was found to have a turnover number of ~43 molecules min-1 on β-HCH and ~13 molecules min-1 on δ-HCH. Additionally, a mutation I253M in the active site of the enzyme was found to drastically decrease the enzyme activity on β-HCH. Taking into consideration the wide range of substrates of haloalkane dehalogenases, such a protocol for inclusion body refolding will contribute to the field of bioremediation technology development for organochlorines, specifically HCH. Such a protocol for refolding of haloalkane dehalogenases from inclusion bodies has not been developed or reported before.

ABSTRACT (AIF09) FEB 04, 12.00-12.10

INCIDENCE OF GROWING ANTIBIOTIC RESISTANT BACTERIAL INFECTIONS IN THE CITY OF RAJKOT IN THE RECENT PAST

Ami Patel1, Sanskruti Thummar1, Dhruti Mungpara1, Rensi Sabhaya1, Nilesh Aghera2, Mousumi Das1, Avradip Chatterjee3 and Debashis Banerjee2.*
1Department of Microbiology, Atmiya University, Yogidham Gurukul, Rajkot, India.
2 Department of Biotechnology, Atmiya University, Yogidham Gurukul, Rajkot, India.
3Department of Biomedical Sciences, Cedars-Sinai Medical Center, Los Angeles, USA.
*Email *debashis.banerjee@atmiyauni.ac.in.*

Growing antimicrobial resistance (AMR) is a worldwide and one of the major healthcare problems, existing at present. AMR is part of the natural process of evolution among microorganisms, but which is expedited manifold by the unregulated and over-the-counter use of antibiotics. This unwarranted exposure to antimicrobial drugs, induces new and more severe resistance mechanisms in the microbes, leading to prolonged infection, disability and even death, caused by them in the host. Also, later these become very difficult to treat with the usually prescribed antibiotics and drugs. WHO had, back in 2014, issued a strict warning in its report about the rising incidence and future threat of AMR globally. According to certain estimates, it has the potential to cause 10 million deaths every year and economic losses to the tune of 100 trillion USD worldwide, by 2050. This epidemiological survey was carried out to evaluate the rising prevalence of antimicrobial resistance in Rajkot, a city located in the western part of India, approximately in the last one year. The data was collected from various clinical settings e.g., hospitals, clinics and diagnostic centers, situated at different locations of the city, mainly by manual surveys, in the form of interviews, questionnaires and documentation. The statistical analysis of the data indicated towards development of high resistance, exhibited by some of the important clinical pathogens such as E. coli, Klebsiella pneumonia, Staphylococcus aureus, Acinetobacter baumannii, etc. against some of common antibiotics used to treat them e.g., ampicillin, piperacillin, ciprofloxacin, levofloxacin and aztreonam. This clearly reflects the growing problem of AMR in Rajkot, as in other parts of the country and the world.

ABSTRACT (AIF10) FEB 04, 12.10-12.20

ANALYSIS OF SPECIFIC ISOFORM USAGE BY BIOFILM LIFESTYLE OF CANDIDA GLABRATA THROUGH A GLOBAL TRANSCRIPTOME-WIDE APPROACH

Khem Raj1, Praveen Rishi1, Shivaprakash M. Rudramurthy2, Dattatray S. Mongad3, Amrita Kaur1, Geeta Shukla1.*
1Department of Microbiology, BMS-Block-I, Sector-25, Panjab University Chandigarh, India.
2Department of Medical Microbiology, Postgraduate Institute Medical Education and Research (PGIMER), Chandigarh
3National Centre for Microbial Resource, National Centre for Cell Sciences (NCCS), Pune, India.
Email khemrajthakur@gmail.com

Eukaryotes utilize alternative isoforms generated through isoform switching mechanism, to thwart various stresses encountered by them. Heretofore, to the best of our knowledge, there is no information pertaining to isoforms switching and differential transcript isoform usage reported in C.glabrata, an opportunistic fungal pathogen. The study was designed to delineate differential transcript expression, transcript isoform switching, their differential usage pattern vis-a-vis their functional impact on biofilm formed by a clinical isolate of C. glabrata. The biofilm formation capacity of the clinical isolate was studied by using crystal violet and XTT assay methods and compared with standard strain C.glabrata (ATCC-2001). Comprehensive bioinformatics investigation of RNA Sequencing data generated from the biofilm growth phase of C.glabrata was performed with the Tuxedo pipeline. IsoformSwitchAnalyzeR was used to identify and visualize switching of isoforms in response to the stresses encountered during the biofilm growth phase. ClueGo, CluePedia and STRING (Search Tool for the Retrieval of Interacting Genes/Proteins) Applications of Cytoscape were used for Gene ontology/Pathways analysis and Protein-protein interactions network visualization. It was observed from differential transcript expression (DTE) and differential transcript utilization (DTU) that C.glabrata utilized 292 significant transcripts isoforms in biofilm formation via isoform switching process. GO/Pathways analysis and PPI interactions further substantiated the functional attribute of switched transcripts isoforms selectively used by C.glabrata to counter the various stress conditions during biofilm lifestyle in rewiring and regulating the carbon metabolic pathways and ribosome biogenesis.

ABSTRACT (AIF11) FEB 04, 12.20-12.30

INSIGHTS INTO THE EVOLUTION OF DRUG RESISTANCE AND POTENTIAL DRUG TARGETS OF MYCOBACTERIUM TUBERCULOSIS USING COMPARATIVE GENOMICS

Helianthous Verma1, 2, Shekhar Nagar3, Shivani Vohra2, 4, Shubhanshu Pandey2,5, Devi Lal2, Ram Krishan Negi3, Rup Lal6, Charu Dogra Rawat1, 2*
1Molecular Biology and Genomics Research Laboratory, Ramjas College, University of Delhi, Delhi -110007, India
2Department of Zoology, Ramjas College, University of Delhi, Delhi-110007, India
3Department of Zoology, University of Delhi, Delhi -110007, India
4 Faculty of Life Sciences and Biotechnology, South Asian University, New Delhi 110021, India
5Department of Biotechnology, Jamia Millia Islamia, Okhla, New Delhi, Delhi 110025
6The Energy and Resources Institute, Darbari Seth Block, IHC Complex, Lodhi Road, New Delhi-110003, India
Email helianthousverma@gmail.com

Mycobacterium tuberculosis is a causative agent of airborne infectious disease tuberculosis (TB). Each year it infects millions of people worldwide and is one of the leading causes of deaths per year. The identification of multidrug resistant (MDR), extensively-drug resistant (XDR) and total-drug resistant (TDR) strains of M. tuberculosis necessitate for the development and implementation of new drug strategies. Here, genomes of 174 strains of M. tuberculosis were retrieved and analyzed to reveal the evolutionary divergence of molecular drug target (MDT) genes. Phylogenomic clustering has shown temporal clustering i.e., based on their time of isolation. We categorised 51 MDT genes into, diversifying (D, dN/dS>0.70), moderately diversifying (MD, dN/dS=0.35-0.70) and stabilized (S, dN/dS<0.35) genes using the information obtained from selection pressure analysis across all 174 M. tuberculosis strains. Among 51 TDR genes, rpsL, gidB, pncA and ahpC were diversifying and Rv0488, kasA, ndh, ethR, ethA, embR and ddn were stabilized. Sequence Similarity Networks (SSN) also showed substantial difference between diversifying and stabilizing protein clusters. At last, we performed protein-protein interactions (PPI) of diversifying and stabilized proteins with human proteins. This suggests that the potential of kasA (dN/dS=0.29), a stabilized gene, as anti-TB drug target as it encodes for KasA which was found to interact with most host proteins. However, homology of KasA with a human mitochondrial beta-ketoacyl synthase protein requires further investigation before designing drug strategies against KasA.

ABSTRACT (AIF12) FEB 04, 12.30-12.40

GLOBAL POPULATION GENOMIC ANALYSIS OF MYCOPLASMA BOVIS ISOLATES REVEALS TRANSCONTINENTAL VARIATIONS AND POTENTIAL VIRULENCE GENES THROUGHOUT ALL CLADES

*Roshan Kumar**
Post-Graduate Department of Zoology, Magadh University, Bodh Gaya
*Email *roshanzhc@gmail.com*

Among more than twenty species belonging to the class Mollecutes, Mycoplasma bovis is the most common cause of bovine mycoplasmosis in North America and Europe. Bovine mycoplasmosis causes significant economic loss in the cattle industry. The number of M. bovis positive herds recently has increased in North America and Europe. Since antibiotic treatment is ineffective and no efficient vaccine is available, M. bovis induced mycoplasmosis is primarily controlled by herd management measures such as the restriction of moving infected animals out of the herds and culling of infected or shedders of M. bovis. To better understand the population structure and genomic factors that may contribute to its transmission, we sequenced 147 M. bovis strains isolated from four different countries viz. USA (n=121), Canada (n=22), Israel (n=3) and Lithuania (n=1). Majority of these isolates were contributed by two host types i.e., bovine (n=75) and bison (n=70). We performed a large-scale comparative analysis of M. bovis genomes by integrating 104 publicly available genomes and our dataset (250 total genomes). Whole genome single nucleotide polymorphism (SNP) based phylogeny revealed that M. bovis population structure is composed of five different clades using M. agalactiae as an outgroup. USA isolates showed a high degree of genomic divergence in contrast to the Australian isolates. We also validated a previous report suggesting minimum divergence in isolates of Australian origin, which grouped within a single clade along with isolates from China and Israel. The function-based analysis of autogenous vaccine candidates (n=10) included in this study revealed that although they are functionally diverse, but in order develop a more broadly spectrum autogenous vaccine it may be necessary to consider isolates from those clades for which there is no representative. Our study also found that M. bovis genome harbors a large number of IS elements and their number increases significantly (p=7.8e-06) as the genome size increases. Collectively, the genome data and the whole genome-based population analysis in this study may help to develop better understanding of M. bovis induced mycoplasmosis in cattle.

ABSTRACT (AIF13) FEB 04, 12.40-12.50

IDENTIFICATION OF BIOSURFACTANT PRODUCING KLEBSIELLA PNEUMONIAE SSP OZAENAE USING VITEK 2 AUTOMATED MICROBIOLOGY SYSTEM

Seema Sangwan, Harpreet Kaur and Pankaj Sharma*
Department of Microbiology, COBS&H, CCS Haryana Agricultural University, Hisar 125004 (Haryana) India.
*Email *seema_sangwan80@yahoo.co.in*

Biosurfactant producing bacterial isolates retrieved from hydrocarbon polluted soil samples were subjected to identification and classification to species and subspecies level using VITEK 2 automated microbiology system utilizing growth-based technology. The system was specifically suitable for identification of industrially important microorganisms based on colorimetric reagent card, electronic records and signatures. Reagent cards have 64 wells each containing an individual test substrate to measure various metabolic activities such as pH alterations, enzymatic hydrolysis and growth in the presence of inhibitory substances. The automated microbiology system revealed 97% probability of the test bacterial isolate being Klebsiella pneumoniae ssp ozaenae. The organism was identified to be harbouring α and β-glucosidase, β-xylosidase, α -galactosidase and phosphatase activities. It was found to be having substrate utilization potential for fermentative carbonsources such as glucose, mannose, sucrose and cellobiose along with non-fermentative carbon sources such as D-mannitol. The confirmation of species was further executed by PCR amplification of 130bp amplicon using species-specific 16S rRNA nucleotide sequence using 5′-ATTTGAAGAGGTTGCAAACGAT-3′ forward primer and 5′-TTCACTCTGAATTTTCTTGTGTTC-3 reverse primer followed by gel electrophoresis. The molecular analysis has also testified its similarity to Klebsiella pnuemoniae ATCC12391. The Gram negative, facultative bacilli, Klebsiella pneumoniae ssp ozaenae was found utilizing dairy waste, vegetable oil for biosurfactant production as can be expected from the biochemical analysis as well.

ABSTRACT (AIF14) FEB 04, 12.50-13.00

METAGENOMIC ANALYSIS OF POND SEDIMENT TO COMPREHEND COMPLEX MICROBIAL INTERACTIONS

Vivek Negi1 and Rup Lal1*
1Molecular Biology Lab, Department of Zoology, University of Delhi, Delhi-110007, India.
*Email *viveknegi2006@gmail.com*

Studies revealing metagenomic profiling of complex community is of interest across the scientific community. Pond sediment near hexachlorocyclohexane (HCH) production site, Indian Pesticide Limited (IPL) located at Chinhat Lucknow, India heaving complex community was selected to identify unique microbial diversity and functional profile at the site. Here we supplement the metagenomic study of pond sediment with different binning approaches and in depth functional analysis, which elucidates its ecology in terms of community dynamics with respect to mechanisms like lin genes implication in HCH degradation pathway, Type VI secretory system (T6SS) with its effector molecules and metagenomic islands (MGIs). Phylogenetic origin of the most metagenomic reads remains anonymous even after approaching widely accessed binning algorithms however metagenomic reassignment approach incredibly improved the taxonomic allocation by 1.02 %. According to functional annotations of the predicted ORFs by database (COG clusters, PFAM families and KEGG GENES) comparison searches (E-value < 1e-5 and Percentage Identity > 20%), pond sediment metagenome encoded proteins for membrane transport, cell signaling, bacterial secretory system, aromatic compound metabolism and two component system. As of now complex community inhabiting pond sediment remains poorly understood however this study highlights the role of novel mechanisms providing deeper insights into the concept of microbial interaction.

ABSTRACT (AIF15) FEB 04, 13.00-13.10

ATRAZINE DECONTAMINATION BY EPIPHYTIC ROOT BACTERIA

Anina James
Pesticide Toxicology and Soil Microbial Ecology Lab, Department of Zoology, University of Delhi.
Email anina_elina@yahoo.co.in

Three epiphytic root bacteria of genus Pseudomonas and Arthrobacter were isolated from the rhizoplanes of emergent hydrophytes Acorus calamus, Typha latifolia and Phragmites karka. Potential of these strains to decontaminate environmentally relevant concentrations of atrazine was determined in liquid atrazine medium (LAM) and Luria Bertani (LB) medium at varying pH and temperature. There was an increase in decontamination by the strains with time upon exposure to 2.5, 5, 7.5 and 10 mg l–1 atrazine over a period of 15 days. Growth in terms of O.D.600 and biomass determined during the same period also showed a corresponding surge. The optimum pH for the strains for decontaminating 10 mg l-1 atrazine was 7 in both media. Strain AACB mitigated atrazine in a wider range of pH (5 to 8). The optimum temperature for the strains AACB and TTLB was between 30 to 40 °C and for strain PPKB, 20 to 30 °C. Strains AACB and TTLB decontaminated >62% atrazine at 10°C. The strains exhibited plant growth promoting (PGP) traits in the presence of 10 mg l–1 atrazine in vitro. The results of the present study indicate the potential of these isolates as bioinoculants. Bioreactors and water treatment plants can be designed comprising the hydrophytes and the strains inoculated into their rhizospheres to improve the efficacy of the biological treatment processes. They can be further used to study plant–bacterium mutualistic symbiosis or any other form of interaction occurring during atrazine mitigation. Also, this phyto-rhizoremediation technique is ostensibly clean and economic.

ABSTRACT (AIF16) FEB 04, 13.10-13.20

DIVERSITY AND POTENTIAL BIOPROSPECTION OF CERTAIN PLANT GROWTH-PROMOTING RHIZOBACTERIA

Shanu Khandelval
Pacific Medical University, Udaipur
*Email *shanu83khandelval@gmail.com*

The rhizobacteria were isolated from roots nodules of Cicer arietinum and Vigna radiata and rhizosphere soil of both plants. The isolation and characterization of various rhizobacteria has been done for their PGP traits and biocontrol activities. Various Rhizobacteria isolated from different agricultural fields and identified by morphological, biochemical and molecular testing. Isolated Rhizobacteria were checked for phosphate solubilization and Nitrogen fixation and carbon source utilization of the potent isolates will be carried out on minimal media containing different carbon sources. Catabolite repression of PGP and Biocontrol activities will be carried out in presence of organic acid and sugar as carbon sources. Gene(s) involved in novel metabolite production or biocontrol activity will be identified by using molecular mechanisms. Generation of rhizobacteria with enhanced or constitutive PGP and biocontrol activities in target rhizospheric bacteria, either repressor gene knockout will be carried out or the target gene will be cloned under a strong constitutive promoter.

ABSTRACT (AIF17) FEB 04, 13.20-13.30

ASSESSMENT OF AG NANOPARTICLES IN SEWAGE SLUDGE

G. Yamal
Department of Botany, Kirori Mal College, University of Delhi
*Email *yamalgupta@gmail.com*

The production of nanoparticles (NPs) and nanomaterials is increasing leaps and bounds, as NPs find application and use in daily commodities. As a result, these engineered NPs are inevitably introduced into environment during different phases of their life cycle (from production to disposal). Silver (Ag) is a precious metal and the nanoparticles of Ag are shown to have anti-microbial properties. Because of the anti-microbial properties, Ag NPs are used in variety of products such as soaps, shampoos, creams, lotions, clothing and fabrics and even in air conditioners, washing machines, catheters, dressings etc. Many studies have demonstrated the toxicity of these Nanoparticles to organisms of main food-chain. Exposure modeling strongly suggest that soil is a major sink of NPs. NPs enter soil through various pathways, such as landfills, agricultural sewage sludge. Sewage sludge has been reported to serve as a good source of plant nutrients and organic constituents. The present study was carried out to determine the presence of Ag in sewage sludge using Atomic Absorption Spectroscopy. Transmission and scanning electron microscopy were also used to find the structure of the Ag NPs present in the sludge. Since a large proportion of NPs are ending up in soil through sewage sludge, it is imperative to assess if sewage sludge application is advisable.

ABSTRACT (AIF18) FEB 04, 13.30-13.40

BIOINFORMATICS ANALYSES OF SARS-COV-2 SPIKE PROTEIN: STEP TOWARDS DESIGNING COVID-19 THERAPEUTICS

*Tikam Chand Dakal1**
1Genome & Computational Biology Lab, Department of Biotechnology, Mohanlal Sukhadia University, Udaipur 313001, Rajasthan (India)
Email tikam260707@gmail.com; tc.dakal@mlsu.ac.in

SARS-CoV-2 is a highly contagious virus that has resulted in a pandemic. In this study, I performed comparative protein sequence analysis, gene expression profiling, molecular docking using authentic tools for unveiling the molecular basis of high infectivity of SARS-CoV-2 and also an integrative approach to predict antigenic sites in SARS-CoV-2 spike receptor binding domain. This study revealed that SARS-CoV-2 harbors an RGD motif which is absent in all other previously known SARS-CoVs. The predicted hypothesis is that the SARS-CoV-2 may be (via RGD) exploits integrins, that have high expression in lungs and all other vital organs, for invading host cells. The molecular docking experiment showed the RBD of spike protein binds with integrins precisely at RGD motif. SARS-CoV-2 spike protein has a number of phosphorylation sites that can induce cAMP, PKC, signalling pathways. These pathways either activate Ca+2 channels or get activated by Ca+2. In fact, integrins have Ca+2 binding sites in vicinity of RGD integrin docking site in our analysis which suggests that RGD-integrins interaction possibly occurs in calcium-dependent manner. Prediction of antigenic sites revealed nine potential antigenic sites. The predicted antigenic sites were then assessed for possible molecular similarity with other known antigens in different organisms. Out of nine, seven sites showed molecular similarity with 54 antigenic determinants found in twelve pathogenic bacterial species. Over-representation of antigenic determinants from Plasmodium and Mycobacterium in all antigenic sites suggests that anti-malarial and antiTB drugs can prove to be clinical beneficial for COVID-19 treatment. Moreover, individuals previously vaccinated or had previous history of malaria, tuberculosis and other diseases are expected to display a considerable degree of resistance against SARS-CoV-2 infection. Altogether, the current study has highlighted possible role of calcium in RGD-integrins interaction for virus invasion into host cells and suggested that lowering Ca+2 in lungs could avert virus-host cells attachment.

ABSTRACT (AIF19) FEB 04, 13.40-13.50

EXPLORING THE POTENTIAL OF MARINE AND SOIL FUNGI FOR ENZYME PRODUCTION

Bhuktar, J. J.
Department of Microbiology, Govt. Institute of Science, Aurangabad.

The present work is focused on screening and production of amylase and protease enzymes from fungi of marine and soil origin. Total eight previously isolated fungi (5 marine and 3 soil fungi) were screened for production of protease, amylase, lipase and cellulase enzymes. All the isolates showed positive activity for amylase and protease enzyme. Only M4 showed negative activity for lipase enzyme and M3 showed negative cellulase enzyme activity. Out of all marine and soil fungal isolates M1 and E3 were observed as an efficient protease producer whereas M3 and E3 as an efficient producers of amylase enzyme. Hence further studies of process optimization were done for protease and amylase production with these isolates. It has been observed that M1 protease production was maximum at pH-8 and temperature 20°C however E3 protease production was optimum at pH 5 and temperature 40°C. And for amylase production M3 showed optimum pH 5 and temperature 40°C whereas E3 requires optimum pH 5 and temperature of 50°C. Enzyme production was also carried out using solid agro-waste such as sugarcane bagasse and fruit waste also studied the enzyme characterization and applications.Keywords: marine fungi, soil fungi, screening, enzyme production, optimization, amylase, protease, agro waste

ABSTRACT (AIF20)

FEB 04, 13.50-14.00

PHYSIO-BIOCHEMICAL POTENTIALS OF SOME ALKALIPHILIC BACTERIAL ISOLATES OBTAINED FROM BAUXITE PROCESSING RESIDUES

Satarupa Dey
Shyampur Siddheswari Mahavidyalaya, University of Calcutta, Ajodhya, Shyampur, Howrah 711312, India
Email dey1919@gmail.com

Bauxite residue, the waste by-product of bauxite ore processing in alumina industry is mostly deposited around the areas of alumina plants leads to a number of environmental and human health problems. In the present study, the physico-chemical and microbiological analysis of bauxite residues were conducted in details. All the samples were characterized by high alkalinity (pH 8.5-12.5) and metal content along with poor organic carbon matter. XRD analysis confirmed the presence of Sodalite, Hematite, Boehmite, Gibbsite, Anatase and Quartz, heavy metal contamination was evaluated by applying contamination factor and pollution load index. The aerobic microbial density as well as activity of the samples were in general very low and ranged from 1.2 - 8.96 ×102cfu/g and 0.32 - 0.96 µg fluorescein/g/h. A total of 12 phenotypically distinguishable bacteria were isolated in pure form which showed significant tolerance to Ni, Cr, Al, Fe, Mn, Mg and Pb, high pH and NaCl and were resistant to a number of antibiotics. Further, tolerance to alkalinity, transformation of waste to neutral one, production of diverse enzymes, extracellular polysaccharide and formation of biofilm, the unique features of these bacterial isolates could be of immense importance for potential applications in bioremediation of the waste materials.

Keywords: Bauxite residue, bauxite ore, alkaliphilic microorganisms, microbial activity, EPS production, biofilm formation

ABSTRACT (AIF21)

FEB 04, 14.00-14.10

EXPLORING THE DIVERSITY AND EVOLUTION OF CHEMOSENSORY AND FLAGELLAR SYSTEMS AMONGST FAMILY VIBRIONACEAE

Gaurav Sharma1,, Shenu Hudson1, Vaishnavi Kolte1, Brittany Bennett2, and Edward Ruby2*
1Institute of Bioinformatics and Applied Biotechnology (IBAB), Bengaluru Karnataka, India
2Kewalo Marine Laboratory, the University of Hawai'i at Mānoa, USA
*Email *gaurav.amit30@gmail.com*

Chemosensory systems (CSSs) are advanced, two-component system-based signalling architectures (a cascade of 6-10 proteins) that govern bacterial motility via rotating flagella/pili mechanosensors (assembled from >40/15 proteins), as well as control alternative cellular activities. Family Vibrionaceae constitutes a diverse group of >150 species distributed across 14 genera with a broad facultative host range (i.e., free-living/ pathogenic/ mutualistic/ commensal) in aquatic (marine/ brackish/ freshwater) habitats. Considering their distinctive physiological nature and ecological niches, this study explores 39 complete genomes to understand the patterns of CSS and flagella-system (FS) diversification and their putative functions using open-source homology search, synteny, clustering, and phylogenomic tools. All CSS and FS were identified and classified into 1-4 CSS (F6, F7, F8, and F9) and 1-3 FS (Primary and secondary) types, amongst which F6-CSS is conserved across all motile organisms except Vibrio qinghaiensis Q67. F6-CSS, located on large chromosome is present up/downstream of the primary FS, therefore, it is putatively involved in flagellar motility. Most of these related organisms have 1-2 additional CSS systems, which are absent in all Aliivibrio and several other Vibrio species. The abundance of CSSs and FSs per organism is not correlated either to each other or with genome size, habitat, or nature. As family Vibrionaceae members have two chromosomes, we found that CSS and FS distributions are relatively biased towards the large chromosome, whereas methyl-chemoreceptor proteins (MCPs) were equally distributed on both. We also performed homology, synteny, and phylogenomic studies of CSSs and their components to understand more about their predicted patterns of evolution and divergence among close relatives. Broadly, this study will provide a platform based on which we might be able to further characterize the roles of unexplored CSS, their MCP proteins, and FS proteins in bacterial communication and adaptation.

ABSTRACT (AIF22)

FEB 04, 14.10-14.20

UNEXPECTED SHIFT IN MICROBIAL COMMUNITIES LEADS TO ENHANCED CRUDE OIL RECOVERY

Akhil Agrawal1 Sandeep Rellegadla2 and Shikha Jain3*
1Energy and Environment Research Laboratory, Department of Microbiology, Central University of Rajasthan, NH-8, Bandarsindri, Kishangarh, Ajmer , Rajasthan 305817
2Department of Chemistry, Manipal University Jaipur, Dehmi Kalan, Jaipur, Rajasthan
*Email *akhilagrawal@curaj.ac.in*

The indigenous microbial communities in oil reservoirs plays significant role in further exploitation of the residual oil after a recovery process. In this study, the shift in indigenous microbial communities for role in enhanced oil recovery (EOR) was performed to post polymer flood. The succession of microbial communities was studied through high-throughput sequencing of 16S rRNA genes and changes in additional oil recovery was analyzed. Data recovered was analysed through QIIME2 pipeline for assessment of microbial community using the SILVA database. The results indicated that the native abundances of resident microbial communities significantly changed, with different polymer treatments. With the intermittent injection of polymer with an electron acceptor as growth promoting agent, microbial communities showed a regular change and were alternately dominated by minority populations such as Dietzia sps., Acinetobacter sps., Soehngenia sps., Paracoccus sps. The most significant change was however observed with injection of galactomannan polymer and nitrate as electron acceptor resulting in growth of Thermus and Anoxybacillus sps. following the injection process. Both these species were found to play role in carbohydrate metabolism (α & β glucosidase). While other than this function, both these communities are found to synthesize biosurfactants and bioemulsifiers which aid the EOR process. While majority of the Thermus sp. are also found to play role in microbial mineralization. This activity favors plugging of high permeability zones in the reservoir due to alteration of petrology of reservoir and favoring dislodging of crude oil in new channels that resulted in the additional recovery of 11.97% of Original Oil in Place. All these results show that microbial population do play role in the recovery process.

ABSTRACT (AIF23)

FEB 04, 14.20-14.30

GENOME METRICS ANALYSIS FOR TAXONOMIC DELINEATION OF PARACOCCUS SPP.

Akshita Puri1, Abhay Bajaj2, Sukanya Lal3, Yogendra Singh4 and Rup Lal5*
1 P.G.T.D, Zoology, R.T.M Nagpur University, Nagpur, 440033, India
2 CSIR-National Environmental Engineering Research Institute (CSIR-NEERI), Nehru Marg, Nagpur, 440020, India
3 Ramjas College, University of Delhi, Delhi, India
4 Department of Zoology, University of Delhi, Delhi, India
5The Energy and Resources Institute Darbari Seth Block, IHC Complex, Lodhi Road New Delhi-110003, India
*Email * akshitapuribajaj@gmail.com*

The genus Paracoccus is characterized by coccus shaped Gram-negative bacteria isolated from diverse range of habitats across the globe with capability to grow on a wide range of substrates, utilising different modes of nutrition. The genus comprises of more than 80 published species at EzTaxon, for which taxonomic characterization was performed using polyphasic methods that integrates phenotypic, chemotaxonomic and single gene based phylogenetic assessment. However, single gene phylogenies have highlighted certain ambiguities in species assignments which could be resolved using genome based methods thereby providing accurate thresholds for species delineation. The present study reports the use of whole genome based comparison methods and multi-gene phylogenies for accurate assessment of species thresholds and refined phylogenetic pattern to overcome the limitation of using single gene 16S rDNA sequence in delineating Paracoccus spp. Based on phylogenomic approach, the genus was identified to cluster into three groups, concordant across all the three multi-gene phylogenies. Furthermore, phylogeny based on pan genome derived single core gene (SCG) clusters for the genus was in congruence with the multi-gene phylogenetic pattern, suggesting robust taxonomic delineation using genome metrics. Using these validated metrics, potential cases of misclassification and presumptive novel species were also identified for this genus. Overall, the advancement in genomics has led to validated genome metric tools which can be used to characterize and assign species rank; however, it would still require to be complemented with polyphasic approach for nomenclature and species description.

AMI/INSCR INNOVATIVE RESEARCH (STUDENTS & SCHOLARS) - ABSTRACTS

Always remember that you are absolutely unique

ABSTRACT (OMOH001)

FEB 05, 09.30-09.40

PROTEIN O-FUCOSYLTRANSFERASE 2 -MEDIATED O-GLYCOSYLATION OF MIC2 IS DISPENSABLE FOR TOXOPLASMA GONDII TACHYZOITE INFECTION

Sachin Khurana 1 , Michael J Coffey 1 , Alan John 1 , Alessandro D Uboldi 1 , My-Hang Huynh 2 , Rebecca J Stewart1 , Vern B Carruthers 2 , Christopher J Tonkin 1 , Ethan Goddard-Borger1 , Nichollas E Scott 3
1The Walter and Eliza Hall Institute of Medical Research, Parkville, Victoria, Australia
2Department of Microbiology and Immunology, University of Michigan Medical School, Ann Arbor, MI
3Department of Microbiology and Immunology, University of Melbourne, Melbourne, Victoria
Email Australiakhuranasach@gmail.com

Toxoplasma gondii is a ubiquitous obligate intracellular eukaryotic parasite that causes congenital birth defects, disease of the immunocompromised and blindness. Protein glycosylation plays an important role in the infectivity and evasion of immune response of many eukaryotic parasites and is also of great relevance to vaccine design. Here, we demonstrate that MIC2, a motility-associated adhesin of T. gondii, has highly glycosylated thrombospondin repeat domains (TSR). At least seven C-linked and three O-linked glycosylation sites exist within MIC2, with >95% occupancy at O-glycosylation sites. We demonstrate that the addition of O-glycans to MIC2 is mediated by a Protein O-fucosyltransferase 2 homologue (TgPOFUT2) encoded by TGGT1_273550. While POFUT2 homologues are important for stabilizing motility associated adhesins and host infection in other apicomplexan parasites, in T. gondii loss of TgPOFUT2 has only a modest impact on MIC2 levels and the wider proteome. Consistent with this, both plaque formation and tachyzoite invasion are broadly similar in the presence or absence of TgPOFUT2. These findings demonstrate that TgPOFUT2 O-glycosylates MIC2 and that this glycan is dispensable in T. gondii tachyzoites.

ABSTRACT (OMOH002)

FEB 05, 09.40-09.50

CUTANEOUS MICROBIOME IN PRETERM INFANTS

Leena and Kiran Nehra*
Department of Biotechnology, Deenbandhu Chhotu Ram University of Science and Technology (DCRUST), Murthal, Sonepat, Haryana
*Email *kaushik24leena@gmail.com*

Premature birth of babies is not only a stressful condition for the parents and family members, but, the preterm birth has also become a global challenge for the paediatricians since such babies have an increasingly high risk of disease because of a weaker immune system. After delivery, from the protected mother's womb, the infantal skin interacts with the gaseous microbe-enriched environment. Infant's skin microbiome serves as a habitat for various bacteria that may result in neonatal sepsis; blood infections in the infants etc., which in turn can have a high chance of becoming one of the most common causes of mortality by stimulating the systematic immune development. A proper development of microbiome at the early phase of life is an essential factor for the maturation of the immune system and other psychological and physiological systems and may be critical to prevent microbial colonization of pathogens. Cutaneous microbiome is helpful in maintaining the cutaneous homeostasis and various stages of inflammatory responses. Presence of site-specific differences in the premature skin microbiome can be easily explained by immature structure of the skin, sweat and sebaceous glands and the environment of the neonatal intensive care unit. There are chances of lowering down of the community richness of microbiome at certain sites in preterm babies because of a regular intake of antibiotics by such babies as compared to full-term babies who are normally not given any antibiotics. Since till now, the skin microbiome development in preterm infants has not been evaluated much at early phases of life; a deeper knowledge of the origin and evolution of this early environment of the skin microbiome will be highly helpful and have strong implications in the prevention and treatment of paediatric skin pathology.

ABSTRACT (OMOH003) FEB 05, 09.50-10.00

AN ASSESSMENT OF ANTIMICROBIAL EFFICACY OF LIQUID SOAP AND ALCOHOL BASED HAND SANITIZER ON REGULAR HAND MICROBIOME

*Siddhi Bangale 1 , Saurav Angnani 1 , Karthik Shivkumar 1 , Nandita Nashikkar 1 , Sunita Bundale 1 **
1 Hislop School of Biotechnology, Hislop College, Nagpur, Maharashtra, India
Email sbundale@gmail.com

The most common way of transmission of microbial infections is through hands coming into contact with contaminated surfaces in our daily routine. Hence the importance of hand hygine cannot be overlooked, particularly in the ongoing Covid 19 pandemic. This study was undertaken to evaluate the antimicrobial efficacy of liquid soap and hand sanitizer of two popular brands, Dettol and Lifebuoy, against hand microflora. Six subjects performed their routine activities without washing their hands for six hours. Handprints of the subjects were taken on trypticase soy agar plates, before and after the application of liquid soap / sanitizer for a visual assessment of the reduction in microflora.The potency of the liquid soaps and hand sanitizers was evaluated by the agar well diffusion method using selected isolates from the agar handprints. Two of the isolates were identified by the Vitek technique. Remarkable reduction in the micro flora was visually observed in the
handprints post washing hands with plain tap water/ application of liquid soaps of both the brands. The sanitizers of both brands were found to be more effective in reducing the microbial load. Twelve out of selected thirteen bacterial isolates were sensitive to liquid soap, whereas only three out of thirteen isolates were sensitive to sanitizers. Two of the isolates were identified as Pantoea spp. and Kocuria kristinae. Thus washing hands with soap and water should be preferred whenever possible.

ABSTRACT (OMOH004) FEB 05, 10.00-10.10

AN ASSESSMENT OF ANTIMICROBIAL EFFICACY OF LIQUID SOAP AND ALCOHOL BASED HAND SANITIZER ON REGULAR HAND MICROBIOME

Vishal Sharma a, MohitaGaur a, Anoop Singh a, Sonam Sharm ab, Anjali a, Ashwani Khanna c, Vishal Khanna c, Neel Sarovar Bhavesh b, Yogendra Singh a**, Richa Misra a,d**
aDepartment of Zoology, University of Delhi, Delhi-110007, India.
bInternational Centre for Genetic Engineering and Biotechnology, New Delhi, Delhi-110067, India.
cLok Nayak Hospital, New Delhi, Delhi-110002, India.
dSri Venkateswara College, University of Delhi, Delhi-110021, India.
Email *s.vishalzoology@gmail.com, **ysinghdu@gmail.com, **richa.1403@gmail.com*

Tuberculosis (TB) is an ancient disease that killed millions of people worldwide and has claimed 1.41 million deaths in 2019 alone. It is caused by Mycobacterium tuberculosis (Mtb), which tends to infect mainly lungs causing pulmonary disease but can also infect any organ of the body as extrapulmonary manifestation. The disease usually presents as a latent infection with no clinical symptoms but may develop into an active disease in the future. This progression from latent to active disease is influenced by many factors such as host immunity, genetic background of the bacilli, age, gender, co-infection and recently gut microbiota has been shown to be associated with the pathogenesis of TB. However, despite the advent of next-generation sequencing platforms that allow profiling these complex microbial communities through 16S rRNA sequencing, the knowledge regarding the gene functional annotation is still sparse. In the present study, we examine the functional readout of the gut community in the host milieu through fecal metabolomics. In particular, 1H-NMR metabolomics was performed for the comprehensive analysis of metabolite composition in the stool samples from the TB infected cases (n=20) and unrelated healthy subjects (n=20). The metabolome analyses showed that few branched-chain amino acids were significantly higher in TB infected groups. The difference in the abundance of different metabolites in TB patients and healthy individuals in our data indicated the role of complex metabolic pathways in the etiology of TB infection. Examination of fecal metabolites provides a non-invasive way to analyse the host-gut microbiome interactions. The findings can potentially go a long way in the development of nutritional and personalized therapies for the restoration of alteration and subsequent relief.

ABSTRACT (OMOH005) FEB 05, 10.10-10.20

LOCAL ECOLOGICAL PARAMETERS FOSTERING VAGINAL DYSBIOSIS CAUSING PATHOLOGICAL CONDITIONS IN WOMEN

Subhasree, Swetha Srikanth, Anvesh Ganta, Srinandan C S*
Biofilm Biology Lab, Anusandhan Kendra-2, Centre for Research on Infectious Diseases School of Chemical and Biotechnology, SASTRA Deemed University, Thanjavur, Tamil Nadu, India
*Email * v.b.s.subhasree@gmail.com,*

The vaginal flora of a woman plays an important role in health and homeostasis. It is highly dynamic and is subjected to timely fluctuations. Certain disruptions in the proportion of bacteria which predisposes towards dysbiosis leading to pathological disorders like bacterial vaginosis, urological infections or severe gynaecological conditions. Mounting evidence indicates that the vagina can harbor uropathogenic bacteria causing urinary tract infection (UTI), bacteriuria and combined urological infections affecting about 50-60% of women. Our study proposes to evaluate the macroecological parameters that alter the native vaginal microbiota leading to pathological conditions. An exhaustive repertoire vaginal microbiota was compiled from the literature survey. The bacteria were classified into their respective phyla. The presence of the species in respective cluster was identified through evolutionary relationship in phylogenetic tree. The Shannon's and Simpson's diversity indices provided the diversity with respect to the habitat and richness respectively. In addition, individual-based modeling (IbM) between Lactobacillus crispatus and Escherichia coli was performed using iDynoMiCS to investigate the competition in the vaginal microenvironment for various factors like nutrients uptake, rate of multiplication for about 72 hours. The vagina microbial community in each cluster was elucidated in exhaustive repertoire. Through phylogeny the species of each cluster were identified as in-group (presence) and out-group (absence). Upon calculating the Shannon and Simpson's diversity indices, BV had more diversity compared to the rest of two clusters. The variance in composition of each cluster was illustrated by taxonomic abundance and diversity variance. A representation model between the most dominant L.crispatus against the pathogenic E.coli in the vaginal milieu is depicted through individual based modelling study-iDynoMiCS. A combination of generalized and personalized treatment owing to the specificity, dynamicity and identicality harbouring the vaginal microbiome, could translate better treatment strategies.

Keywords: Vaginal Microbiome, Dysbiosis, Lactobacillus spp., Bacterial Vaginosis

ABSTRACT (OMOH006) FEB 05, 10.20-10.40

IN SILICO IDENTIFICATION AND CHARACTERIZATION OF CADMIUM, COPPER METALLOPROTEINS AND CYSTEINE-RICH PROTEINS INVOLVED IN CELL DEFENSE IN THE FRESHWATER CILIATE

*S Sripoorna a, Jeeva Susan Abraham a, Swati Maurya a, Renu Gupta b, Seema Makhija a and Ravi Toteja a**
aCiliate Biology Laboratory, Acharya Narendra Dev College, University of Delhi, Delhi, India
bZoology Department, Maitreyi College, University of Delhi, Delhi, India
Email spoorna4@gmail.com

Heavy metals are increasing in the environment in an exponential way due to anthropogenic activities. Living organisms are exposed to different environmental stressors including heavy metals. Heavy metals generally enter the living cells and induce oxidative damage to macromolecules by the excessive generation of ROS (reactive oxygen species). Heavy metals are also known to interfere with the functioning of important metalloproteins (proteins containing metal ions as cofactors) by modifying or replacing the essential divalent ions. Some of the essential metalloproteins play important role in cell defense and help to combat heavy metal stress. Ciliated protozoans are considered to be better model systems for monitoring freshwater pollution by heavy metals. In this pioneering study systematic bioinformatics approach has been employed to identify and characterize metalloproteins (cadmium, copper, and cysteine-rich) involved in cell defense mechanisms from the whole genome data of freshwater ciliate, Tetmemena sp. SeJ-2015 (GenBank accession number LASU02000000). The first 4,769 contigs of Tetmemena sp. SeJ-2015 were annotated from the total of 25,217 contigs where 1,777 were Cd-binding proteins, 1,574 were Cu-binding proteins and 1,066 contigs were Cys-rich proteins. Heat-shock protein and antioxidant enzymes have been detected and characterized from Cd- and Cu-metalloproteins. Among cysteine-rich proteins involved in cell defense mechanism, phytochelatin synthase has been reported and characterized for the first time from spirotrich ciliates. Also, the catalytic sites of these annotated metalloproteins have been elucidated using molecular docking techniques. This study is thus conducted to understand the role of these metalloproteins in metal detoxification and regulation of stress-responsive genes in ciliates.

ABSTRACT (OEAM001)

FEB 05, 09.30-09.40

SPECIES DELINEATION AND GENOMIC SIMILARITY AMONG EXIGUOBACTERIUM STRAINS: A PAN-GENOME ANALYSIS

Alok Kumar Srivastava1, Ruchi Srivastava1, Anjney Sharma1, Akhilendra Pratap Bharati1, Praveen Kumar Tiwari1, Alok Kumar Singh1, Anchal Kumar Srivastava1, Prem Lal Kashyap2, Hillol Chakdar1 and Anil K. Saxena1*
1 ICAR-National Bureau of Agriculturally Important Microorganism, Kushmaur, Mau 2751032
2 ICAR- Indian Institute of Wheat and Barley Research (IIWBR), Karnal, Haryana, India
*Email *aloksrivastva@gmail.com*

The species and subspecies characterization in evolving bacterial genera species are complex, however the new bioinformatic algorithms to calculate genome-to-genome distance (GGD) and DNA–DNA hybridization (DDH) for comparative genome analysis have rejuvenated the exploration of species and sub-species characterization. The present study reports pan-genome analysis of 70 different genomic sequences of Exigubacterium strains devoid of a species taxon on the basis of GGD and the DDH. The analysis identified that eight genomes are analogous to the E. profundum PHM11 at species level and may be characterized as E. profundum. The ANI value and phylogenetic tree analysis also support the same. Further, the comparison of the PHM11 with other eighteen type strains of Exiguobacterium on the basis of 16S ribosomal RNA and the phylogenetic tree analysis showed the two major branching further divided in two clades. The two branches have an intermediate strain E. flavidum. The E. profundum shares clade with the E. marinum and E. aestuarii.The 16S ribosomal RNA sequence similarity between the PHM11 and the E. profundum (10C) type strain by pairwise sequence alignment exhibited that ~58 nucleotide sequences are missing (gap) in the type strains which were present in the PHM11. The results regarding pan-genome analysis provide a convincing insight for delineation of these strains to species.

Keywords: DNA-DNA hybridization, Pan-genome, Exiguobactreium, Delineation

ABSTRACT (OEAM002)

FEB 05, 09.40-09.50

CULTIVABLE DIVERSITY OF THERMOPHILIC ANAEROBIC LIGNOCELLULOLYTIC BACTERIA FROM INDIAN HOT-SPRINGS

*Sai Hivarkar1,2, Vikram Lanjekar1, Prashant Dhakephalkar1, Sumit Singh Dagar1**
1Bioenergy, MACS-Agharkar Research Institute, Pune, India
2Savitribai Phule Pune University, Pune, India
*Email *ssdagar@aripune.org*

India is privileged to have approximately 400 hot-springs across different geographical sites which are known to harbour diverse and unique microbial groups. Due to the prevailing extreme conditions within hot-springs, inherent microbes have evolved specialized mechanisms which are of great biotechnological importance. Among several extremophiles, thermophilic anaerobic lignocellulolytic bacteria have numerous industrial applications, especially in biofuel production. However, due to the limitations associated with the cultivation of anaerobes, Indian hot-springs were hitherto least explored for the presence of thermophilic anaerobic lignocellulolytic bacteria.Hence, in this study, we collected water and sediment samples from six different hot-springs spread across India's three geothermal provinces to cultivate targeted bacteria. Initially, 208 enrichments were set up for ligninolytic, cellulolytic and xylanolytic anaerobic bacteria at the temperature ranges of 40-85 ℃. Following incubation of up to 15 days, 35 enrichments were scored positive based on turbidity, substrate degradation and gas production. In total, nine cellulolytic, fourteen xylanolytic, while no enrichment for lignin-degrading was obtained. Isolations were performed from positive enrichments using Hungate's roll bottle technique, following which, 85 pure isolates were identified using morphomolecular methods. Overall, the isolates were nearest to the genera Bacillus, Caldicoprobacter, Caloramator, Clostridium, Pseudoclostridium, Tepidimicrobium, Thermoanaerobacter and Thermoanaerobacterium.Interestingly, three cultures showed <95% sequence similarity with their closest neighbour, hence, classified as putatively novel genera within family Dysgonomonadaceae, Lachnospiraceae and Limnochordaceae. Similarly, two cultures showed <98.7% while one culture showed <96% sequence similarity with the closest neighbour of genera Thermoanaerobacterium and Caldicoprobacter, respectively, hence, classified as putative novel species. To the best of our knowledge, this is the first study documenting the community of thermophilic anaerobic bacteria which reveals Indian hot-springs as a biological hotspot for efficient fibrolytic anaerobic bacteria.

Keywords: Bioenergy, bioethanol, biohydrogen, cellulase, lignocellulose, xylanase

ABSTRACT (OEAM003) FEB 05, 09.50-10.00

ISOLATION, CHARACTERIZATION AND IDENTIFICATION OF PESTICIDE TOLERATING BACTERIA FROM AGRICULTURE SOIL

Priyanka M Gajjar1, Hiral R Shah2*
1Department of Microbiology and Biotechnology, School of Sciences, Gujarat University Ahmedabad 380009, India
2Ananya Institute of Science, KIRC Campus, Ahmedabad – Mehsana highway, Kalol (N. G) 382721, India
*Email *pu6889@gmail.com*

Pesticides are the chemicals used for the prevention, repelling or destroying agricultural pests. The frequent use of such pesticides results in the residual deposition in the soil vis-a-vis entering the ecosystem and affecting the living system causing serious effects like diseases of various systems, cancer or foetal abnormalities in pregnant ladies. Therefore, it is an absolute necessity to develop the method for excluding or converting the soil residual pesticides into non/less toxic substances. Bioremediation is one of the methods, which is eco-friendly, inexpensive and easily applicable to the soil. Hence, the study has been conducted to identify and characterize the micro-organism that are resistant to Mancozeb pesticide (bisdithiocarbamate non-systematic fungicide), widely used in potato farming. The study has been performed on 10 nos. soil samples collected from the Banaskantha District, Gujarat. An enrichment culture technique has been applied on the soil samples to isolate microbial isolates and such isolates are subjected to morphological and biochemical tests for their identification. Various parameters of microbial isolates like optimum temperature of the growth, pH scale and NaCl concentration have also been determined. Total 8 nos. pesticide resistant bacterial isolates viz. PM1, PM3, PM5, PM7, PM8, PM9, PM10 and PM11 have the ability to degrade Mancozeb. These selected isolates have also been tested for their antibiotic susceptibility and different enzyme production. The presented findings are useful in designing the multi-resistant microorganisms that can be used efficiently for the bioremediation of Mancozeb.

ABSTRACT (OEAM004) FEB 05, 10.00-10.10

PROMOTION OF MICROBE- MEDIATED PRACTICES AND ORGANIC AMENDMENTS AT FARMERS FIELD THROUGH FRONT LINE DEMONSTRATIONS (FLDS)

Pooja Yadav, Renu, Adarsh Soni, Garima Rai, Rajan Singh, Rahul Kumar Gupta, Sudheer Kumar Yadav, Ashish Kumar Vishwakarma, Astha Tiwari, Nagesh Tiwari, Amit Yadav, Anil Kumar Saxena*
ICAR- National Bureau of Agriculturally Important Microorganisms, Kushmaur, Maunath Bhanjan 27510 I, India
*Email *renui nri@rediffrnail.com*

Organic farming is not a new concept to the Indian farmers as they have practiced it from ages. Organic farming system rely on crop rotation, crop residues, animal manure, green manure, off farm wastes and biological pest control. Yields in organic farming is lower than chemical farming during initial years and it takes time to stabilize, but if practiced in the long run and properly monitored then yields can be enhanced reducing dependency on chemical fertilizers. Field experiments were conducted under DST-SSTP project "Promotion of microbe-mediated farm-centric approaches to improve soil and plant health and generate livelihood for farmers in Mau (UP)"at ICAR-NBAIM, Mau fields on various crops such as wheat, rice, pea, moongbean, and chickpea using different combinations of microbial inoculants such as Trichoderma, Pseudomonas, Bio-NPK, Mycorrhiza, Bio-shakti and organic amendments such as Gomutra and organic compost. Further the objective of the project is to make these practices reach at the end users i.e., farmers. To fulfill this purpose 4 field trials were planned on crops such as wheat, (HD-2967), chickpea and brinjal (Fl Hybrid No.704) during Rabi (2020-21). The owners of these fields are small and marginal farmers with <2 hectares land and follow Rice-Wheat cropping system. Different combinations of microbial inoculants were provided to farmers and sowing/transplating after treatment was done with proper demonstration and supervision. In two FLDs on wheat and chickpea, microbial inoculants used were Bio-NPK + Trichoderma and Bioshakti with 30% reduced dose of chemical fertilizers. Initial grO\vth parameters such as seed germination percentage, shoot height and root height were recorded at 30 DAS. Preliminary results in wheat have shown better performance ofBio-NPK and Trichoderma in comparison to control with full dose of fertilizers practiced by farmers. Microbial treatment for FLO on Brinjal includes Bio-NPK, and Bio-NPK+Trichoderma + Compost at 30% reduction of chemical fertilizer as in normal practice. Data was recorded at 30 DAS, 60 DAS, 90 DAS on parameters such as Plant height, number of flowers, number of fruits, and presence of any disease. It was found that there was no decrease in yield on reducing chemical fertilizer and the fruits were healthier, longer and shinier than that in control. According to the farmer, use of Bio NPK and Trichoderma has given excellent results in terms of yield, fruit size, color and resulting in better economic returns in the local market.

ABSTRACT (OEAM005)

FEB 05, 10.10-10.20

MICROBIAL FORTIFICATION ENHANCES PLANT GROWTH AND ANTIOXIDANT DEFENCE SYSTEM IN RICE (ORYZA SATIVA L.)

Garima Rai, Renu**, Adarsh Soni, Pooja Yadav, Rajan Singh, Rahul Kumar Gupta , Sudheer Kumar Yadav, Ashish Kumar Vishwakarma, Astha Tiwari , Nagesh Tiwari, Amit Yadav, Anil Kumar Saxena*
ICAR- National Bureau of Agriculturally Important Microorganisms, Kushmaur, Maunath Bhanjan 275101, India
*Email *raigarima26@gmail.com, **renuiari@rediffmail.com*

The usage of inorganic fertilizers excessively has led to several environmental problems like degradation of soil, negative effect on organic matter and carbon in soil, leaching of nitrogen, other properties of soil such as its compaction which requires attention.For agricultural and environmental sustainability use inoculants of biological origin i.e. bio-fertilizers could reduce the dependency on chemical fertilizers.A field experiment was designed to check the effect of the microbial fortification in rice (Oryzasativa L.) varieties CO51, MTU-7029 and RNR with microbial inoculants viz., Trichodermaasperellum, Pseudomonas fluorescensas, Nostoc, Anabaenaand Bio-NPK via seed coating, seedling root inoculation on growth promoting parameters and antioxidant enzymes in plants.Three treatments of co-inoculation of microbial inoculants were (i) Pseudomonas+Trichoderma+Nostoc+Anabaena; (ii) Bio-NPK and (iii) Bio-NPK+Pseudomonas+Trichodermaa two recommended doses of fertilizers i.e., 100% and 75%. Each treatment has four replicates following CRD. Growth parameters taken were shoot length, number of tillers, fresh weight and dry biomass at regular time interval (30 DAS, 60 DAS, 90 DAS). Highest fresh shoot weight was obtained in Bio NPK with 100% RDF (CO-51) and Bio-NPK+Pseudomonas+Trichoderma with 100% RDF(RNR) followed by other treatments while in freshrootweight was found highest in Pseudomonas+Trichoderma +Nostoc+Anabaena with 60% RDF(CO-51) followed by Bio-NPK+Pseudomonas +Trichoderma with 60% RDF(CO-51).Application of microbial inoculants increased total polyphenolics, flavonoids and protein content in the leaves of plants. Highest record of DPPH, Fe-ion reducing power and Fe-ion chelation were found in plants treated withBio-NPK+Pseudomonas+Trichoderma in RNR and CO-51 varieties reflecting high non-enzymatic antioxidant (free radical scavenging) activities in polyphenolics-rich leaf extracts.Improved ROS scavenging was observed upon Bio-NPK+ Pseudomonas+Trichoderma treatment reflected by enhanced phenylalanine ammonia-lyase (PAL), superoxide dismutase (SOD), catalase (CAT), peroxidase (PO) and ascorbate peroxidase (APX) activities in rice plants as compared to other treatments. The results suggest the role of microbial inoculants in enhancing the growth and development of rice plants at physiological and biochemical level.

ABSTRACT (OEAM006)

FEB 05, 10.20-10.30

ENDOPHYTIC FUNGUS SERENDIPITA INDICA COLONIZATION IN ROOT REDUCES ARSENIC MOBILIZATION FROM ROOT-SHOOT-FRUIT IN THE TOMATO PLANT

*Jagriti Shukla1, 2 Manoj Kumar1, 2**
1Environmental Microbiology Lab CSIR-IITR Campus Vishvigyan Bhavan, 31, Mahatma Gandhi Marg, Lucknow, Uttar Pradesh, India
2Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, Uttar Pradesh, India
*Email *manojkumar@iitr.res.in*

Arsenic (As) contaminated agricultural soil is a serious issue in a large region of the world due to various natural and anthropogenic activities. Various studies suggested that crops growing in these As contaminated soil contain elevated levels of As in their edible part which is also a major route of As exposure in humans besides drinking water. Unlike drinking water, there is no technology available to remove/reduce arsenic from soil and therefore As transfer from water-soil-plant is a growing concern. However, the use of microorganisms has been a promising tool to diminish this problem. Mycorrhizal like endophytic fungus Serendipita indica (S. indica) has As resistance capacity and it can be grown upto 5 mM As concentration. We use S. indica and studied various phenotypic, metabolic, and physiologic parameters like seed germination, fungus colonization, plant growth, reactive oxygen species (ROS) measurement, antioxidative enzyme activities glutathione, proline measurement, and As estimation in the root, shoot, and fruit of tomato plant under As stress. Our investigation suggests that interaction of S. indica results in alleviation of arsenic toxicity at the germination stage and increases plant growth, reduction of ROS accumulation through modulating antioxidative enzyme activities in plants. Colonization of fungus also enhances antioxidative metabolites glutathione and proline in As stressed plants. The fungus colonization study shows that As induces hyper colonization of S. indica in the root which results in arsenic accumulation exclusively in root and quite a low fraction of As mobilized from root to shoot/fruit of the plant. Thus our study suggests that S. indica is able to restrict mobilization from root to shoot and fruit by decreasing the availability of arsenic in the rhizosphere. The phenomenon of immobilization of arsenic by fungus may be exploited to grow safer crops in arsenic-contaminated agricultural areas.

ABSTRACT (OEAM007)

FEB 05, 10.30-10.40

BACTERIAL TRANSFORMATION AND CHEMOTAXIS OF HEAVY METALS

*Rupali Mishra, Pankaj Kumar Arora**
Department of Microbiology, Babasaheb Bhimrao Ambedkar University, Lucknow, India
*Email *arora484@gmail.com*

An arsenic-resistance bacterial strain PKA-200 was isolated from a water sample collected from Hindan River, Ghaziabad. Strain PKA-200 was identified as a member of the genus Pseudomonas on basis of the 16S rRNA gene sequencing. Pseudomonas sp. strain PKA-200 was able to oxidize highly toxic arsenite [As (III)] to less toxic arsenate [As (IV)]. Minimal inhibitory concentration of As (III) for strain PKA-200 was 600 mg/L. Furthermore, Pseudomonas sp. strain PKA-200 exhibited positive chemotaxis towards As (III) in semi-solid and soil media. Several methods including drop plate assay, big circular plate assay, and fabricated tray assay used to demonstrate chemotactic potential of strain PKA-200. This is a first report of bacterial chemotaxis towards As (III) in soil by any bacterium.

Keywords: Arsenic, Pseudomonas, Arsenite-oxidising bacterium, Biotransformation, chemotaxis

ABSTRACT (OEAM008)

FEB 05, 10.40-10.50

DECIPHERING GENETIC AND FUNCTIONAL DIVERSITY OF CHASMOPHYTE (WILD CHENOPODIUM) ASSOCIATED BACTERIA

*Sudipta Das1, 2, Shaloo Verma1, Hillol Chakdra1, Rajni Singh2 and Anil Kumar Saxena1**
1 ICAR-National Bureau of Agriculturally Important Microorganisms (NBAIM), Mau-275103, Uttar Pradesh, India
2Amity Institute of Microbial Technology, Amity University, Noida-201301, Uttar Pradesh, India
*Email *saxena461@yahoo.com*

Chasmophytes are plants growing on cracks and crevices of rocks. They survive under nutrient and water limited conditions. Epiphytic and endophytic microbes present in chasmophytes may play a critical role in their survival. In the present study, from wild Chenopodium plants collected from hills of Tsomoriri, Ladakh, 262 different bacterial morphotypes were isolated using six different media. Among, 124 isolates were positive for siderophore produce, 36 for P solubilization, 10 for K solubilization, 25 for Zn solubilization, 31 for ACC deaminase production and 46 for IAA production. Production of IAA by the isolates ranged from 4.7-232 µg/ml.The culture was screened for tolerance to range of temperature (4o-50o), salinity (0-15%) and pH (7-11). Among the culture screened, 196 could grow at 50oC while 155 showed growth at 4oC .In general, 96 isolates exhibited the ability to grow over a range of temperature (4-50oC).More than 50% isolates could tolerate 10-15% NaCl concentration and almost all could tolerate till pH11. Restriction profiling of 16s rRNA gene using three different restriction enzymes viz. RsaI,TaqI, HaeIII revealed 16 and 44 operational taxonomic units (OTUs) in gram negative and gram positive bacteria respectively at 75% similarity level. The results indicated that genetically and functionally diverse microflora is associated with wild Chenopodium that might be helping these plants to effectively mine nutrients and water under extreme conditions.

ABSTRACT (OEAM009)

FEB 05, 10.50-11.00

EFFECT OF SULFUR OXIDIZERS ON MUSTARD YIELD AND OIL CONTENT

Mohammad Tarique Zeyad, Shiv Charan Kumar, Ruchi Srivastava, Anjney Sharma, Murugan Kumar, Anil Kumar Saxena*
ICAR- National Bureau of Agriculturally Important Microorganisms, Mau Nath Bhanjan, Uttar Pradesh-275103, India
*Email *kumarmic84@gmail.com*

Sulfur (S) is one of the essential plant nutrients and an important ingredient in some amino acids. Sulfur undergoes several chemical alterations in soil which are exclusively operated by microorganisms. Oxidation of sulfur is the most important step as it leads to sulfate ions which are readily absorbed by plants. S is required in quantities equal to phosphorus in oil seed crops, especially mustard. In this context it is required to develop microbes that can oxidize sulfur in soil and make them available to crop plants. A total of 36 sulfur oxidizers were isolated from different niches. They were evaluated for their ability to solubilize elemental sulfur. Four sulfur oxidizing isolates were selected for identification and further studies. They were identified as Bacillus firmus SS1, Pseudomonas azotoformans SC14 and Alcaligens sp. BS104 and Staphylococcus haemolyticus CA101. Three of them were tested for their ability to improve yield and oil content in mustard with different treatments; T1-Recommended dose of NPK (NPK);T2-NPK + Elemental Sulfur (NPKS); T3-NPK + SS1; T4-NPKS+SS1; T5-NPK+SC14; T6-NPKS+SC14;T7-NPK+BS104;T8-NPKS+BS104;T9-NPK+Gypsum. Treatment with gypsum recorded the highest yield although application of BS104 + sulfur resulted in yield statistically on par with gypsum treatment. With regards to oil content the highest oil content was recorded with BS104 + sulfur treatment closely followed by gypsum treatment and SC14 + sulfur treatment. Alcaligens sp. BS104 is identified as a potential sulfur oxidizing inoculant for Mustard crop.

Keywords: Sulfur oxidizing bacteria, Mustard, Alcaligens sp.

ABSTRACT (OEAM010)

FEB 05, 11.00-11.10

STUDY ON REMOVAL OF HEAVY METAL FROM INDUSTRIAL EFFLUENT USING MICROORGANISMS

Gagana S, Ishwarya P R, Marni Devika Krishna, Monisha D R, Roopa K B*
Department of Biotechnology, Siddaganga Institute of Technology, Tumkur, Karnataka, India
*Email *gagana191999@gmail.com*

Heavy metal contamination is one of the biggest problems today due to its great impact on the surface, groundwater and even in catchment areas. Uranyl acetate dihydrate (UAD) is formed when Uranium is in the VI oxidation state. It was observed that UAD causes oxidative damage, respiratory diseases, cancer and fatigue in human beings. In an effort to overcome this problem bioremediation is employed in our studies. In comparison to physical and chemical methods of uranium removal, bioremediation is a promising strategy, with advantages of reduced energy demand and environmental impact. In our present study, a sample was collected from an electroplating industry. From the collected sample, microorganisms were screened for degradation of UAD and were identified by performing staining and various biochemical tests. The organism was confirmed to be Bacillus subtilis by 16S rRNA sequencing. Titrimetric analysis was performed to check the amount of UAD removal by the selected organism and it was able to remove 95.18% of UAD with the incubation period of 48hrs. Further to understand the surface topography of the organism, the sample was subjected to SEM (Scanning electron Microscopy) analysis and observed that UAD was removed by mechanisms of biosorption and bioaccumulation. Further to analyze, the parameters that influence the removal of UAD, Response surface methodology needs to be conducted.

ABSTRACT (OEAM011)

FEB 05, 11.10-11.20

EFFECT OF SULFUR OXIDIZERS ON MUSTARD YIELD AND OIL CONTENT

Rishit Soni1, Shilpa Jani2, Aarti Thakker3*
1Shree P. M. Patel
1 Institute of Biosciences, Anand-388001, India
2J & J Science College, Nadiad-387001, India
3President Science College, Ahmedabad-389001, India
*Email *sonirishit8@gmail.com*

Keratin is an insoluble protein and it's not easily degraded by normal proteolytic microorganisms. Keratinous waste samples viz. rock samples from Dalhousie, Himachal Pradesh, hair debris were collected from Fatepura village salon and poultry farm waste from Sheriyaj, Gujarat. Keratinase producing microorganisms were isolated from keratinous waste. Initially, alkaline protease producing microorganisms were screened based on the zone of casein hydrolysis. The isolates were tested for their relative enzyme activity on skimmed milk agar media. The isolates were characterized based on their morphological characters, biochemical activity, spore nature, growth patterns, and pigmentation, and 16 S rRNA sequencing. The potent isolates were analyzed for feather degradation capacity to screen out keratinase producers. Isolates were identified as novel Streptomyces spp. and Saccharothrix xinjiangensis. The chicken feathers were degraded successfully within 48 hours at 37°C and 40°C simultaneously by isolate A1 and A2. The feather degraded samples were analyzed for release of various essential amino acids by TLC-Thin Layer chromatography. The amino acids detected were histidine, lysine, tryptophan, and methionine. Isolates were found to possess a major keratinolytic activity and should serve a dual purpose for the degradation of poultry waste and production of amino acid rich feed supplement. Isolates were also employed for the production of keratinase and it was found that they produced keratinase optimally at 72 hours and 48 hours respectively. The optimal pH and temperature for production of the keratinase enzyme were found to be 8.5 pH and 40°C for A1 and 9.5 pH and 40°C for A2.
Keywords: Keratinase, Keratinic, Actinomycetes, Feather Degradation, Production.

ABSTRACT (OEAM012)

FEB 05, 11.20-11.30

FUNGAL DIVERSITY ANALYSIS OF SOIL SAMPLES FROM NAGALAND AND THEIR ROLE IN SOIL HEALTH

Anchal Kumar Srivastava1, Manish Roy1, Alok Kumar Singh1, Anjali Singh2, Jagriti Yadav1, Praveen Kumar Tiwari1, Ruchi Srivastava1, Alok Kumar Srivastava1, Anil Kumar Saxena1*
1 ICAR-National Bureau of Agriculturally Important Microorganism, Kushmaur, Mau 275103, India
2 S.M.T.D.College, Bahadurpur, Ballia, Uttar Pradesh 277001, Ballia, India
*Email *aloksrivastva@gmail.com*

Soil fungi represent one of the most important microbial groups that are actively involved in the enhancement of environmental quality and plant nutrient supply. In the present study an attempt was made to map the fungal diversity in the soil from various places of Nagaland, India. The samples were collected during March 2020 at the temperature of 32°C max and 16°C minimum with 75% humidity. The soil samples were collected from the Rukitalang forest (Sample 1), Medziphema pineapple crop field (Sample 2), Lalmati Elev 970 M (Sample 3) and Kohima crop field (Sample 4). Total 51 fungi isolates were obtained on PDA through dilution plating. The isolates were further screened and characterized for Plant growth promoting traits viz: production of siderophore and solubilization of zinc, potassium and phosphate. Twenty four strains were recorded as potential candidates for plant growth promotion and were identified through sequencing of the ITS region. These isolates were identified as Alternaria alternata, Aspergillus flavus, A. aculeatus Talaromyces flavus, Mortierella alpina, M. ambigua, Gongronella butleri, Keithomyces carneus, Trichoderma koningiopsis, T. caribbaeum, and T. asperellum, etc. and the sequences were submitted at NCBI Genbank. Three most prominent fungal isolates (NL2F5, NL3F6, and NL4F18) were further evaluated for PGP activity in maize, NL2F5 and NL3 F6 showed significant increment in root length, root volume, shoot length and shoot fresh weight as compared to control. These isolates have a better prospect for development of formulations and provide an alternative to already commercialized species.

ABSTRACT (OEAM013) FEB 05, 11.30-11.40

DECIPHERING THE REGULATORY ROLE OF MIRNAS IN C. ANNUUM L. DURING P. CAPSICI INFECTION

Tilahun Rabuma1, Om Prakash Gupta2, Vinod Chhokar1*
1Department of Bio and Nano Technology, Guru Jambheshwar University of Science and Technology, Hisar, Haryana, India
2 Scientist, Division of Quality and Basic Sciences, ICAR-Indian Institute of Wheat and Barley Research, Karnal-132001, Haryana, India
*Email *tilahun.rabuma@wku.edu.et, *tilefire@gmail.com*

miRNAs are un-translated, tiny (20-25 ntds.) riboregulator of genes associated with regulation of every stage of plant's life cycle including stress responses. Despite several efforts made in identifying the regulatory role of miRNAs during defense response in many host-pathogen interactions, their involvement during C. annuum-P. capsici pathosystem largely remains under explored. Therefore, the current study was aimed at identifying novel as well as known conserved miRNAs associated with defense response in two chilli pepper genotypes viz. GojamMecha_9086 (Resistant) and Dabat_80045 (Susceptible) during infection with P. capsici infection. The small RNA deep sequencing resulted in 79 known miRNAs corresponding to 24 miRNAs families and 477 novel candidate miRNAs. The expression analysis revealed that around ~29 known & ~157 novel miRNAs and ~30 known & 176 novel miRNAs were differentially expressed in RC vs RI and SC vs SI leaf sample, respectively. A total of 22,895 potential target genes were predicted among which 29 genes were associated with defense response against P. capsici infection. Furthermore, RT-qPCR analysis of eight randomly selected miRNAs genes validated the result of Illumina NextSeq500. Our results provide new insight into the miRNA mediated defense mechanism of C. annuum L. under P. capsici infections. Further functional validation of miRNAs and their corresponding defence related genes using reverse genetic approach could impart more in-depth understanding of the role of miRNAs during C. annuum-P. capsici pathosystem.

Keywords: C. annuum, P. capsici, miRNA sequencing, known miRNA, novel miRNAs, target gene, regulatory mechanism

ABSTRACT (OEAM014) FEB 05, 11.40-11.50

PHYSIOLOGICAL AND BIOCHEMICAL PERSPECTIVES OF HD-2967 WHEAT CULTIVAR DURING MICROBIAL INTERACTION AGAINST SALINITY STRESS

Madhulika Singh1,2, Jai Gopal Sharma1, Bhoopander Giri2*
1Department of Biotechnology, Delhi Technological University, Delhi, India
2Department of Botany, Swami Shraddhanand College, University of Delhi, Delhi, India
*Email *madhu.ssnc@gmail.com*

Salinity is one of the most devastating abiotic stresses that hinders plant growth and productivity. In order to alleviate salinity impact and to increase agricultural productivity, the efficient resource management and crop improvement approaches are required, however, such approaches are cost intensive. Among low-cost methods for mitigating salinity stress, the microbial mitigation of salinity stress could play a significant role in managing soil fertility and sustainable development of crop productivity. In this study, we investigated the response of HD-2967 wheat cultivar inoculated with the fungus, Piriformospora indica and plant growth-promoting bacteria (PGPB) under four different levels of salinity (0 mM NaCl, 50 mM NaCl, 100 mM NaCl, 200 mM NaCl having electrical conductivity (EC) value 0.01, 5.84, 11.50, 21.4 mS cm-1respectively). The results of this study showed that, the P. indica and PGPB inoculated HD-2967 wheat plants had a greater root and shoot biomass and leaf area as compared to uninoculated HD-2967, subjected to different levels of salinity. Microbial inoculation of HD-2967 wheat plants also restored better photosynthetic rates, transpiration, stomatal conductance, relative membrane permeability, internal CO2, chlorophyll and carotenoid levels under salinity stress. Moreover, microbial inoculation increased the accumulation of glycinebetaine, total sugars and proteins, whereas the activity of lipoxygenase enzyme and MDA content decreased significantly. Inoculation of HD-2967 cultivar with PGPB showed significant increase in the accumulation of proline content as compared to that of the P. indica and uninoculated plants under all levels of salinity. Result of this study showed that the salinity tolerance was more pronounced in the PGPB inoculated than P. indica inoculated plants. Such microbes may be considered as potential bioinoculants to alleviate salinity stress in HD-2967 wheat cultivar; however, a detailed study at molecular level needs to be done, to understand the mechanism by which microbes alleviates salinity stress in HD-2967 wheat cultivar.

ABSTRACT (OEAM015) FEB 05, 11.50-12.00

GENOME OF EXTREMELY SALT RESISTANT BACTERIUM EXIGUOBACTERIUM PROFUNDUM PHM 11 VIEWED FROM THE PERSPECTIVE OF COMPARATIVE GENOMICS

Alok Kumar Srivastava1, Praveen Kumar Tiwari1, Ruchi Srivastava1, Sudipta Das1, Alok Kumar Singh1, Anchal Kumar Srivastava1, Prem Lal Kashyap2, Hillol Chakdar1, Anil K. Saxena1*
1 ICAR-National Bureau of Agriculturally Important Microorganism, Kushmaur, Mau 2751032
2 ICAR- Indian Institute of Wheat and Barley Research (IIWBR), Karnal, Haryana.
*Email *aloksrivastva@gmail.com*

Advances in the next generation sequencing (NGS) technologies and new algorithms to calculate DNA-DNA hybridization (DDH) and genome-genome distance (GGD) for comparative genome analysis have invigorated the exploration of microbial genomes in retrieving the hidden traits and species and subspecies characterization. In this study, we performed the whole genome sequencing of a halotolerant Exiguobacterium profundum PHM 11 and compared with the genome of six well characterized Exiguobacterium. The PHM 11 genome has a size of 2.92 Mb with G+C content of 47.93%. Chromosome map of PHM 11 showed the presence of lysogenic phage DNA. The PGP traits were validated by pot trials on Zea mays showed enhanced growth and development of shoot as well as roots. Functional annotations of the genome showed the different hidden inherent metabolic pathways and protein families. We found the total 3033 genes were protein coding and 33 genes were non protein coding. Out of these, 2316 were characterized and 737 were hypothetical. The predicted proteome was compared with other six Exiguobacterium sp. Results showed that these species from 3806 clusters, out of which a total of 2723 clustered were shared by PHM 11, 1639 clusters were common and 131 were singletons. A total of 112 GO (Gene Ontology) terms were allocated for biological processes, 28 GO terms for molecular function and 5 GO terms were assigned for cellular functions.
Keywords: DDH, GGD, Exiguobacterium

ABSTRACT (OEAM016) FEB 05, 12.00-12.10

MICROBIAL DERIVED BIOSURFACTANTS FOR THEIR APPLICATION IN ENVIRONMENTAL BIOREMEDIATION AND AS DISINFECTANTS

*Vivek Kumar Gaur1,2, Natesan Manickam1**
1Environmental Biotechnology Laboratory, Environmental Toxicology Group, CSIR-Indian Institute of Toxicology Research, Vishvigyan Bhawan, 31 Mahatma Gandhi Marg, Lucknow-226001, Uttar Pradesh, India
2Amity Institute of Biotechnology, Amity University Uttar Pradesh, Lucknow Campus, Lucknow-226010, India
*Email *nmanickam@iitr.res.in*

Biosurfactants belong to a class of biological origin surfactants derived from bacteria and fungi. Biosurfactants exhibit several advantages such as reduced toxicity, biodegradability, and high substrate specificity as compared to their synthetic counterparts. We report here the biosurfactants derived from Lysinibacillus sphaericus strain IITR51 and Candida glabrata CBS138 exhibiting difference in haemolysing capabilities, thus indicating their application. Liquid chromatography–mass spectrometry (LC-Mass), and nuclear magnetic resonance (NMR) spectroscopic analysis revealed that strain IITR51 and CBS138 produced sophorolipid and rhamnolipid, respectively. Based on the positive haemolysis observed for rhamnolipid, it was studied for environmental bioremediation. It was observed that the rhamnolipid at a concentration of 90 mg/L exhibited enhanced dissolution of chlorinated pesticides α-endosulfan (7.2 folds), β-endosulfan (2.9 folds), γ-hexachlorocyclohexane (1.8 folds) and crude oil contaminants (2.7 folds). Both rhamnolipid and sophorolipids were found to exhibit bactericidal activity against pathogenic strains viz., Bacillus subtilis strain MTCC441 and Escherichia coli strain MTCC723. Higher concentrations of sophorolipid biosurfactants increased the generation of reactive oxygen species when tested against gram+ve and gram-ve bacteria. Furthermore, an increased concentration of cellular materials in the test system suggests that sophorolipid mediated cell disruption leading to the cell lysis. Sophorolipid at 5 mg/L combined with penicillin at 1 mg/L exhibited a synergistic effect against B. subtilis strain 441 leading to its early cell death. Both the biosurfactants when used at a concentration of 600 mg/L did not exhibit toxic effect on keratinocyte cell line (HACAT), in vitro, suggesting their non-toxic nature. Therefore, biosurfactants isolated and characterized in this study can be used in environmental cleanup of chlorinated pesticides. Also, as evident by its bactericidal properties these biologically derived surfactants can be employed in any suitable formulation of disinfectant to prevent the spread of pathogenic bacteria which in turn may help in reducing the use of synthetic antibiotics.
Keywords: Bioremediation, Biosurfactant, Antibiotic, Bactericidal

ABSTRACT (OEAM017) FEB 05, 12.10-12.20

AN OVERVIEW OF RESIDUAL CONTAMINATION AND BACTERIAL DEGRADATION OF ORGANOPHOSPHATE PESTICIDES AND INVESTIGATION OF PESTICIDE USAGE PATTERNS AND FARMERS PERCEPTION ON PESTICIDE USE

Mohd Ashraf Dar, Garima Kaushik***
Department of Environmental Science, School of Earth Sciences, Central University of Rajasthan, Bandarsindri, Ajmer, 305817, Rajasthan, India
*Email *darashraf9@gmail.com, **garimakaushik@curaj.ac.in*

Utilization of pesticides has proved to be a mandatory input in agriculture as they have frolicked a major role in boosting agricultural yield by providing shield to crops against pest infestations. But intensive agricultural development implies that more harmful chemicals are increasingly entering the environment which leads to harmful impacts on the biological system. In view of their extensive application, stability, toxicity, and bioaccumulation, they are among the most lethal substances which contaminate all vital life saving needs including air, food, and water. Among different pesticides, organophosphate (OPs) are the most widely used pesticide group because of their lower persistence and higher efficiency. However, due to the extensive utilization of OPs their residues have become an unavoidable part of the environment, as they have been regularly detected in every fragment of the environment especially in food items, through which they are mostly dangerous to living organisms including humans. Every year, their deliberate or accidental take-up causes a huge number of deaths and severity. Keeping in view the contamination and toxicity of OPs their monitoring has been often carried out globally with the initiation of field and laboratory studies in the natural environments. Present study highlights many cases where OP residues have been detected surpassing their respective MRL (maximum residual level) values. Some OP detected are hazardous to that point that even WHO has classified them into Ia and Ib hazardous group. Because of higher OP toxicity, research is carried out worldwide to design and develop viable and proficient methodologies/solutions for OP elimination and its associated metabolites from the environment. Different techniques for detoxifying these pesticides are currently available, but microbial degradation mostly by bacteria has demonstrated to be profoundly effective, economical, and eco-friendly. In this way, this study provides a framework of recent research events on this topic and describes the evidence of OP pollution and analyse the theoretical analysis of latest research finding on pesticide degradation by bacterial strains. Present study also undertook a survey to study the pesticide usage patterns, and farmer's perception towards pesticides. Data were collected via structured questionnaire, formal and informal interviews. Results indicated the easy availability, manual application, and extensive application of pesticides in crop fields. The pattern of pesticide use among farmers therefore needs improvement.

Keywords: Pesticide, Organophosphates, Maximum residual level, Toxicity, degradation

ABSTRACT (OEAM018) FEB 05, 12.20-12.40

ISOLATION AND CHARACTERIZATION OF BACTERIOPHAGES AGAINST XANTHOMONAS ORYZAE PV. ORYZAE AS A POTENT BIO-CONTROL FOR BACTERIAL LEAF BLIGHT OF RICE

Lata Jain, Vinay Kumar, S.K. Jain*
ICAR-National Institute of Biotic Stress Management, Baronda, Raipur, Chhattisgarh, India
*Email *jain.lata59@gmail.com*

Xanthomonas oryzae pv. oryzae (Xoo), is one of the most important bacterial pathogens causing Bacterial Leaf Blight (BLB) in rice. Due to ineffectiveness of chemicals in controlling the disease, development of effective and eco-friendly bio-control methodology like phage therapy can be an alternate approach in the present era of anti-microbial resistance. In this study, we attempted to isolate the bacteriophage against Xoo. About 128 water and soil samples from rice field were collected from Chhattisgarh and all adjoining states and processed for phage amplification by co-culturing with Xoo using liquid culture method and isolation by agar overlay method. A total of 16 bacteriophages against Xoo were isolated indicated by clear round plaques and clearance of bacterial growth around phage streaked lines. The isolated phages were characterized in terms of the plaque size, plaque forming count (PFU) and effect of temperature (4 to 90°C), pH (range 2-12), chemicals, UV-light and sunlight on viability of the phage. The plaque size of phages varied from 2 to 10 mm in diameter while PFU count ranges from 3 x 106 to 6.2 x 109/ml. Effect of temperature on phage viable count ranged from 100% viability at 4°C to 40°C; 66% at 50°C; 30% at 60°C and less than 1% viability at 70°C or more. Similarly, phages were found to have about 99-100% viability at pH range of 6-8; about 80% at pH 5 and 9; 40% at pH 4 and 20% at pH 10 while they are not viable at pH 2, 3, 11 and 12. Upon chemical treatment of phage for their viability, 40% formalin has maximum lethal effect on phage up to 99.9% followed by 1% SDS (90-97%); 10% chloroform and 5% aqueous phenol (80-90%). Phages were found to survive UV-light (365nm) for up to 2 minutes and direct sunlight at 12 noon in the month of December for 1 hour. All the 16 phage were found highly host specific and they have no bactericidal effect against heterologous host viz., Bacillus spp., Serratia, Salmonella, Escherichia coli, Staphylococcus. Efficacy study of individual bacteriophages for their bactericidal activity against Xoo was conducted in-vitro using liquid culture assay. On co-infection/co-culture of phage with Xoo pathogen at 0.1 multiplicity of infection (MOI), isolated phages were found to kill in a range of 85% to 95% bacteria within 24 hours as evident by decreased visible turbidity and total viable count of bacteria. The isolated phages can be used as bio-control agents for the management of devastating BLB disease.

ABSTRACT (OEAM019) FEB 05, 12.30-12.40

ENDOPHYTE MEDIATED MODULATION OF NUTRIENT TRANSPORTERS AND ROOT ARCHITECTURE IMPROVES FE AND ZN UPTAKE IN MAIZE

Shaloo Verma, Kumar M, Hillol Chakdar, Anil Kumar Saxena*
ICAR- National Bureau of Agriculturally Important Microorganisms (NBAIM), Kushmaur, Mau, Uttar Pradesh, 275103, India
*Email *hillol.chakdar@gmail.com*

Microbe mediated biofortification of micronutrients could be a sustainable alternative to available agronomic and genetic approaches. In the present study, two groups of maize endophytes- (1) Zinc solubilizers: Microbacterium hydrothermale M10 and M. jejuense B2 (2) siderophore producers: Bacillus sp. C7 and Pseudonocardia alni M29 were evaluated for their potential to improve Zn and Fe uptake in maize under hydroponics. Confocal laser scanning microscopy (CLSM) revealed successful colonization of the endophytes inside the maize roots. Inoculation of maize seeds with combination of M. jejuense B2 and P. alni M29 resulted in increased Fe localization in roots whereas inoculation of M. hydrothermale M10 resulted in higher localization of Zn in root. These bacterial endophytes, especially, P. alni M29 significantly influenced root architecture. P. alni M29 resulted in ~3 folds higher expression of ZmIRT1 in root while in shoot, ZmZIP3 and ZmZIP4 were up-regulated by ~5 and ~3 folds respectively. Combination of M. hydrothermale M10 and P. alni M29 also showed ~4 folds increase in the expression of ZmZIP4 in shoot. This particular combination of M. hydrothermale M10 and P. alni M29 resulted in significantly higher expression of ZmZIP3 gene both in roots and shoots. The results of the present study revealed that the endophytes could modulate the expression of nutrient transporters and also improve the root architecture so as to increase the uptake and transport of Fe and Zn from root to shoot.

ABSTRACT (OEAM020) FEB 05, 12.40-12.50

SIMPLIFICATION OF SOIL MICROBIOLOGICAL TECHNIQUES TO PROMOTE TECHNOLOGY TRANSLATION IN AGRICULTURE AND ALLIED SECTORS

Aparna K, Sivaprasad V*
Central Sericultural Research and Training Institute, Berhampore-742101, West Bengal, India
*Email *aparna.micro@gmail.com, *aparna.k@csb.gov.in*

Advancements in the field of agricultural and soil microbiology have generated an amplitude of information on physiological and molecular characterization of microorganisms and microbiomes; only a very small fraction of the information is actually being translated into utilizable technologies for real farming situations. Despite the fact that soil microorganisms act as ideal indicators of soil fertility and health, their niche is least exploited in soil testing for determining fertilizer and fungicide dosage recommendations. The complexity associated with microbiological assessment methods is the root cause of such a gap. Two novel simplified microbiological methods discussed here, dye reduction assay (DRA) for soil microbial activity and split agar technique (SAT) for soil antifungal activity, are cost effective and have better scope in soil testing laboratories overcoming the tediousness of conventional soil testing procedures. DRA is designed based on the ability of microorganisms to utilize cell permeable redox indicators as terminal electron acceptors in their respiratory electron transport chains. The colour change on reduction due to microbial activity is quantified spectrophotometrically. The test permits visual assessment of microbial activity for classification of soil health into broader categories. As the results proportionally correlate with soil organic carbon (correlation coefficient 0.6) and soil dehydrogenase activity (correlation coefficient 0.7), dosage of macronutrients (CNPK) is calculated based on principles of balanced fertilization. Fungicides are one of the most potent agrochemicals causing deleterious effects on soil health, rationalizing their use necessitates a test to assess the natural suppressive ability of soils towards crop-specific soil pathogens well before scheduled planting/sowing. The split agar assay is a novel agar diffusion assay to quantify the potential of soil microbes to produce antifungal metabolites and offers an integrated expression of suppressiveness as actidione equivalents per gram of soil. DRA/SAT techniques could transform application schedules of agrochemicals for effective improvement in crop productivity and soil health.

ABSTRACT (OEAM021) FEB 05, 14.15-14.25

COST EFFECTIVE SUBSTRATES FOR PRODUCTION OF BIOSURFACTANT USING STAPHYLOCOCCUS LENTUS AND EXPLORATION OF EXTRACTION METHODS

Harpreet Kaur, Seema Sangwan, Pankaj Sharma, Mukesh Kumar*
Department of Microbiology, CCS Haryana Agricultural University Hisar-125004, Haryana, India
*Email *seema_sangwan80@yahoo.co.in*

Biosurfactants are the surface-active biomolecules produced by a variety of microbes that play an imperative role in numerous fields. The commercial uses of biosurfactants in various industries like cosmetics, pharmaceutical, oil recovery, environmental sectors and interestingly in the agricultural sector are known well. Therefore, heavy research is underway including the use of low-cost substrates in promising amounts and media optimization strategies by exploring various extraction techniques. In the present study, different zero cost substrates such as waste mobile oil, used frying oil, molasses and whey were used for biosurfactant production under shaking conditions at 30 °C and 7 pH using mineral salt medium. Maximum biosurfactant production was achieved with whey at 10% (w/v) concentration as observed from oil displacement of 8.7cm after 5 days of incubation. Acidification of culture supernatant was executed for biosurfactant production. Culture supernatant was collected by centrifugation at 10,000 r/min for 15 min and the pH of the supernatant was adjusted in the range of 1-6 using 6 M HCl. pH has a direct influence on biosurfactant production as significant decrease in the values were observed with increasing pH. Maximum yield of crude biosurfactant was obtained at pH 2 (14 g/L) while values were minimal at pH 6 (9.4g/L). Therefore, the discovery of such a low-cost substrate with an optimized extraction process may account for the industrial production of biosurfactants.

ABSTRACT (OEAM022) FEB 05, 14.25-12.35

AN ACCELERATED METHOD FOR IN SITU DECOMPOSITION OF AGRICULTURAL WASTES: A NEED OF THE HOUR

V. Mageshwaran, Adarsh Kumar., Renu and A.K. Saxena*
ICAR-National Bureau of Agriculturally Important Microorganisms, Kushmaur, Mau, Uttar Pradesh-275 103, India
*Email *mageshbioiari@gmail.com*

Agricultural residues/Agro-residues are annually generated lignocellulosic biomass and available in large quantities. India contributes more than 30 % of global agricultural residues production. On an average, 1 to 2 tonnes of these residues are generated per hectare of land. In practice, these residues are burnt in the field which causes serious environmental problems including soil fertility deterioration and air pollution. In northern India, the burning of paddy stubble after harvest of paddy causes severe air quality deterioration and health hazards. The consistent efforts are being made by researchers, environmentalists and industrialists to explore the possible potential of biomass in food/feed/fuel/fine chemical/fertilizer application and to overcome the environmental problems caused by agro-residues. Among the various applications, the recycling of agro-residues in the field itself receives more attention due to nutrients balance in the environment and overcoming the logistics problem of biomass as seen in other applications. The lignin content varies with the type of residue and it is highly recalcitrant for decomposition. Thus, the use of suitable microbial consortium containing efficient lignocellulose degrading microbial strains become inevitable for rapid agro-residue decomposition especially under paddy-wheat cropping system in northern India where the window between the two crops is narrow and it is usually less than 25 days. Unlike conventional composting process, in situ method attempts to decompose the agro-residue after harvest per se without collection and heaping. In the present study, four different microbial consortia (C-I, C-II, C- III and C-IV) were applied to evaluate in situ decomposition of paddy stubbles at the farm of ICAR-NBAIM, Mau. The soil CO2 evolution was recorded at 10 and 20 days after application of microbial consortia. The results showed CO2 evolution was higher at 10 days and the maximum (14.52 mg of CO2 evolved per day) was recorded at C-II applied soil.

ABSTRACT (OEAM023) FEB 05, 14.35-14.45

CHARACTERIZATION AND PURIFICATION OF EXTRACELLULAR POLYMERIC SUBSTANCES (EPS) PURIFIED BY HALOMONAS SP. DK4: BIOSORPTIONAL PROPERTIES OF EPS COATED MAGNETIC MAGNETITE NANOPARTICLE FOR RAPID TREATMENT OF REAL CHROME ELECTROPLATING WASTEWATER

Vidhi Kalola, Chirayu Desai***
Department of Biological Sciences, P. D. Patel Institute of Applied Sciences, Charotar University of Science and Technology, CHARUSAT campus, Changa, Gujarat, India
*Email *vidhikalola93@gmail.com, **chirayudesai.bt@charusat.ac.in*

The extracellular polymeric substances (EPS) originated from Halomonas sp. DK4 was independently studied to explore its possible application in biosorption of Cr(VI). The maximum EPS production of 2.9 mg/L was noted when the bacterium was grown under optimized conditions at 30°C in modified minimal salt medium (MSM). The Box-Behnken response surface methodology showed a positive correlation of sucrose, yeast extract, and Cr(VI), with the production of EPS by Halomonas sp. DK4. In presence of Cr(VI) the EPS production in Halomonas sp. DK4 was enhanced by 23.36%. The purified EPS was thermostable with a degradation temperature (Td) of 300°C as determined using thermo-gravimetric analysis (TGA). A stable EPS coated magnetic nanoparticle with core Fe3O4 structure was developed and its adsorption efficiency compared to sole EPS was studied. The effects of various factors, such as pH, contact time and initial concentration of metal ions were also investigated. The adsorption isotherm model and adsorption kinetics were studied which showed that maximum adsorption of Cr(VI) at equilibrium using EMNPs (EPS coated magnetic nanoparticles) was 217.39 mg/g with a regression value of 0.96 and n>1. The results obtained using adsorption-isotherm modeling suggested that the EMNPs-Cr(VI) interactions are based on chemisorption mechanism which can be best described using the Langmuir isotherm model. The results of FT-IR analysis confirmed that the carboxyl, hydroxyl, alkyl group along with sugar monomers and carbohydrate moieties in the EPS were responsible for Cr(VI) adsorption. The energy dispersive X-ray analysis (EDAX) revealed the change in phosphate, sodium and potassium ions after Cr(VI) adsorption. In summary, the newly purified EPS from Halomonas sp. DK4 was found to be thermostable and soluble biopolymer with adhesive properties. In addition the results suggested the potential application of EPS coated nanoparticle having a remarkable capability for adsorption of Cr(VI) from industrial wastewater.

Keywords: Extracellular polymeric substances, Cr(VI), Box-Behnken design, magnetic nanoparticles, Adsorption isotherm models, Halomonas sp.

ABSTRACT (OEAM024) FEB 05, 14.45-14.55

BIOCONVERSION PROCESS FOR COMPOST PRODUCTION FROM AGRICULTURAL RESIDUE

*Kamla Malik *, Meena Sindhu, Sunita Rani*
Department of Microbiology, Chaudhary Charan Singh Haryana Agricultural University, Hisar-125 004, India
*Email *kamlamalik06@gmail.com*

Bioconversion of agricultural residual wastes into value added compost for enhancing crop productivity and improving soil health and attaining popularity among the farmers. Therefore, present investigation was carried out, microorganisms play an important role in the recycling of agricultural wastes for compost production. Cattle dung, biogas slurry and paddy straw had 14.86, 11.23 and 15.66% total solids with organic carbon 45.11, 40.13 and 50.42%, respectively. The C/N ratio was observed 35:1 in cattle dung, 34:1 in biogas slurry and 87:1 in paddy straw. The nitrogen content was 1.04, 1.0 and 0.62%, respectively in cattle dung, biogas slurry and Paddy straw. The C/N ratio dropped from 42.38 to 27.65 and maximum amount of humic acid was observed in T7 treatment after 60 days of composting. Volatile solids ranged from 60 to 67.7 % of TS in all treatments after 60 days of composting. There is definite need to intensify research on novel effective microorganisms to prepare high quality compost in a relatively shorter duration and new technologies for large-scale production.

Keywords: Bioconversion, Composting, Paddy straw, Cattle dung

ABSTRACT (OEAM025) FEB 05, 14.55-15.05

EVALUATION OF PSEUDOMONAS SP. FOR ITS MULTIFARIOUS PLANT GROWTH PROMOTING POTENTIAL AND ITS ABILITY TO ALLEVIATE BIOTIC AND ABIOTIC STRESS IN TOMATO (SOLANUM LYCOPERSICUM) PLANTS

*Shikha Gupta1, Sangeeta Pandey2**
1 Amity Institute of Biotechnology, Amity University, Noida, Uttar Pradesh-201313, India
2 Amity Institute of Organic Agriculture, Amity University, Noida, Uttar Pradesh-201313, India
*Email *spandey5@amity.edu*

1-Aminocyclopropane-1-carboxylate (ACC) deaminase activity is one of the most beneficial traits of plant growth promoting (PGP) rhizobacteria responsible for protecting the plants from detrimental effects of abiotic and biotic stress. The strain S3 with ACC deaminase activity (724.56 nmol α-ketobutyrate mg-1 protein hr-1) was isolated from rhizospheric soil of turmeric (Curcuma longa), a medicinal plant, growing in Motihari district of Indian state, Bihar. The halotolerant strain S3, exhibited optimum growth at 8% (w/v) NaCl. It also exhibited multiple PGP traits such as indole acetic acid production (37.71 µg mL-1), phosphate solubilization (69.68 mg L-1), siderophore, hydrocyanic acid (HCN) and ammonia production as well as revealed antagonism against Rhizoctonia solani. The potential of isolated strain to alleviate salinity stress in tomato plants was investigated through pots trials by inoculating strain S3 through-seed bacterization, soil drenching, root dipping as well as seed treatment + soil drenching. The strain S3 inoculated through seed treatment and soil drenching method led to improved morphological attributes (root/shoot length, root/shoot fresh weight and root/shoot dry weight), photosynthetic pigment content, increased accumulation of osmolytes (proline and total soluble sugar), enhanced activities of antioxidants (Catalase and Peroxidase) and phenolic content in salt stressed tomato plants. The biochemical characterisation, FAMEs analysis and 16S rRNA gene sequencing revealed that strain S3 belongs to the genus Pseudomonas. The overall findings of the study revealed that Pseudomonas sp. strain S3 can be explored as an effective plant growth promoter which stimulates growth and improves resilience in tomato plants under saline condition.

Keywords: ACC deaminase, Biofertilizer, Indole acetic acid, PGPR, Rhizosphere, Antioxidative enzymes

ABSTRACT (OEAM026) FEB 05, 15.05-15.15

ISOLATION, SCREENING, AND CHARACTERIZATION OF SAPONIN PRODUCING ENDOPHYTIC FUNGI FROM ROOTS OF ASPARAGUS RACEMOSUS

Monika Rani1,Sandeep Jaglan2, Vinod Chhokar1*
1Department of Bio and Nano Technology, Guru Jambheshwar University of Science and Technology, Haryana, India
2CSIR-Indian Institute of Integrative Medicine, Jammu 132001, J &K, India
*Email *monikapanwar35@gmail.com*

The aim of this study was to identify saponin producing endophytic fungi from the roots of Asparagus racemosus. A total number of 35 endophytic fungi were isolated out of which five fungi were found to efficiently saponin producing after screening. Identification was carried out by 18s rDNA sequencing. The crude extract of endophytic fungi was screened using HPLC for qualitative and quantitative analyses of saponin.Extract performed by high-performance liquid chromatography (HPLC) with diode array detector (DAD) detector on C18 column under isocratic mobile phase (30:70) elution at 231 nm. Maximum saponin was found in E.F-1 strain (5441.54 ng/mg). The crude extract of endophytic fungi also evaluated under FTIR and mass spectrometry and most similar bonding pattern with saponin standard was found in all five fungi. Antimicrobial activity detected by MIC well diffusion assay revealed that at 50µg/ml concentration of Y-2 crude extract shows antibacterial activity whereas in case of antifungal activity E.F-12 and E.F-7 showed best antifungal activity at 100µg/ml concentration.Antioxidant activity were detected by DPPH free radical method. The maximum antioxidant activity was exhibited by the E.F-7.

ABSTRACT (OIMB001) FEB 05, 10.30-10.40

INSIGHT INTO THE STRUCTURAL AND FUNCTIONAL ASPECTS OF OSMO/HALO-RESPONSIVE PROTEINS IN YEAST

Athira M Menon, Tikam Chand Dakal***
Genome & Computational Biology Lab, Department of Biotechnology, MohanlalSukhadia University, Udaipur 313001, Rajasthan
*Email *aathimenon143@gmail.com, **tikam260707@gmail.com, **tc.dakal@mlsu.ac.in*

Zygosaccharomyces rouxii is an osmo/halo-tolerant, yeast species especially found in high sugar/salty niches. Owing to the unavailability of crystal structures of transmembrane proteins, the genetic and molecular basis of phenotypic and fundamental diversity of the species is less understood. Modeling of these proteins is not done yet as conventional methods require an ultra-purified form of proteins which is a limiting factor for large transmembrane delicate fragment proteins. In this study, we have employed a multi-phasic computational biology approach to obtain high resolution, energy minimized, three-dimensional structures of transmembrane proteins involved in the cation homeostasis. Also, we scanned the promoter region of 50 osmo/halo- tolerant genes in Zygosaccharomyces rouxii to understand their distinct regulation during osmo or halo- stress condition. The primary structure of the proteins was retrieved and three-dimensional structures were constructed followed by atomic-level energy minimization and structural refinement. In their promoter region, we have focused on the stress regulatory elements (STREs), repetitive elements, and the transcription factor (TF) binding sites of the genes. On analyzing the promoter, we came to know that out of 50 genes analyzed, 18 genes possess STREs, 26 genes harbor tandem repeat sequences and 18 genes have transcription factor binding sites in their promoter region. Acknowledgment of these factors along with characterized ATP and ion binding sites suggested plausible functional impact which can lead to the development of a better understanding of the physiological mechanisms of tolerance against osmo/halo-stress in the genus Zygosaccharomyces.

ABSTRACT (OIMB002) FEB 05, 10.40-10.50

XYLANASE PRODUCTION BY FUNGI USING POST METHANATED DISTILLERY SPENT WASH

P. Mahla and N. Bhatt***
P.G. Department of Microbiology & Biogas Research Center, Faculty of Sciences & Applied Sciences, Gujarat Vidyapith, Sadra, Dist: Gandhinagar, Gujarat, India
*Email *priti.mahla@gmail.com, **bhattnikhil2114@gmail.com*

Melanoidin linked dark brown colored organically rich components possessing post methanated distillery spent wash is still objectionable after one-time anaerobic digestion. So, our study included that it could be used as a nutrient for xylanase production by fungi. Isolation of potent xylanase production fungi was from spent wash contaminated soil collected from different areas of South and North Gujarat, India. Nine different isolated fungi BPN1, BPN2, BPN3, BPN4, SPN1, SPN2, SPN3, SPN4 and SPN5 coded and were enriched by using potato dextrose agar and PMDSW amended medium. Among all, SPN2 was selected as potent fungi. The effect of several parameters on xylanase activity such as various carbon and nitrogen sources, moisture content, medium concentration, inoculums size, pH, temperature, metal ion, and incubation time were obtained as optimum conditions required for maximum xylanase activity. After optimization the SPN2 exhibited excellent xylanase activity.
Keywords: Xylanase, PMDSW, fungi, Melanoidin, Optimization

ABSTRACT (OIMB003) FEB 05, 10.50-11.00

BIO-BUTANOL PRODUCTION ON POST METHANATED WASTE WATER BY BATCH FERMENTATION

P. Aghera, N. Bhatt***
P.G. Department of Microbiology & Biogas Research Center, Faculty of Sciences & Applied Sciences, Gujarat Vidyapith, Sadra, Dist: Gandhinagar, Gujarat, India
*Email *agherapayal07@gmail.com, **bhattnikhil2114@gmail.com*

The huge amount of sugar industrial water is considered as waste water because it contains a high amount of carbohydrate source, high COD and toxic chemicals that can be converted into various different value added products by fermentation. The present work emphasizes on production of citric acid from treated distillery spent wash using lab scale biofermenter. Pre-treatment of distillery spent wash was studied in anaerobic digestion by a suspended growth system under varying hydraulic retention time (HRT) and organic loading rate (OLR) as well as physicochemical parameters. Anaerobic culture APBN5 was applied for butanol production using post methanated waste water as a raw fermentation medium and high amount of carbohydrate source. Potent strain APBN5 was identified by morphological, cultural and molecular characterization. For enhancement of butanol production was carried out in different nutritional and environmental parameters such as inoculum size (5 to 10 % v/v), incubation period (24 to 120 h), pH (4 to 7), temperature (25 to 40 °C), nitrogen source (organic and inorganic), yeast extract concentration (0.1 to 0.5 %). The detection of intracellular and extracellular enzymes activities indicated that the pyruvate carboxylation pathway was enhanced, which suggested carbon flux to butanol was redistributed in strains. Analysis of biosynthesized products by Gas chromatography. Initial sugar and consumed sugar determined by Anthrone and DNSA method and also estimated cell dry weight.

Keywords: Butanol, Fermenter, Distillery spent wash, Anaerobic reactor, Intracellular and extracellular enzymes

ABSTRACT (OIMB004) FEB 05, 11.00-11.10

CULTIVATION OF MICRO-ALGAE FOR EXTRACTION OF VALUABLE PRODUCTS: AN ADVANCEMENT IN ALGAL-REFINERY

Sanjeet Mehariya, Roberto Lavecchia, Antonio Zuorro*
Department of Chemical Engineering, Materials and Environment, Sapienza University, 00184 Rome, Italy
*Email *sanjeet.mehariya@uniroma1.it*

Microalgae is a photosynthetic organism, which can grow under different cultivation modes. These organisms synthesize various natural compounds, including β-carotene, lutein, astaxanthin, fatty acids during their growth phase, which have several human health benefits. Nowadays, the large-scale cultivation of microalgae for production of various bioactive compounds has gained significant interest due to commercial application in nutraceutical sector. For the enhancement of their exploitation, a sustainable cultivation and extraction method is fundamental to reach high productivity and extraction efficiency. Therefore, phototrophic cultivation offers numerous environmental advantages over mixotrophic and heterotrophic cultivation. Moreover, after the biomass cultivation efficient extraction methods need to be employed for complete recovery of intracellular compounds from harvested biomass. Thus, a well-known CO2 supercritical fluid extraction (CO2-SFE) technology can be used for extraction of intracellular compounds. CO2-SFE uses CO2 as a safe solvent and operates in mild conditions avoiding thermal degradation and light exposure to intracellular compounds. Also, CO2-SFE method is advantageous over solvent extraction due to reduction of solvent use, easy for compound purification and lesser extraction time with higher extraction yield. However, the CO2-SFE of carotenoids from microalgae have still needed to be enhanced the purity of extracted compounds. For the optimization of this technique, key parameters should be tested based on microalgae biomass characteristics. Therefore, this study summarizes the effect of different operative conditions for cultivation of microalgae and extraction of high value added chemicals from algal biomass. In summary, this study may allow for development of sustainable cultivation of microalgae biomass for efficient extraction of intracellular compounds, which have several industrial applications.

Keywords: Microalgae, high value-added compounds, CO2 mitigation, nutraceuticals and circular economy.

ABSTRACT (OIMB005) FEB 05, 11.10-11.20

DIVERSITY AND CHARACTERIZATION OF MODERATELY HALOPHILIC BACTERIA PRODUCING ALKALINE PROTEASE

Ami D. Varia1, Viral Y. Shukla1, Devayani R. Tipre2*
1Department of Microbiology and Biotechnology, School of Sciences, Gujarat University, Ahmedabad 380 009, India
1L.J. Institute of Applied Sciences, L.J. Campus, Between Sarkhej Circle and Kataria Motors, S.G. Road, Ahmedabad 382 210
2 Department of Microbiology and Biotechnology, School of Sciences, Gujarat University, Ahmedabad 380 009, India
*Email *amivaria89@gmail.com*

Haloalkaliphilic bacteria are a choice of bacteria and still progressively studied for their microbial and biotechnological potential to produce enzymes. These enzymes are extraordinarily stable and speedily working at alkaline pH, high temperature and higher salt applications. These adaptable specific features are alluring in various microbial fermentation and biotechnological industries. Basic need of salts for elemental growth is important for the operating of most of the metabolism tracks assembled by enzymes which make them appropriate for use in industrial operations that include high salts application. Production of haloalkaliphilic bacterial enzymes for industrial use, isolation and characterization of new rising strains using massive medium component source is a constant process. In this context the presented work was initiated. Haloalkaliphilic protease producing bacteria were isolated from saline soil samples collected from different areas of Bhavnagar and Uncha Kotda city, Gujarat. High protease producers were isolated and screened using haloalkaliphilic agar plate having 5% skimmed milk, 10% NaCl and medium pH of 10-10.5. Total 55 bacterial isolates were isolated and selected at the end of primary screening. The primary screening was done based on relative protease enzyme activity on the haloalkaliphilic agar medium plates at pH 10-10.5. Secondary screening was carried out at pH 9, 10, 11 and NaCl concentration 10%, 15%, 20%, 25%, 30% further 20 isolates were selected based on their haloalkaliphilic protease activity in the production medium for tertiary screening. Selected isolates showed haloalkaliphilic protease production between 41.4 to 283.1 U/mL at 48 h of incubation under 180 rpm shaking condition at room temperature (36±3 °C) in modified production medium at pH 11 and 20% NaCl concentration under the experimental condition. Diversity study of the isolates were also carried out in terms of colony morphology, cell morphology and biochemical characterization. Detailed results will be discussed.

ABSTRACT (OIMB006) FEB 05, 11.20-11.30

CHARACTERIZATION AND IMMOBILIZATION OF LIPASE PRODUCED FROM PSEUDOMONAS PLECOGLOSSICIDA S7

Prassan Choudhary1,3, Arpan Bhowmik2, Shaloo Verma1, Shilpi Srivastava3, Hillol Chakdar1, Anil Kumar Saxena1*
1Microbial Technology Unit-II, ICAR-National Bureau of Agriculturally Important Microorganisms, Maunath Bhanjan - 275103
2ICAR-Indian Agricultural Statistics Research Institute (IASRI), New Delhi - 110012, India
3Amity Institute of Biotechnology, Amity University, Uttar Pradesh-226028, India
*Email *hillol.chakdar@gmail.com*

Lipases are serine hydrolases that catalyze the conversion of triglycerides into glycerol and free fatty acids. It is due to this unique catalysis that lipases have applications in food, pharmaceutical, biofuel industries. In the present study, we characterized free and alginate immobilized lipase from Pseudomonas plecoglossicida S7. The lipase was active over a range of 30-50° C temperature and pH ranging from 7-10. The free enzyme did not show any activity in acidic pH. The enzyme was tolerant to various solvents like chloroform, methanol, 1-butanol, acetonitrile, dichloromethane (2% v/v) and retained 60% of its activity in the presence of Sodium Dodecyl Sulphate (0.5% w/v). The free enzyme, when immobilized onto Ca-alginate beads showed an improved activity of lipase over a temperature range of 20-60° C retaining 72% of its activity at 60° C. The bound enzyme retained its activity in acidic pH and showed relative stability (27-34% less activity) in presence of organic solvents (2% v/v). Such immobilized lipases can be used in detergent formulations, wastewater treatments, and biodegradation of oil in the environment.

Keywords: Lipase; Pseudomonas; Immobilization; Solvent stability

ABSTRACT (OIMB007) FEB 05, 11.30-11.40

PURIFICATION, CHARACTERIZATION AND FUNCTIONALITY ANALYSIS OF HIGH PURITY ANALYTICAL GRADE C-PHYCOCYANIN FROM NON-HETEROCYSTOUS CYANOBACTERIUM PHORMIDIUM SP. CCC 316 ISOLATED FROM RAJASTHAN, INDIA

Diya Roy and Sunil Pabbi*
CCUBGA, Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi-110012, India
*Email *diyaroyubkv@gmail.com*

C-Phycocyanin (C-PC) is a well known algal biopigment of industrial significance due to several valuable features and properties. However, these properties differ and are dependent on the strain and the environment from where the isolation has been done. Cyanobacteria found in extreme environmental conditions may serve as a desirable feedstock of phycocyanin from industrial perspective as it may have enhanced antioxidant activity because of the organism's ability to survive under stress conditions. But, its application is highly regulated by the downstream processing i.e extraction and purification of the pigment. In the current study, Phormidium sp. CCC 316 isolated from Rajasthan, India and maintained in germplasm of CCUBGA, IARI, New Delhi was evaluated for its phycocyanin content. Extraction through conventional freezing thawing method resulted in 0.402 mg/ml phycocyanin. Fractionation of the crude extract with 65% ammonium sulphate itself resulted in analytical grade purity of 4.25 with a recovery percentage of 95.32% and a final purity of 5.56 was obtained via anion exchange chromatography. Validation of purification was done by SDS-PAGE which showed two distinct bands of approximately 17 and 19 kDa representing α and β subunits of phycocyanin. Spectral analysis of phycocyanin depicted a single peak at 620nm and fluorescence emission spectrum of purified phycocyanin recorded a prominent peak at 645nm. Functional property in terms of antioxidant activity of phycocyanin showed 82.88 ± 0.63% free radical scavenging activity at 200 µg/ml of phycocyanin concentration as determined by DPPH assay. The study presents a potential cyanobacterial strain with high purity C-PC with very high antioxidant activity.

Keywords: Chromatography, Phycocyanin, Antioxidant, Cyanobacteria.

ABSTRACT (OIMB008) FEB 05, 11.40-11.50

OPTIMIZATION OF POLYHYDROXYBUTYRATE (PHB) PRODUCTION BY BACILLUS ENDOPHYTICUS MTCC 13038

Sweeta Soni, Vinod Chhokar, Vikas Beniwal, Mukesh Jangra, Hemlata Badgujar, Shruti Dudeja, Rohit Chauhan, Anil Kumar*
Department of Bio & Nano Technology, Guru Jambheshwar University of Science and Technology, Hisar, Haryana
*Email *sonigjust@gmail.com*

Polyhydroxybutyrate (PHB) is a natural, biodegradable polymer produced by several bacteria. It is accumulated in the form of carbon and energy reserve granules under certain nutrient limitations. Due to its enormous properties and environmental sustainability, PHB can be a suitable alternative to petroleum-based polymers. The present study aimed to isolate PHB producing bacteria and optimization of medium components to enhance PHB yield. Potent PHB accumulating bacterial strain was isolated from oil spilled soil. Sudan Black B staining method was used to detect PHB granules and affirmed by using Fourier Transform Infrared Spectroscopy (FTIR). The isolate was initially subjected to various standard biochemical tests such as Urease test, β- galactosidase activity test, Oxidase test and Catalase test, Nitrate reduction and various carbon sources utilization test followed by molecular characterization. Based upon 16S rRNA and phylogenetic tree analysis, the isolate was identified as Bacillus endophyticus. Combinations of various carbon sources and nitrogen sources were used to enhance PHB accumulation in which Glucose and Potassium nitrate were found effective. It was observed that PHB production was higher in the case of monosaccharide and low when the complexity of carbon sources increased. Bacillus endophyticus was found to accumulate up to 2.21g/L PHB when media was supplemented with glucose as a carbon and Potassium nitrate as a nitrogen source.

ABSTRACT (OIMB009) FEB 05, 11.50-12.00

YEAST MEYEROZYMA GUILLIERMONDII YK22 MEDIATED BIOSURFACTANT PRODUCTION USING LOW COST INDUSTRIAL WASTE AND ASSESSMENT OF ITS EXTRACTION METHODOLOGIES

Pankaj Sharma, Seema Sangwan, Harpreet Kaur and Mukesh Kumar*
Department of Microbiology, COBS&H, CCS Haryana Agricultural University, Hisar 125004, Haryana, India
*Email *seema_sangwan80@yahoo.co.in*

Biosurfactants are surface-active compounds produced by microorganisms such as bacteria, yeast and fungi. These offer lower toxicity, inherent good biodegradability and ecological acceptability over chemical surfactants. However, the industrial production of biosurfactants is still constrained owing to their higher production costs which could be dropped down by employing high yielding microbial strains and low cost substrates along with the proficient downstream processing methodologies. Present investigation was designed to produce biosurfactant by yeast Meyerozyma guilliermondii YK22 using dairy industry waste as a low cost substrate. The biosurfactant production was carried out under previously optimized cultural conditions and was evaluated in terms of oil displacement technique and emulsification index. The culture supernatant generated by yeast gave a maximum oil displacement of 8.2cm along with an emulsification index of 68% after five days of incubation. Surprisingly the yeast pellet retrieved after centrifugation also generated an oil displacement of 7.8cm along with an emulsification index of 64%. The biosurfactant extraction was carried out using five different methods namely acid precipitation, solvent extraction, ammonium sulfate and zinc sulfate precipitation by using the approach of activity-guided-fractionation. The method of acid precipitation was evaluated by acidifying the culture supernatant at different pH levels and it gave a maximum yield of 15.20g/L at the pH 3. However, the crude biosurfactants maintained their activity when retrieved using acidification of culture supernatant at other different pH ranges. The ammonium sulfate precipitation gave a maximum yield of 3.42g/L at the 30% saturation whereas the biosurfactant retrieved using zinc sulfate precipitation did not generate any oil displacement.

ABSTRACT (OIMB010) FEB 05, 12.00-12.10

CHARACTERIZATION OF TWO PROMOTERS FROM ZYMOMONAS MOBILIS AND THEIR FUNCTIONALITY IN E. COLI

Rohit Khandelwal, Preeti Srivastava, Virendra Swarup Bisaria*
Department of Biochemical Engineering and Biotechnology, Indian Institute of Technology, Hauz Khas, New Delhi, 110016, India
*Email *krohit.iitd@gmail.com*

Zymomonas mobilis is a Gram-negative ethanologen which possesses the Entner-Doudoroff pathway for carbon metabolism, and used for industrial production of bio-products. It produces high amount of ethanol with low biomass production which makes it useful for various product-targeted applications. But limited information on genetic tools in this bacterium has hindered the applicability to an extent. It is crucial to study promoters to understand gene expression in an organism. This study presents two promoters, Pchap and Pmpe from Z. mobilis which regulate the expression of chaperonin and metallophosphoesterase genes, respectively. Considering their important roles in cell viability, they were successfully characterized in E. coli. Further, their promoter strengths were checked at different pH and temperatures, which suggests their use for wide-range pH and temperature applications. These promoters will be used for expression of genes in Z. mobilis in future.
Keywords: Zymomonas mobilis, E. coli, Promoter, Chaperonin, Metallophosphoesterase.

ABSTRACT (OIMB011) FEB 05, 12.10-12.20

INVESTIGATION OF KRAFT LIGNIN DEGRADATION BY BACILLUS ARYABHATTAI SP. K13 ISOLATED FROM COMPOST

Kishor Sureshbhai Patil1,2, Jong-Chan Chae1*
1Division of Biotechnology, Jeonbuk National University, Iksan 54596, South Korea
2Department of Biological Sciences, P. D. Patel Institute of Applied Sciences, Charotar University of Science and Technology (CHARUSAT), Changa 388421, Gujarat, India
*Email *kspatelbt@gmail.com*

The bacterial strain Bacillus sp. K13 was isolated from the compost environment by enrichment of the Kraft lignin substrate. The ability of strain K13 to degrade Kraft lignin and a variety of aromatic carbon sources has been examined by series of laboratory-scale growth experiments in aerobic conditions. Structural characterization by SEM, FTIR, and XRD had revealed significant structural changes that appeared in surface morphology, functional group assignments and crystallinity of lignin polymer which confirmed depolymerization of a native compound has taken place by ligninolytic enzyme. The analysis of Kraft lignin degradation products by GC-MS analysis revealed the formation of low molecular weight aromatic compounds such as eugenol, 4-vinyl-guaiacol, acetovanillone, vanillin, vanillic acid, and guaiacol. Interestingly, all these compounds were a metabolic intermediate product of coniferyl monolignol type, belonging to (G) units of softwood lignin. Studies with mono-aryl lignin derivatives showed that strain could grow on almost all mono-aryl compounds. Vanillin was found to be the central metabolite in lignin metabolism. The metabolic pathway in lignin and coniferyl alcohol or ferulic acid had shared similar biochemical routes. Strain K13 displayed the adaptation of the mechanism to convert toxic phenolic compounds to less toxic forms to release metabolic stress of cell and produced a number of industrially important compounds. Together with its Kraft lignin depolymerization, high tolerance towards phenolic acids and biotransformation and product accumulation abilities, strain K13 represents a promising candidate for the biotechnological production of high market value products. Genomic analysis justified our findings, as putative peroxidase, phenolic acid decarboxylase were among the important functional genes detected in the genome along with the other aromatic compound degrading genes. Overall, this study demonstrates that the presence of a multiple-aromatic-catabolic bacterium as a “microbial sink” improves the extent of lignin depolymerization.

ABSTRACT (OIMB012) FEB 05, 12.20-12.30

EFFECT OF SHIITAKE (LENTINUS EDODES) MUSHROOM ON ANTI-INFLAMMATORY RESPONSE IN CARAGEENAN INDUCED RATS

Sujata Makkar1,2, Kiran Nehra1, Ajay Singh2*
1Department of Biotechnology, Deenbandhu Chhotu Ram University of Science & Technology, Murthal-131039, Sonipat, Haryana,
2Maharana Pratap Horticultural University (MHU) Regional Mushroom Research Centre, Murthal, Haryana, India
*Email *sujata.makkar@gmail.com*

Lentinula has immunomodulating properties. The objective of present study was to evaluate the anti-inflammatory effect of different strains of Lentinula edodes mushroom in relation to inflammation induced by Carrgeenan in rat’s model. In this study, 24 healthy young adult male rats aged 8 weeks were used. Rats were distributed into four cages containing six in each, in which Group I was control and treated with 1% CMC. Group II was inflammation induced by 0.1 ml of 1.0% carrageenan and Group III & IV rats were orally administered with single dose level 500 mg/kg of DMRO-34 and DMRO-356 strains of Lentinula edodes. The finding showed that there was significant enhance in the paw edema volume up to 8 hours in carrageenan induced group. The percentage enhancement of paw edema was found high in this group i.e. Group II. On other hand, Group III and IV rats, the paw edema volume was found low in comparison to carrageenan induced group. The highest inhibition of paw edema volume was found in DMRO-356 treated rats as compared to DMRO-34 treated rats. On the basis of the above findings, it is clear that the DMRO-356 is most effective for the management of inflammation in comparison to DMRO-34 of Lentinula edodes mushroom.

Keywords: Lentinula edodes; immunomodulating; inflammation; Carrgeenan; paw edema.

BIOFERMENTATIVE PRODUCTION OF D-LACTIC ACID FROM WHEY PERMEATE FROM CEESH MANUFACTURING INDUSTRY: A POLYMER FOR BIOPLASTIC PRODUCTION

Dipanjana Banerjee1, Nanthakumar Kuppanan1, Senthilkumar Sivaprakasam2, Banwari Lal1*
1Environmental and Industrial Biotechnology Division, The Energy and Resources Institute Lodhi Road, New Delhi -110003,
2Department of Biosciences and Bioengineering, BioPAT Laboratory, IIT Guwahati, Guwahati-781039, India
*Email *k.nanthakumar@teri.res.in*

Whey is the main by-product of cheese making industries, which is the liquid remaining after the milk has been curdled and strained. About 85-95% of the milk volume is cheese whey, retaining milk nutrients of about 55%; with high chemical COD and BOD, making it a threat to the environment. The most abundant nutrient of cheese whey is lactose which constitute about 4.5-5% w/v, followed by soluble proteins (0.6-0.8% w/v), lipids (0.4-0.5% w/v) and mineral salts (8-10% of dried extract). The whey permeate is used as a cheap source of raw material for the production of D (-) Lactic acid (DLA). More recently, production of optically pure DLA has received much importance due to the application of bioplastic in biomedical devices. Samples like cheese whey, fermented fruits and vegetables were collected for isolation of potential Lactobacillus strains, which were initially isolated based on the cultural, physiological and biochemical characteristics followed by 16s rRNA identification. Fermentation media was prepared using cheese whey permeates as the carbon source to find the strain which has more potentiality in the production of DLA. One strain from Mozzarella cheese water showed high optically pure DLA production of 98.9 with the yield of 0.12 g of lactic acid/g of lactose. Response surface methodology-central composite design (RSM-CCD) is used to find out the optimum condition for DLA production. For the set of experiments, the conditions which were chosen are cheese whey permeate, yeast extract, pH and inoculum size. All the experiments were conducted in a shaker incubator with fermentation temperature at 37°C for 72 hours. The maximum DLA concentration under optimum experimental condition was found to be 8.15 g/L. The DLA production is further studied under up-scale production using whey permeate.

A STUDY ON CILIATE DIVERSITY OF DELHI USING TRADITIONAL MICROSCOPIC AND MODERN MOLECULAR METHODS

*Jeeva Susan Abraham 1 , S. Sripoorna 1 , Swati Maurya 1 , Utkarsh Sood 2 , Vipin Gupta 3 , Rup Lal 2 , Renu Gupta 4 , Ravi Toteja 1 , Seema Makhija 1 **

1 Ciliate Biology Laboratory, Acharya Narendra Dev College, University of Delhi, Delhi, India

2 The Energy and Resources Institute, Delhi, India

3 PhixGen Private Limited, Gurugram, India

4 Maitreyi College, University of Delhi, Delhi, India

*Email *jeeva18.SA@gmail.com, **seemamakhija@andc.du.ac.in*

Ciliates are single-celled eukaryotic microorganisms exhibiting unique structural and functional features. Ciliates are present in freshwater, marine, and soil ecosystems. They are an integral part of the microbial loop as they function as recyclers and remineralizers of the organic material and also prey upon the bacteria and smaller protists thereby maintaining the ecosystem balance. The study of ciliate diversity is important in managing and maintaining ecosystems. Diversity reports from the freshwater bodies of Delhi are scarce. In the present study, ciliates from three freshwater bodies from Delhi namely, Okhla Bird Sanctuary (OBS), Sanjay Lake (SL), and Raj Ghat pond (RJ) were identified using traditional microscopic and modern molecular biological methods. Microscopic methods include live-cell observation, Protargol staining, wet silver nitrate staining, and Feulgen staining. About 48 species belonging to 8 classes, 16 orders, 28 families, and 38 genera were identified on the basis of classical methods. Maximum diversity was observed in the OBS site and maximum species were reported from the class Spirotrichea. Molecular analysis like DNA metabarcoding approach was used in the present study. The V4 region of 18S rRNA gene was used as a barcode to decipher the ciliate diversity in the environmental DNA samples. Using this method one class of ciliates and about 11 unidentified species were additionally observed. Though, about 22 species observed by the microscopic method were not observed by the metabarcoding approach. Hence, it is suggested to integrate both traditional and molecular methods to have 'total evidence' about ciliate diversity.

SPECIES DELIMITATION USING INTEGRATIVE TAXONOMY:CASE STUDY OF STYLONYCHIA NOTOPHORA SENSU SAPRA AND DASS 1970

Harpreet Kaur1, Shashi2, R. K. Negi1*, Komal Kamra2*

1Department of Zoology, University of Delhi, Delhi, India

2 Ciliate Biology lab, SGTB Khalsa College, University of Delhi, Delhi, India

*Email *hk2171@gmail.com*

Advancements in the classical and molecular approach in species delimitation has resulted in accurate descriptions and resolution of synonymous species. Taxonomic status of the spirotrichean ciliate species reported from India, Stylonychia notophora sensu Sapra and Dass 1970, has been questioned several times stating that it is not S. notophora Stokes 1885 but is an Indian population of Tetmemena pustulata (Müller, 1786) Ehrenberg 1835, but this has never been confirmed due to lack of detailed description. In the present study, an integrative approach has been used to characterize six populations of Tetmemena sp. isolated from different locations along the River Yamuna which were similar in morphology to Stylonychia notophora sensu Sapra and Dass 1970. Intra-clonal variations and inter population variations in inter-cirral distances and positional coordinates of cirri among six populations were similar. Based on the comparisons among these populations with previous descriptions of T. pustulata and S. notophora sensu Sapra and Dass 1970, minor morphological variations were observed. Morphogenetics stages were also similar. Inter population variations in pairwise distances based on 18S rDNA and variations found between S. notophora and T. pustulata ranged from 0.1-2.1%. In phylogenetic analyses based on 18S rDNA, all six populations of Tetmemena sp. from the present study showed polytomy with other available sequences of S. notophora and T. pustulata and clustered within Tetmemena pustulata vorax complex. Evidence from the present study support the contention that S. notophora sensu Sapra and Dass 1970 is a T. pustulata population and not S. notophora Stokes 1885.

PHARMACOLOGICAL EVALUATION OF SOME PLANT DERIVED NATURAL INGREDIENTS AGAINST SARS-COV-2 INFECTION

*Bhanupriya Dhabhai, Athira M Menon, Tikam Chand Dakal**
Genome and Computational Biology Lab, Department of Biotechnology, Mohanlal Sukhadia University, Udaipur
Email bhanupriyadhabhai@gmail.com, tc.dakal@mlsu.ac.in

The novel coronavirus, SARS-CoV-2 infected by a new strain of human coronavirus has engulfed the whole globe with its vicious potential to eradicate humankind. The pandemic has emerged from the Wuhan provinces of China with high transmissibility. Researchers are rushing to discover vaccines and drugs for the disease which is not known yet. In this study, we have focused on the in-silico screening of phytochemicals occurring naturally in plant extracts that could possibly interact with Receptor binding Motif (RBM) of spike protein and thereby inhibit virus-cell interaction. In this study, we have taken 100 phytochemicals that have been studied in various viral interactions and have shown antiviral properties. Initially, these compounds were analysed based on their physicochemical and pharmacokinetic properties, biological activities, possible target interactions, similar compounds in humans, and gene regulations and were filtered out based on immunobiological activities and expression of genes involved in cytokine storm regulation and immunostimulation. Further, they were docked with the RBD domain of spike protein in the SARS-CoV-2. We observed that two phytochemicals namely, orientin and apigenin interact directly in the receptor-binding motif of the spike protein. These phytochemicals were also screened for their pharmacokinetics and physicochemical activities which make sure that the compound holds efficient drug-like properties. This could be a robust test of an iterative framework of inhibiting virus- receptor interaction with the help of phytochemicals.Keywords: Phytochemicals, SARS-CoV-2, Pharmacokinetics, Molecular Docking

ABSTRACT (OMP001)

FEB 05, 14.15-14.25

SALMONELLA STRAIN SPECIFICITY DETERMINES POST-TYPHOID CENTRAL NERVOUS SYSTEM COMPLICATIONS: INTERVENTION BY LACTIPLANTIBACILLUS PLANTARUM AT GUT-BRAIN AXIS

*Amrita Kaur1, Kanwaljit Chopra2, Indu Pal Kaur2, Praveen Rishi*1*
1Department of Microbiology, Panjab University, Chandigarh, India;
2University Institute of Pharmaceutical Sciences, Panjab University, Chandigarh, India
Email amritakaurvirdi@gmail.com

Neurological complications occurring due to Salmonella infection in some typhoid patients remain a relatively unexplored serious complication. This study firstly aimed to explore whether disseminative ability of Salmonella from gut to brain is strain specific or not and on the basis of bacterial load, histopathology, and behavioral changes, it was observed that Salmonella enterica serovar Typhimurium NCTC 74 did not cause brain infection in murine model in contrast to Salmonella Typhimurium SL1344. Simultaneously, alarming escalation in antimicrobial resistance, making the existing antibiotics treatment inefficacious, prompted us to evaluate other bio-compatible strategies as a potential treatment option. In this context, the role of gut microbiota in influencing behavior, brain neurochemistry, and physiology by modulating key molecules associated with gut-brain axis has captured the interest of the scientific community. Followed by in vitro screening of potential probiotic strains for beneficial attributes, efficacy of the selected strain was systematically evaluated at various levels of gut-brain axis against Salmonella induced brain infection. Analysis of behavioral (depression, anxiety, and locomotor), neurochemical [gamma amino butyric acid and acetylcholinesterase (AChE)], neuropathological (brain and intestinal histology; bacterial burden), and immunohistochemical studies (tight junction proteins expression) revealed its role in preventing serious manifestations and proving its potential as “psychobiotic.” To the best of our knowledge, this is the first report elaborating strain specificity of Salmonella in causing post-typhoidal neurological manifestations and simultaneous use of probiotic in managing the same by influencing the pathophysiology at gut-brain axis.

ABSTRACT (OMP002)

FEB 05, 14.25-14.35

DIRECT-DIFFERENTIAL SLIDE AGGLUTINATION ASSAY FOR BRUCELLA DETECTION USING ANTIBODY CONJUGATED WITH FUNCTIONALIZED GOLD NANOPARTICLES

*Richa Hans1, Duraipandian Thavaselvam **
1 Division of Biodetector Development Test and Evaluation,Defence Research and Development Establishment, Defence Research and Development Organization, Jhansi Road, Gwalior, Madhya Pradesh, 474002 – India
*Email *dtselvam@drde.drdo.in*

Brucellosis is caused by Brucella which is an endemic, re-emerging and highly infectious bacteria causing zoonosis world-wide. It belongs to class ‘Alphaproteobacteria’ and is intracellular, facultative, gram-negative coccobacilli infecting both livestock and humans. Among Brucella species, most infectious are Brucella abortus, Brucella melitensis, Brucella canis, Brucella suis and Brucella ovis. It is known as potential bio-threat agent and preferentially transmits through occupational, food-borne and re-creational routes. In our present study, we have developed a direct-differential slide agglutination assay using polyclonal antibody (pAbs) derived against rOmp28 recombinant outer membrane protein of Brucella melitensis 16M. Highly sensitive and specific, affinity purified IgG pAbs were bio-conjugated with Gold Nanoparticles (AuNps) using N-(3-Dimethylaminopropyl)-N’-ethylcarbodiimide hydrochloride (EDC) and N-Hydroxysuccinimide (NHS) for WC detection of Brucella at detection limit (LOD) of 104 CFU mL-1. Standard ‘Turkevich Method’ was used for preparing AuNps of 50 nm particles size at an absorbance peak of 523 nm and characterized using SEM-EDAX and TEM with indexed polycrystalline SAED patterns. For chemical analysis, Fourier Transform Infrared Spectroscopy (FTIR) and X-Ray Diffractions (XRD) were performed. Functional capping and linking (1% Tri-Sodium Citrate, Sodium Borohydride along with self-assembled monolayer’s producing 16-Mercaptohexadecanoic acid) of AuNps allowed enhanced amine-coupling of antibodies with nanoparticles for binding affinity. On evaluation, no cross-reactive agglutinations were observed with 26 closely related bacterial species and specificity of the assay was validated using spiked clinical and non-clinical matrices. For sensitivity, 9 standard species of Brucella were tested and positive agglutinations were obtained at LOD of 104 CFU mL-1. Hence, the developed assay is easy to perform and can detect intact WC of Brucella more rapidly in comparison to S-ELISA with minimum time of performance, high capacity for multiple sample screening, cost-effective, offers no false positive/negative results and requires minimum 5 to 10 minutes for direct agglutination in early disease detection and diagnosis.
Keywords: ‘Brucella’; ‘Brucellosis’; ‘Agglutination’; ‘Gold-Nanoparticles’; ‘Whole Cell Detection’.

ABSTRACT (OMP003) FEB 05, 14.35-14.45

DEVELOPMENT OF SYBR GREEN BASED REAL TIME PCR ASSAY FOR MOLECULAR DIAGNOSIS OF BURKHOLDERIA PSEUDOMALLEI

*Pranjal Kumar Yadav, Duraipandian Thavaselvam**
Division of Biodetector Development Test and Evaluation, Defence Research and Development Establishment, Defence Research and Development Organization, Jhansi Road, Gwalior, Madhya Pradesh – 474002, India.
*Email *dtselvam@drde.drdo.in*

Burkholderia pseudomallei is a soil-borne β-proteobacteria and causal organism of melioidosis. Melioidosis is a fatal endemic disease with a high mortality rate accounts for nearly 89,000 deaths around the globe annually. Specific and early diagnosis of the pathogen is a crucial factor in disease control and prevention. The present study was designed to identify a novel sequence and the development of specific and sensitive molecular assay for B. pseudomallei detection. Initially, a unique and conserved 287 base pair region within the gene BPSL1655 of B. pseudomallei was identified. This novel target was used for the SYBR Green based real-time PCR assay development. The developed real-time PCR assay was highly sensitive and could detect 23 fg of genomic DNA, equivalent to 3 GE copies of B. pseudomallei per reaction. The developed assay can detect up to 14 whole cells of B. pseudomallei spiked in water. In artificially spiked human whole blood, this assay could detect 28 CFU per reaction of B. pseudomallei and no cross reactivity was observed with human blood DNA. Further, this assay was highly specific as tested positive for four standard strains, ten clinical isolates and four soil isolates of B. pseudomallei and no amplification was observed with twenty five other closely related and non-related species. Hence, the real-time PCR assay developed in this study targeting a novel sequence can be successfully applied for the detection and discrimination of B. pseudomallei from other related and non-related species.

Keywords: Burkholderia pseudomallei, Melioidosis, Molecular Diagnosis, SYBR Green Real-Time PCR

ABSTRACT (OMP004) FEB 05, 14.45-14.55

ENDOPHYTIC ACTINOBACTERIA ASSOCIATED WITH BRYOPHYLLUM PINNATUM (LAM.) OKEN: ISOLATION AND ASSESSMENT OF THEIR ANTIMICROBIAL ACTIVITY

Sujata Yadav and A. K. Gupta**
**Microbiology Research Laboratory, School of Studies in Life Science,Pt. Ravishankar Shukla University, Raipur-492010, Chhattisgarh, India*
Email yadavsujata1892@gmail.com, akguptarsu@gmail.com***

Endophytic actinobacteria represent one of the proven pharmaceutical resources and extremely versatile producers of bioactive natural products to combat frequently emerging multidrug-resistant (MDR) pathogens. Thus, in the present study endophytic actinobacteria associated with different parts of Bryophyllum pinnatum were isolated and screened for potential utilization of their antimicrobial activity. Total ten isolates were obtained, five, three and two from root, leaves and stem respectively. Antibacterial activity of all the isolates were screened against eight clinical and eight MTCC bacterial pathogens by cross streak method. Among the ten isolates, three exhibited antagonistic activity against both Gram positive and negative pathogens whereas one isolate exhibited inhibitory activity against Gram positive pathogens. Out of four potent isolates, BpR-4GER from root of Bryophyllum pinnatum showed the highest antibacterial activity against clinical as well as MTCC bacterial cultures. The screening results infer possibility of high antibacterial activity of the endophytic actinobacteria isolated from Bryophyllum pinnatum. The studies at hand will envisage further conferment.

ENDOPHYTIC RARE ACTINOALLOTEICHUS CYANOGRISEUS SIR5 (MK793584) FROM MEDICINAL WEED SPHAERANTHUS INDICUS LINNAEUS: ANTIMICROBIAL EFFICACY AGAINST DRUG RESISTANT HUMAN PATHOGENS

Geetika Wag, Ashwini Kumar Gupta*
Microbiology Research Laboratory, School of Studies in Life Science, Pt. Ravishankar Shukla University, Raipur-492010, Chhattisgarh, India
*Email *geet.mun08@gmail.com*

The emergence of antibiotic resistance in infectious microorganisms is currently imposing serious medical issues worldwide. To address this problem, our research aimed to look for endophytic actinobacteria, which could be a significant source of efficient antibiotics. In our study, endophytic actinobacteria SIR5 was isolated from roots of Sphaeranthus indicus Linnaeus and its 16S rRNA sequence revealed 100% similarity with Actinoalloteichus cyanogriseus DSM 43889 AUBJ01000042. The gene sequence of A. cyanogriseus SIR5 was submitted to NCBI, which verified and assigned an accession number, MK793584 to the organism. A. cyanogriseus, a rare actinobacteria, has been reported as an endophyte for the first time in this study. The antimicrobial potential of A. cyanogriseus SIR5 was tested against 20 human pathogens including both Microbial Type Culture Collection (MTCC) and Clinical Cultures (CC) and it was found to be effective against 16 pathogens. Significant zone of inhibition were recorded against CC E. coli (15.33±0.33 mm), MTCC B. subtilis (13.33±0.16 mm), MTCC P. aeruginosa (13.33±0.33 mm), MTCC S. epidermidis (12.33±0.33 mm), CC Candida albicans (12.83±0.44 mm), CC B. cereus (12.16±0.16 mm), CC S. epidermidis (11.50±0.28 mm) and MTCC B. cereus (11.16±0.16 mm). Antimicrobial potential of A. cyanogriseus SIR5 was enhanced by optimization using one factor at a time (OFAT), and increased antibiotic production was achieved with modified ISP-4 medium (starch-1% w/v, ammonium nitrate-1% w/v, calcium carbonate-2g/l, dipotassium phosphate-1g/l, magnesium sulphate-1g/l, sodium chloride-1g/l, trace solution-1ml/l) with inoculum size-13%, incubation period-16 days, pH- 8.0 and temperature- 28oC.

ANTIMICROBIAL AND ANTI-BIOFILM ACTIVITY OF GREEN SYNTHESIZED ZNO NANOPARTICLES AGAINST ESBL PRODUCING AND BIOFILM FORMING UROPATHOGENS

*Renu Jagdish and Kiran Nehra**
Deenbandhu Chhotu Ram University of Science and Technology, Murthal, Sonipat, Haryana
*Email *nehrakiran@gmail.com*

UTIs are among the most common and the most neglected infections worldwide. More recently, it has been observed that an imprudent usage of antibiotics has been leading to a rapid rise of antimicrobial resistance among uropathogens. Most of these resistant strains have been observed to be ESBL (Extended Spectrum Beta Lactamases) producers and biofilm-formers that make the major antibiotics, viz., β- lactams, cephalosporins, and fluoroquinolones ineffective against these uropathogens. Such highly multi-drug-resistant (MDR) uropathogens need to be dealt with alternative therapeutic measures so that the mortality and morbidity caused by UTIs can be limited. In this direction, ZnO nanoparticles which have been enlisted as GRAS (generally recognized as safe) by US FDA have been observed to hold a high potential. In the present study, the authors collected ESBL and biofilm-producing clinical uropathogens and synthesized ZnO nanoparticles against these by green synthesis method using Bryophyllum pinnatum plant leaf extract. Various analytical techniques including UV-Vis spectroscopy, FTIR and XRD were used for characterization of these nanoparticles. The synthesized nanoparticles act by binding to the plasma membrane of the pathogenic microbes and result in the inhibition of crucial life-saving mechanisms of the cell, and thus cause death of the pathogenic cells. ZnO nanoparticles synthesized in the present study were found to exhibit high antibacterial and anti-biofilm activity against both ESBL-producing and the biofilm-forming uropahogens. Thus, based on the present study, the authors concluded that ZnO nanoparticles can be used as alternate antimicrobial agents for curing UTIs.

Keywords: Antimicrobial resistance, Biofilm, ESBL, MDR, UTI

ABSTRACT (OMP007)

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NOVEL VALIDATED CARBAPENEMASE INHIBITORS ACTIVE AGAINST CLINICAL KPC-2 PRODUCING STRAINS

*Perwez Bakht1, Mangal Singh1 *, Marc Boomgaren2, Annette Bayer2 , Hanna-Kirsti S Leiros3, Ranjana Pathania1*
1Department of Biotechnology, Indian Institute of Technology Roorkee, Roorkee 247667, India.
2Department of Chemistry, Faculty of Science and Technology, UiT The Arctic University of Norway, N-9037 Tromsø, Norway
3The Norwegian Structural Biology Centre (NorStruct), Department of Chemistry, Faculty of Science and Technology, UiT The Arctic University of Norway, N-9037 Tromsø, Norway
Email perwezbakht@gmail.com

Antimicrobial resistance (AMR) is the propensity of microorganisms to grow despite exposure to their inhibitory substances, which is the major global health concerns. Bacteria have evolved sophisticated mechanisms of drug resistance to avoid killing by antibiotics such as target site mutation, overexpression of drug resistance of efflux pumps or antibiotics degrading enzymes. Carbapenemases are an example of such antibiotic inactivating enzymes that confer bacteria the ability to resist the action of carbapenems, the last resort antibiotics. Klebsiella pneumoniae Carbapenemase-2 (KPC-2) is the most widespread and swiftly disseminating carbapenemases in gram-negative pathogens that are associated with high mortality and morbidity in the clinic. There is an urgent and continuing need to look for strategies and identify inhibitors against these notorious enzymes. The overall aim of the study was to develop inhibitors against carbapenemases. Based on the molecular docking and crystal structure information available of KPC-2 with phenylboronic acids, six phenylboronic acid derivatives were synthesized and validated with biophysical and structural characterization using SeeSAR software. Furthermore, these compounds were tested for synergistic combination study with meropenem for inhibitory activity against clinically relevant strains harbouring KPC-2 (K. pneumoniae ATCC 1705 and K. pneumoniae K47-25). Some of the compounds displayed an excellent reduction in MIC of meropenem by 512 fold against the tested KPC-2 producer strains. We attempted to gain more insight into the mechanism of action of these compounds by conducting detailed kinetic characterization of their interaction with purified KPC-2. These compounds were also shown to be potent progressive inactivators of KPC-2 with nanomolar (nM) range of IC50, fast rate of acylation (Kon) and slow rate of deacylation (Koff) corresponded to longer residence time confirming the mode of action as KPC-2 inhibition. This is a significant leap towards the availability of an inhibitor that is likely to help in the effective treatment of resistant infections in the long run.

ABSTRACT (OMP008)

FEB 05, 15.25-15.35

MODULATION OF STREPTOCOCCUS MUTANS BIOFILM GROWTH BY LACTOBACILLUS RHAMNOSUS

Niranjan, Rashmi a, Dubey, Amrita a, Agrawal, Guncha b, Patil, Sachin b, Locha b, Bimlesh b, Priyadarshini, Richa a ***
a Department of Life Sciences, Shiv Nadar University, NH9 Tehsil Dadri, Greater Noida, Uttar Pradesh, 201314, India
b Department of Chemistry, Shiv Nadar University, NH9 Tehsil Dadri, Greater Noida, Uttar Pradesh, 201314, India
*Email *rn161@snu.edu.in, ** richa.priyadarshini@snu.edu.in*

Streptococcus mutans is facultative anaerobic coccus commonly found in the human oral cavity being highly efficient at forming biofilms contributing significantly to cariogenesis. Previous studies have suggested use of lactobacillus and bifidobacteria as probiotics preventing the biofilm formation by S. mutans. The objective of this study is to evaluate the inhibitory effect of antimicrobial compounds produced by Lactobacillus rhamnosus on S. mutans biofilm formation. For this, rhamnosus was screened by coculturing with S.mutans and static biofilm of S. mutans was seeded with L. rhamnosus. Crystal violet quantification method was used for biofilm quantification. Our results show inhibitory effect with L. rhamnosus cells when co cultured with S. mutans. Use of cell free supernatant of lactobacillus on S. mutans showed similar inhibitory effect. Lactobacillus species are known to produce organic acid causing pH reduction, which might be the cause of biofilm inhibition. To eliminate we used pH adjusted conditional medium, which also recapitulated the phenotype. Phase separation of cell free supernatant was performed. Organic phase showed increased antibiofilm activity in comparison to aqueous phase. To understand which genes are being affected by our metabolite, gene expression studies were performed by qPCR with lactobacillus treated and untreated S. mutans cells. The expressions of genes involved in TCSTS, quorum sensing, EPS formation and cell surface adhesins was down regulated in rhamnosus treated S.mutans cells. Our data indicates that lactobacillus species is probably producing a small organic molecule which may be responsible for biofilm suppression of S. mutans

Keywords: Streptococcus mutans; Biofilm inhibition; Lactobacillus rhamnosus; antibiofilm; qPCR

ABSTRACT (OMP009) FEB 05, 15.15-15.25

ROLE OF HORIZONTAL GENE TRANSFER AND IS6110 TRANSPOSITION IN THE EVOLUTION OF CRISPR-CAS SYSTEM IN MYCOBACTERIUM TUBERCULOSIS

Anoop Singh1, Mohita Gaur1, Vishal Sharma1, Palak Khanna1, Ankur Bothra2, Asani Bhaduri3, Anupam Kumar Mondal2, Debasis Dash2, Yogendra Singh1**, Richa Misra1,4****
1Department of Zoology, University of Delhi, Delhi, India,
2CSIR-IGIB, Sukhdev Vihar, Mathura Road, New Delhi, India,
3Cluster Innovation Centre, University of Delhi, Delhi, India,
4Department of Zoology, Sri Venkateswara College, University of Delhi, Delhi, India
*Email *anoop1792@gmail.com, **ysinghdu@gmail.com, ***richa.1403@gmail.com*

Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) and CRISPR-associated (Cas) genes are conserved genetic elements in many prokaryotes including Mycobacterium tuberculosis, the causative agent of tuberculosis. Although the knowledge of CRISPR locus variability has been utilized in M. tuberculosis strain genotyping, its evolutionary path in Mycobacteriaceae is not well understood. In this study, we have performed a comparative analysis of 141 mycobacterial genomes and identified the exclusive presence of the CRISPR-Cas type III-A system in M. tuberculosis complex (MTBC). Our global phylogenetic analysis of CRISPR repeats and Cas10 proteins offers evidence of horizontal gene transfer (HGT) of CRISPR-Cas module in the last common ancestor of MTBC and Mycobacterium canettii from a Streptococcus-like environmental bacterium. Additionally, our results show that the variation of CRISPR-Cas organization in M. tuberculosis lineages, especially in Beijing sub-lineage of lineage 2, is due to the transposition of insertion sequence (IS) 6110. The direct repeat (DR) region of CRISPR-Cas locus acts as a hotspot for IS6110 insertion. We show in M. tuberculosis H37Rv that the repeat at 5' end of CRISPR1 of forward strand is an atypical repeat made up partly of IS-terminal inverted repeat and partly CRISPR DR. By tracing an undetectable spacer sequence in DR region, the two CRISPR loci could be theoretically joined to reconstruct the ancestral single CRISPR-Cas locus organization, as seen in M. canettii. This study retracing the evolutionary events of HGT and IS6110-driven genomic deletions helps better understand the strain-specific variations in M. tuberculosis lineages.

ABSTRACT (OMP010) FEB 05, 15.45-15.55

MODULATION OF STREPTOCOCCUS MUTANS BIOFILM GROWTH BY LACTOBACILLUS RHAMNOSUS

*Surbhi Agarwal, Garima Sharma, Kavita verma, Vartika Mathur**
Animal-Plant Interactions Lab, Department of Zoology Sri Venkateswara College, Dhaula Kuan, New Delhi-110021, India
*Email *vmathur@svc.ac.in*

In various parts of the world, ants are consumed either in the form of nutrient and protein rich diet or as a source of medicine provided by traditional healers. These ants, similar to other animals, form mutualistic relationship with the microbes that live inside them as endosymbionts. Endosymbionts perform several crucial functions in their host such as digestion, nutritional upgrading, nitrogen recycling and pathogen defence. However, some of these microbes may be harmful to human beings due to their pathogenic nature. For example, a number of endosymbionts found in insects confers antimicrobial resistance (AMR) in humans. Our study on the gut microbiome of Oecophylla smaragdina (red weaver ant) suggests that this ant harbours many species that may be pathogenic to humans and may confer antimicrobial/ multidrug resistance (MDR). Metagenome analysis of Oecophylla revealed that 18 isolates belonging to the classes Gammaproteobacteria, Actinobacteria, Bacilli, Alphaproteobacteria and Bacteroidia have AMR/MDR, with resistance to many antibiotics including vancomycin, cephalosporin and quinolones. Direct or indirect contact by humans (through food, air, water, soil) with such microbes leads to increased morbidity and mortality as well number of hospitalizations depending on the severity of infection. This study, thus, discusses the role of such endosymbionts in transmitting AMR to humans and the risk in direct consumption of ants either as food or medicine.

ABSTRACT (OMP011) FEB 05, 15.55-16.05

RUTIN CAPPED COPPER NANOPARTICLES EXERT POTENT ANTIBIOFILM EFFECT AGAINST KLEBSIELLA PNEUMONIAE AND CURTAIL PLANKTONIC GROWTH IN ZEBRAFISH INFECTION MODEL

*Anvesh Ganta**1, Sankar Mahesh R1, Subhasree V 1, Swetha S1, Robert Lotha1****
*All the authors have equally contributed.
1 *Robert Lotha, Department of Chemistry, School of Chemical and Biotechnology, SASTRA Deemed to be University, Thanjavur, Tamil Nadu-613401, India,
Email **anveshganta1@gmail.com *** robertngullie1@gmail.com

Rutin a common dietary flavonoid known to have diverse therapeutic properties are being exploited in human medicine for antimicrobial, antiallergic, anti-inflammatory, antiproliferative, and anticarcinogenic properties. In our present study, Rutin was isolated from Elsholtzia griffithii and was capped on copper nanoparticle (Rutin@CuNPs), by a biogenic nanoparticle synthesis1. The fabrication of Rutin@CuNPs was confirmed using UV-visible spectroscopy and XRD. The morphological characterization was achieved using FE-SEM, TEM image, HR TEM and SAED for the crystalline nature of the Rutin@CuNPs whereas surface charge and stability of Rutin@CuNPs were determined by Zeta potential respectively. The amount of Cu (II) ions released in the presence of Klebsiella pneumoniae was determined by Alizarin Red Assay. The enhanced antimicrobial/antibiofilm potential of Rutin@CuNPs to curtail the planktonic cells/ biofilm formation was quantified through MIC/MBC/MBIC at 4/32/2 (µg/mL)1,2. Time kill kinetics indicates the deceleration phase of the K. pneumoniae. Image captured from crystal violet staining and fluorescence imaging shows > 50% inhibition of biofilm formation at sub MIC. The morphology and bacterial adhesion under SEM image depicted no microcolony formation in the treatment group. Mechanistic studies showed, statistically significant changes in hydrophobicity nature, alteration in membrane permeability potential of bacterial cells and the release of reactive oxygen species. In vivo zebrafish infection study showed ~3 log fold reduction in CFU and further confirmation with histopathology indicated no severe damage of liver cells.
Keywords: Anti-Microbial resistance (AMR), synergistic approach, Nanoparticles, Zebra fish model.

ABSTRACT (OMP012) FEB 05, 15.35-15.45

PLANKTONIC AND SESSILE MICROBIAL GROWTH HINDERED BY HERBAL EXTRACTS AND THEIR NANOPARTICLE

Mohammad Riyaz and Khem Raj*
Department of Microbiology, Panjab University, Chandigarh, 160014
*Email *riyazbiology@gmail.com*

Anticipatory behaviour & microevolution in fungal cell along with increased used of medical devices, prophylactic use of antibiotics has increased the risk of resistance in the Candida glabrata and can bring new fungal disease. ‘Bio-medically’ multiple determinants of pathogenicity and resistance to antibiotic in the biofilm. ‘Socio- anthropologically’ lack of identical global biomedical model and irrational prescription of antibiotics. This scenario to see the biofilm problem have evolved the need for a holistic approach to solving them. Latterly, phytochemicals alone and in combination with nano-particles have been exploited to fight out the microbial resistance and also complimented with prescribed medicine.In the present study, the medicinal plants and their nano particle are enumerated qualitatively & quantitatively for antimicrobial & antibiofilm activity; well diffusion assay, MIC, MBC and Microtiter plate assay (crystal violet and XTT assay). Nano-particles were characterized by UV-VIS, FTIR and TEM. The ethanol extract of medicinal plants has shown the minimum inhibitory concentration (MIC) ranging 0.0097 to 0.0312 mg/ml against different strains of Candida glabrata. When used at multiple MIC, the plant extracts and their nano particles resulted in reducing the fungal count up to 99.9% (R 2 = 0.89 to 0.93) within 4-18 h depending on the plant extract used and fungal strain used.The plant extracts and nano particles significantly inhibited biofilm formation at MIC/16 ($p<0.001$) and also, eradicated 5-day old biofilm at 64 MIC ($p<0.001$). This work incisively showed the antimicrobial potential of the medicinal plant extract and their nano particle’ role in inhibition and removal of biofilms. Potent antimicrobial activity, antibiofilm potential and biosafety of medicinal plants extract and also nano particles reveal the prospective active principle for the biofilms, resistome jeopardy and drug development.

ABSTRACT (OMP013) FEB 05, 15.45-15.55

PHAGE THERAPY AS AN ALTERNATIVE TREATMENT FOR MRSA INFECTION

*Archana Loganathan1, Prasanth Manohar2, Ramesh Nachimuthu1**
1School of Bioscience and Technology, Vellore Institute of Technology (VIT), Vellore, Tamil Nadu, India
2Zhejiang University-University of Edinburgh (ZJU-UoE) Institute, Zhejiang University, School of Medicine, Haining, Zhejiang 314400, P.R. China
Email larchana720@gmail.com

Staphylococcus aureus is a bacterium that endanger health., and the treatment of MRSA has become complicated. Phage therapy is one such an alternative treatment option to cure MRSA infections. Clinical Staphylococcus aureus was collected from clinical laboratories located in Chennai and Trichy. Collected isolates were characterized for resistance profile by phenotypic and genotypic methods, and bacteriophages were enriched from water and environmental samples collected from the regions of Tamil Nadu. The individual phages were characterized by their lifestyle pattern and the host range specificity, stability and morphological characterization (transmission electron microscopy). In vitro phage-antibiotic synergy was evaluated to improve the therapeutic index. Out of 100 S. aureus (non-repetitive), 97 isolates were Multiple Drug-Resistant with a Multiple Antibiotic Resistance index range of 0.25 to 0.80. Minimum inhibitory concentration test against oxacillin and ciprofloxacin showed resistance in 60% and 89% of the isolates respectively. Genomic analysis showed the mecA gene presence in 60% of the isolates. A total of seven bacteriophages were isolated against MRSA, out of which one phage, vB_sau_s1 showed broad-host-range activity against 72/100 isolates tested. Microscopic examination of vB_sau_s1 depicted the phage belongs to Siphoviridae family with the icosahedral head of 71±0.7 nm and a tail length of 230±0.3 nm. The multiplication cycle showed; absorption time of 15 min, time of lysis at 29th min and at the end of each cycle with a burst phage progeny of 105 phages/infected cell. The isolated phage, vB_sau_s1 can be used to treat MRSA infections and their therapeutical potential can be enhanced using phage-antibiotic synergy.

ABSTRACT (OMP014) FEB 05, 15.55-16.05

DEVELOPMENT OF BBZ AS POTENT BROAD-SPECTRUM ANTIBACTERIAL AGENT ACTIVE AGAINST CLINICAL MDR STRAINS

*Raja Singh1, Stuti Pandey2, Vibha Tandon1,**
1Special Center for Molecular Medicine, Jawaharlal Nehru University, New Delhi 110067, India
2Department of Chemistry, University of Delhi, Delhi-110007, India
Email t.rajasingh1786@gmail.com, vtandon@mail.jnu.ac.in

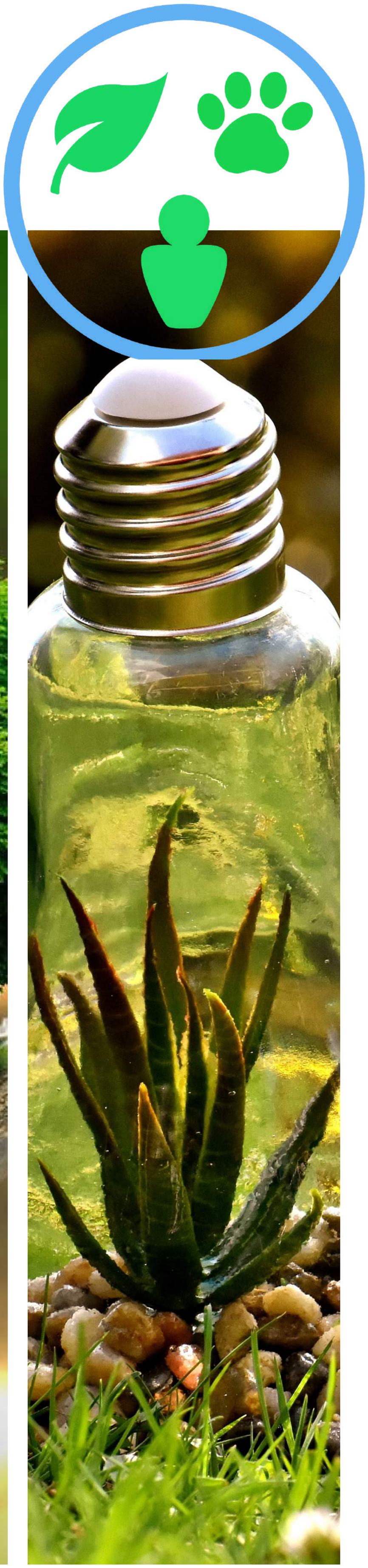
The discovery and development of a new class of broad-spectrum antibacterial agents with a clinically validated novel mode of action is required to fight against microbial resistance (AMR). In the pursuance of a drug discovery program, we synthesized novel bisbenzimidazoles (BBZ) and explored their broad-spectrum antibacterial activity. In the present study, we report the development of PPEF and BPVF as broad-spectrum bactericidal agents against global priority pathogens (GPP) listed by the World Health Organization (WHO). PPEF and BPVF target topoisomerase IA and topoisomerase III caused severe bactericidal backlash marked by cellular filamentation, juxtaposed with cellular distress, proven by chromosomal condensation and generation of focal points. We demonstrate the increase in the number of mutations in the active site decreased the binding affinity of PPEF towards topoisomerase. Genomic analysis of PPEF treated EC*555* and PPEF tolerant E.coli K12-R strain suggested no topoisomerase IA and III mutation. The study of whole transcriptome data of E. coli K12-R and PPEF treated EC*555* (MDR clinical strain) suggested that PPEF induced a complex set of metabolic perturbations in E. coli, as validated by glucose utilization ineptitude, carbon catabolism, amino acid degradation, gridlocked DNA synthesis, and replication, along with differential regulation of efflux genes and upregulation of transcription repressors. PPEF treatment upregulates cAMP, a negative regulator of virulence, biofilm formation genes; finally, it curtails bacterial SOS adaptive response and inciting bacterial dissolution. We propose that PPEF and BPVF are potential lead candidates to be developed as antibiotics as they target type IA topoisomerases and induce a plethora of changes in the transcriptional regulatory network of bacteria, causing cell death.

POSTER PRESENTATIONS ABSTRACTS

There are no shortcuts to any place worth going

THEME 1

Microbiome and one health



ABSTRACT (PMOH001)

EXPLORING THE MICROBIOME: A REVIEW

*Yashika Thakran and Jasvinder Kaur**
Gargi College, University of Delhi
*Email *jasvinder.kaur@gargi.du.ac.in,*

The microbiome is the most intimate link with the external environment that an organism has. In fact, the microbiome plays a crucial role in preserving equilibrium in the internal environment. Scientists are only beginning to understand what these microbes do, how they function, and how to manipulate them in order to improve human health. The science of microbiome is based mainly on interactions between the microbiome and disease, not health. It is therefore important to know how the microbiome is directly involved not only in causing or preventing certain diseases, but also in diet and sustaining good health. Thus, most dietary therapies now focus on altering host biology through their effect on the microbiome. Therefore, the connection between the microbiota and the brain, gut and consciousness is reviewed here. A bidirectional connection between the cardio-vascular system and the microbiota of the gut is also present. This is further expanded to address the idea of the theory of hologenomes. A vast amount of microbial diversity, however, continues to be discovered. Consequently, in the near future, in the era of precision medicine and drug discovery, microbiome technologies are expected to play a crucial role.

ABSTRACT (PMOH002)

TO REVIEW THE EFFECT OF ULTRA- PROCESSED FOOD ON HEALTH AND GUT MICROBIOTA

*Vanshi Bali, Garima Badhan and Jasvinder Kaur**
Gargi College, University of Delhi, Siri Fort Road, New Delhi-110049
*Email *jasvinder.kaur@gargi.du.ac.in*

This article reviews the effect of ultra-processed food on the human body and its functions. Result analysis from various studies indicates excessive food processing not only alters the nutritional quality of food material, but also alters the healthy gut-microbiota. Studies conducted over various population groups in different countries have successfully investigated the relationship between ultra-processed food consumption and non-communicable diseases (NCDs). Participants with high consumption of ultra-processed food were found to have a much higher risk of developing various non-communicable diseases. This is due to the fact that packaged food has low nutritional value, high amount of sodium; trans-fats (IL-6, TNF-α), contain additives like TiO2, glutamates, emulsifiers, sulfites, neoformed contaminants (acrylamide and acrolein), and even toxic material (bisphenol A). All these factors contribute to the development of a plethora of health risks and diseases leading to a low-quality life. On the other hand, the natural and organic food contains not only the nutrients we need, but also the substrate and medium for gut bacteria's sustenance and growth. Skewed diet would eventually influence composition of types of bacteria in the gut. There is an increasing number of studies linking the effect of diet on altering the gut microbiota. The essential focus again from this review is that high consumption of ultra-processed foods can alter gut microbiota as well as cause inflammation. To indicate the relationship between diet and inflammation in different populations, a dietary inflammatory index has also been proposed and tested by certain research groups. At last, in some animal studies, it has been found that these effects may be transferred to later generations via epigenetic change. In conclusion, diets rich in fruits, vegetables, legumes and whole grains offer a healthy microbiota gut profile that leads to decrease in inflammatory markers and even a reduction in insulin resistance, as is supported by various studies.
Keywords: Ultra-processed food, Non-communicable diseases (NCDs), additives

ABSTRACT (PMOH003)

ASSESSMENT OF LARVICIDAL EFFICACY OF ENDOPHYTIC ACTINOBACTERIA ISOLATED FROM BLUMEA LACERA AGAINST FILARIASIS VECTOR CULEX QUINQUEFASCIATUS

Sunita Datla and A. K. Gupta**
**Microbiology Research Laboratory, School of Studies in Life Science, Pt. Ravishankar Shukla University, Raipur- 492010, Chhattisgarh, India*
*Email *ksunita.887@gmail.com, **akguptarsu@gmail.com*

Resistance development in mosquitoes along with environmental toxicity due to non- judicious application of synthetic insecticides necessitated biologically safer alternatives. Actinobacteria are well known for its unparalleled ability of producing precious bioactive natural products. Thus, the present investigation deals with isolation and assessment of the mosquito larvicidal potential of endophytic actinobacteria from a weed Blumea lacera against Culex quinquefasciatus which act as a potent vector of lymphatic filariasis, an infectious debilitating disease affecting a major population in this region and also affecting people around the world. The isolation and cultural characteristics study revealed 15 actinobacteria from different parts of Blumea lacera (four, nine and two isolates from roots, stem and leaves, respectively) on Starch M- protein agar medium. Blood fed female Cx. quinquefasciatus were collected from household areas, reared and maintained in the insectary of Pt. Ravishankar Shukla University, Raipur, Chhattisgarh. For screening of larvicidal efficacy, the 3rd instar larvae were exposed to cell free culture filtrates of actinobacteria. Of the eight isolates investigated, the bioactive metabolites of three actinobacterial strains exhibited significant larvicidal activity. The results suggest the potentiality of endophytic actinobacteria as a candidate for environment friendly larvicides. Further, characterization and identification of the potent actinobacteria and their larvicidal metabolites is in progress.

ABSTRACT (PMOH004)

NAÏVE METABOLIC MODELLING OF SIMPLE MICROBIAL COMMUNITIES RECAPITULATES EXPERIMENTALLY OBSERVED DIVERSITY PATTERNS

Silvia Talavera, Daniel Aguirre de Carcer*
Universidad Autonoma de Madrid
Email Spainstalaveramarcos@gmail.com

Microbiomes have a preeminent role in the biogeochemical cycles that sustain life on Earth and establish close and intricate relationships with most macroorganisms. The patterns of microbial diversity observed in nature indicate the plausible existence of common community assembly rules. However, these common rules are still not properly understood in spite of their perceived economical and scientific impact. Here, we use a naïve metabolic modelling approach to explore the factors governing experimentally observed diversity patterns; it only relies on experimentally-derived 16S rRNA gene amplicon sequencing data and genome sequences deposited in the databases. The experimental dataset consisted on 16S rRNA gene amplicon sequencing data generated by culturing a diverse range of complex natural communities ex-situ on two simple carbon and energy sources (glucose and citrate) [Obtained from Goldford, J. et al. Science 361, 469-474 (2018)]. In addition to providing an in-depth characterization of the phylogenetic signal observed in the datasets, our naïve metabolic modelling approach of simple microbial communities built on the basis of experimentally observed phylogenetic signal and freely available genome sequences predicts community compositions close to those experimentally observed and provides additional information that may help explain the ultimate causes of observed diversity patterns.

ABSTRACT (PMOH005)

EXPLORING THE BACTERIAL MICROBIOME AND ANTIBIOTIC RESISTOME OF THE RIVER GANGA

Ankita Srivastava and Digvijay Verma*
Department of Microbiology, Babasaheb Bhimrao Ambedkar University, Lucknow, India
*Email *ankita09srivastava11@gmail.com*

The Ganga river is vital for the survival of humans as well as other organisms thriving upon it. However, it is in danger due to several anthropogenic activities such as direct disposal of domestic and industrial wastes into the river Ganga which eventually results in increased organic load, heavy metals, complex chemicals, other recalcitrant pollutants and antibiotic- resistant bacteria (ARB) and ARGs have been also observed in the river Ganga. Thus, deteriorating water quality and disturbing native microflora. Identification of antibiotic resistance microorganisms has further elevated this problem multi-fold. It has been broadly accepted that some environmental pollutants especially antibiotics exert selective pressures on microbial communities persistently and facilitate the progression and propagation of antibiotic resistance genes (ARGs). We have limited information on the microbial communities of river Ganga and its associated ARGs. With the advancement in Next Generation Sequencing (NGS) technology, now it has become possible to understand the microbial diversity of a habitat using its metagenome. We have employed culture-dependent as well as independent approaches to explore the microbial diversity of the river Ganga. Preliminary screening of the river Ganga revealed a high microbial load of bacteria ranges 100-350 CFU per ml of water. Of the isolated distinct bacteria, several of them showed antibiotic resistance towards a range of antibiotics such as chloramphenicol, tetracycline, rifampicin, Erythromycin, Gentamycin, Bacitracin. Majority of them belong to phyla Proteobacteria and Firmicutes. Identification and characterization of these bacteria are underway. Besides, high- molecular weight, humic acid-free metagenomic DNA have also been isolated from respective water samples of the river Ganga. Amplification and NGS based sequencing of V3-V4 hypervariable region of bacterial specific 16S rDNA are under progress for analyzing the bacterial composition of the river Ganga. These outcomes will assist to understand the bacterial microbiome and its association with antibiotic-resistant genes in the river Ganga.

ABSTRACT (PMOH006)

CULTURE-DEPENDENT AND INDEPENDENT APPROACHES FOR IDENTIFY BACTERIAL COMPOSITION OF SMOKELESS TOBACCO PRODUCTS OF INDIA

Akanksha Vishwakarma and Digvijay Verma*
Department of MicrobiologyBabasaheb Bhimrao Ambedkar University, Lucknow, Uttar Pradesh-226025, India
*Email *akansha.181097@gmail.com*

Smokeless tobacco (SLT) is one of the terrible causes for 1.5 million disability-adjusted life years (DALYs) among 113 countries together with India. The presence of approximately four thousand chemicals in SLT and similar products makes it a risky chewing/smoking product. Of these chemicals, many belong to the group of toxicants and carcinogens such as tobacco-specific nitrosamines (TSNAs), polyaromatic hydrocarbons (PAH), volatile aldehydes, metals, and metalloids. The inhabitant microorganisms on the surfaces of SLT and their products further elevate the problems associated with several oral diseases with cancer. We have limited information on inhabitant microflora of smokeless tobacco in India, where the prevalence of tobacco consumers is highest. These microorganisms play a significant role in various transformations of alkaloids such as TSNA formation. We have employed both traditional cultivations as well as metagenomic approaches for exploring bacterial diversity from commercial SLT products of various cities of India. Enumeration of bacteria revealed that SLT products harbour a high microbial load where 400-952 x 105 CFU/gm SLT were obtained. Preliminary screening of the distinct isolates showed that these bacteria are highly diverse. The majority of these bacteria were aerobic, Gram-negative rods followed by cocci. We are in process of their identification using bacterial specific 16S rDNA based signature sequences. We have also extracted metagenomic DNA from the respective SLT products for enhancing our understanding of the inhabitant microorganisms of SLT products. We have successfully amplified bacterial V3 and V4 regions from all the samples. At present, we are analyzing the bacterial composition of these SLT products using QIIME2 pipeline.

ABSTRACT (PMOH007)

EVALUATION OF PROBIOTIC PROPERTIES OF LACTOBACILLUS PENTOSUS ISOLATED FROM COW MILK

Disha P. Senjaliya John J. Georrge**
**Christ College, Rajkot, Gujarat, India*
*Email *dishasenjaiya99@gmail.com, **johnjgeorrge@gmail.com*

Numerous reports have suggested the presence of beneficial microorganisms in Cow Milk. This microorganisms affects several benefits to the host health. Lactobacillus is an significant probiotic and has several claims in the the food preparation. We isolated and assessed the potential probiotic bacteria from Cow Milk. All the isolates were tested for primary screening. Out of twenty-six, twelve isolates were preserved for further analysis; furthermore out of twelve isolates one strain of Lactobacillus species, L.pentosus CMGC4 was identified from the two breeds of cow milk by 16S rRNA sequencing. It showed good aggregation activity (75%), excellent hydrophobicity against all three solvents (>50%), resistance in acidic pH (pH 2), tolerance towards phenol (0.4%) and bile (0.3%) conditions. Evaluation of the probiotic attribute indicated that Lactobacillus pentosus had antagonistic and bacteriocins activity against all tested organisms. Furthermore, it also showed antifungal activity and was sensitive towards all tested antibiotics. In conclusion, Lactobacillus pentosus isolated from Cow milk is an ideal candidate which provides health beneficial microbes . However, several tests need to be performed before its use as a potential probiotic.Keywords: Cow milk, Lactobacillus, 16S rRNA sequencing, antagonistic, Bacteriocin

ABSTRACT (PMOH008)

GUT MICROBIOTA AND NEURODEGENERATIVE DISORDERS

Sheeba Khan, Dr. M.S. Parihar, Rekha Khanna*
Government Madhav Science College, Vikram University Ujjain
*Email *k.shibakhan@gmail.com*

Human intestine is inhabited with thousandfold microbial species and this not only includes bacterial species that are unculturable but also archaea, protozoan, fungi and viruses which are found in the gastrointestinal tract. Commensal bacteria shortly after birth colonises the human intestine and remain there for lifetime. The mostly found phyla which constitute the 70-75% of the microbiota are Firmicutes and Bacteroidetes. Additionally Proteobacteria, Actinobacteria, Fusobacteria, Verrucomicrobia occurring in lower quantities. Various factors which affect the microbiota are food, age factor, metabolic activity, topology, tension and antibiotic therapy. Throughout the world the various cases of neurodegenerative diseases like Alzheimer's disease, Parkinson's disease, Multiple Sclerosis, Major Depressive disorders, Prions disease, Hypertension are increasing but their developmental pathways are not clear and even effective treatment of these disorders are still unrevealed. Brain Gut Microbiota (BGM) axis was also given to focus the importance of these interrelationships. The interaction of the Central Nervous System (CNS) and gut microbiota takes place in two ways. For example, the psychological and physical stresses taking place, causes the CNS to create a response which regulates gut performance which ultimately affects movability, excretion and immunity. Apart from these various physiological and microchemical changes are also caused due to change in gut microbiota. The BGM through the vagus nerve, adrenal hypothalamic pituitary axis, and various cytokines controlling the gastrointestinal interact and CNS. To find out the role of microbiome in the growth, route and therapy of Parkinson disease, Multiple Sclerosis, Major Depressive Disorder, Prion Disease, and Alzheimer's disease various studies are going on. Recent advanced technology, open accessible data libraries allow microbial examination and their role in helping to diagnose neurological health.

ABSTRACT (PMOH009)

BIOPROSPECTING AEROBIC RICE MICROBIAL INTERACTIONS FOR HIGHER PRODUCTIVITY

Ekta Narwal, K Annapurna1, Jairam Choudhary2, YV Singh1*
1Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi- 110012, India
2ICAR-Indian Institute of Farming Systems Research, modipuram- 250110, India
*Email *enarwal@gmail.com*

Production of rice in a well-drained, non-puddled unsaturated field is known as aerobic rice production. Despite of yield losses as compared to low land cultivation this method is important for sustainable rice production with water and labour saving. Therefore twenty rice varieties (ten upland and ten lowland) were grown under aerobic and flooded condition with identical nutrient management. Soil microbial activities were 22-40% higher under flooded conditions as compared to the aerobic conditions but native mycorrhizal colonization was very low under flooded condition. Rice rhizosphere under aerobic conditions was mainly occupied by Alcaligenes, Bacillus, Pseudomonas, Rhizobium, Stenotrophomonas, Enterobacterium, Achromobacter, Agrobacterium etc with greater percentage of gram negative bacteria (157 isolates) as shown by 16S rDNA partial gene sequencing results. Out of total 216 isolates isolated from rice rhizosphere, total 131 showed in vitro nitrogenase activity with highest in Rhizobium sp. Ekn 04 (167.79 nmoles/mg protein/h) followed by Pseudomonas protegens Ekn 03 (164.02 nmoles/mg protein/h). Apart from good invitro nitrogenase activity P. protegens Ekn 03 showed faster growth, IAA production, cellulase and pectinase activities with highest antibiotic tolerance which makes it capable for faster colonization into the soil and plant. Mycorrhizal inoculation of rice plant resulted in increased shoot dry weight, chlorophyll content, nutrient uptake, grain yield (10%), straw yield (10%) and reduced accumulation of proline, high amount of glutathione and ascorbate as compared to uninoculated plants. Co-inoculation of rice plant with strain P. protegens Ekn 03 and AMF resulted in increased plant height, tiller number, dry weight, chlorophyll content, higher N and P content in plants.

ABSTRACT (PMOH010)

COMPARATIVE GENOME ANALYSIS OF CAMPYLOBACTER SPECIES

*Twinkle yadav, Charu Tripathi**
Molecular Biology Laboratory, Department of Zoology, CMP College, University of Allahabad, Prayagraj, India
*Email *charutripathi89@gmail.com*

Campylobacter is gram negative bacteria they are comma or S shaped, and are non-motile. Campylobacter species can infect humans and causing campylobacteriosis, a diarrhoeal disease in humans. Studies on Campylobacter species suggest that several species of Campylobacter have ability to cause disease in humans like C. consicus cause inflammatory bowel disease, C. jejuni and C. coli have been also recognized as human and animal pathogens. In this study comparative genome analysis of different Campylobacter species has been done and identify species specific gene and gene clusters by comparative analysis of orthologs, paralogs, core genome and pan genome. Phylogenetic analysis has been also performed which gives an insight into genetic classification, events that occur during evolution and evolutionary relationships among species.

ABSTRACT (PMOH011)

EMOTIONS, BEHAVIOUR AND MICROBIOME CHEMISTRY: A REVIEW

Yousuf Khan, Yash Verma and Ram Sunil Kumar Lalji*
Department of Chemistry, Kirori Mal College, University of Delhi, Delhi – 110007, India
Email yousuf26k@gmail.com

Multiple studies over the years have explored the detrimental impact of chemical exposure and toxicity on animal microbiome. Herein, we present a summary of the contrary approach of utilising chemistry and biotechnology to influence the microbiome and its effects on emotions, behaviour and chemical communication in organisms. Building upon the One Health principle, we look into studies where microbial and chemical exposure, inter alia in
animal models, have been employed to target and manipulate the microbiome-gut-brain axis. We look into interdisciplinary areas such as nanochemistry, food science, psychobiotics etc. and ways they can be better integrated for improving patient outcomes, for example in mental health, by active exposure of microbiome to external manipulation.
Key Words: Microbiome, chemical exposure, behavioural changes, mental health and disorders, emotions

ABSTRACT (PMOH012)

IDENTIFICATION OF SIGNIFICANT GENES IN BASAL CELL CARCINOMA (BCC) OF EYELID USING BIOINFORMATICS ANALYSES.

*Pranjal Vats 1 , *Perumal Jayaraj 2*
1 Department of Life Sciences, Sri Venkateswara College, Benito Juarez Marg, Dhaula Kuan, New Delhi-110021
2 Department of Zoology, Sri Venkateswara College, Benito Juarez Marg, Dhaula Kuan, New Delhi-110021
Email pranjalvats2000@gmail.com, jayaraj@svc.ac.in

BCC of skin is the most common malignancies worldwide with significant morbidity. Patients often report enlarging nonhealing lesion that may sometimes bleed. They may also describe pruritus or no symptom leading to poor prognosis of the disease mechanisms. The objective of this study was to identify the key genes in BCC of eyelid and underlying mechanisms by bioinformatics approach. Gene expression profiles of GSE103439 (BCC Eyelid) and GSE53462 (BCC Skin) were downloaded from GEO Database. The common Differentially expressed genes (DEGs) of both datasets were identified and pathway enrichment was done using Kegg and DAVID. String was employed to analyse and evaluate interaction among DEGs followed by construction of PPI network using Cytoscape Software. A total of 181 common DEGs were filtered and were incorporated into this study. According to analyses in PPI network; 42 genes were found in close network among which CTNNB1, EGFR, GNG2, BTRC and MAPK14 had higher degree of connectivity and participated in majority of important pathways like Wnt signaling. Ras signaling and Cancer signaling pathways. Our study suggested that CTNNB1, EGFR, GNG2, BTRC and MAPK14 may play key roles in the progression of BCC in eyelid which will be useful in study of underlying mechanisms and will help in advancement of therapeutic treatment. However, furthur experimental studies like immunohistochemistry can be performed to validate the findings. Keywords: Basal cell carcinoma (BCC), Eyelid, Bioinformatic analyses, Differentially expressed genes (DEGs), Protein – Protein Interaction (PPI) Network

THEME 2

Environmental and agricultural microbiology

ABSTRACT (PEAM001)

PLANT GROWTH PROMOTING BACILLUS ARYABHATTAI STRAIN KMT-4 EFFECTIVELY CONTROLS MELOIDOGYNE JAVANICA INFECTION

Sonam Antil, Rakesh Kumar, D.V. Pathak*
Department of Microbiology, College of Basic Sciences & Humanities, CCS Haryana Agricultural University, Hisar, Haryana 125004, India
*Email *sonamantil.sa@gmail.com*

Root infecting nematodes (Meloidogyne spp.) are a major reason behind crop yield reduction worldwide. The management of such pests via biological means is an emerging trend these days. Because of excessive use of chemical nematicides and awareness towards their ill effects, Bacillus aryabhattai strain KMT-4 was isolated from nematode affected tomato rhizosphere at research farms, CCS Haryana Agricultural University, Hisar and examined for its biological control potential against Meloidogyne javanica along with its effect on plant growth. During in vitro studies, hatching and mortality of M. javanica were significantly affected due to the antagonistic behaviour exhibited by the bacterium. Apart from this, the bacterium also exhibited various direct as well as indirect plant growth promoting attributes like siderophores production, growth hormone (IAA) production, ammonia excretion, hydrogen cyanide production and chitinase activity. A pot house experiment conducted on brinjal resulted in 80% reduction in galls and nearly 73% reduction in eggs in the plant root compared to control and chemically treated plants. Also, a notable enhancement in plant growth was observed. Similar results were observed in field experiments on brinjal and cucumber conducted in years 2018 and 2019. Hence it can be concluded that plant growth promoting Bacillus aryabhattai KMT-4 is also a potent biocontrol agent against M. javanica.

ABSTRACT (PEAM002)

BIODESULFURIZATION OF DIBENZOTHIOPHENE AND SIMULTANEOUS PRODUCTION OF BIOSURFACTANT FROM A BACTERIAL STRAIN IITR112

*Varsha Tripathi1,3, Vivek Kumar Gaur1, Ravindra Singh Thakur2,3 and Natesan Manickam1**
1Environmental Biotechnology Laboratory, Environmental Toxicology Group,
2Analytical Chemistry Laboratory, Regulatory Toxicology Group
3Academy of Scientific and Innovative Research (AcSIR)CSIR-Indian Institute of Toxicology Research, Vishvigyan Bhawan, 31 Mahatma Gandhi Marg, Lucknow-226001, Uttar Pradesh, India
*Email *nmanickam@iitr.res.in*

Abundance of sulphur contents in coal and petroleum products poses serious threat to the environment by causing corrosion and generation of gases containing oxides of sulphur. Organic sulphur in the form of thiols, sulphides and thiophenes are present in petroleum products which are covalently linked to a molecular matrix. This study is aimed to isolate and characterize the dibenzothiophene (DBT) utilizing bacteria and explore the pathway for DBT degradation. Crude oil contaminated soil was collected from ONGC oilfield of Baruch, Ankleshwar Gujarat. Seven different bacteria were isolated by the successive enrichment using DBT as the sole source of energy for detailed studies. These bacteria were characterized by 16S rDNA gene sequencing and other biochemical methods. Among them, one of the bacteria designated as strain IITR112 was found to metabolize DBT for its growth and formed an orange coloured metabolite in 8 days of incubation. Strain IITR112 was able to utilize DBT up to 100 mg/L. The metabolites formed during degradation are being confirmed using Gas chromatography–mass spectrometry (GC-MS). The strain IITR112 was found to produce biosurfactant in presence of DBT which was further identified by Fourier transform infrared spectroscopy (FTIR). The efficiency of the isolated surfactant to increase the solubility of different hydrophobic compounds such as hydrocarbons present in crude oil is evaluated. This study provides more insights into the understanding of a biodesulfurization bacterium isolated from a hazardous oil contaminated site.

Keywords: Crude oil, Dibenzothiophene, Biosurfactant, Solubilization.

ABSTRACT (PEAM003)

ISOLATION AND CHARACTERIZATION OF PHTHALATE ESTERS DEGRADING BACTERIA FROM WASTE- DUMP SITES

*Saurabh Singh1,2, Raj Kumar Regar1 and Natesan Manickam1**
1Environmental Biotechnology Laboratory, Environmental Toxicology Group,
2Academy of Scientific and Innovative Research (AcSIR), GaziabadCSIR-Indian Institute of Toxicology Research, Vishvigyan Bhawan, 31 Mahatma Gandhi Marg, Lucknow-226001, Uttar Pradesh, India
*Email *nmanickam@iitr.res.in*

Phthalic acid esters (PAEs) have been used in industrial applications as the most commonly used plasticizer due to which they are widespread and omnipresent in various environments. Recent studies on PAEs have focused primarily on their environmental fate and toxicological risk assessment. As it has various potential health implications and being a threat to biodiversity, PAEs has drawn global attention for their elimination from diverse niches. In this study, soil and water samples were collected from a municipal dump waste site located in Lucknow, The physico-chemical properties of soil and water samples were determined and found to have high Nitrogen, Chloride Also, qualitative and quantitative analysis of the samples lead to identification of organic and inorganic compounds and present in the range of 1.44 to 2522.28 ug/g in soil and 6.2 to1112.0 mg/l in water samples respectively. GCMS profiling of samples revealed the presence of several phthalate derivatives namely Dimethyl phthalate, Dibutyle phthalate, Diethyl phthalate, Di-n-butyl phthalate, Benzyl butyl phthalate, Bis (2-ethyl hexyl) adipate (DEHA), Bis(2-ethyl hexyl) phthalate (BEHP). Through enrichment method using phthalate esters as substrate, we were able to isolate three different bacteria which are able to utilize phthalic acid, dimethyl phthalate and dibutyl phthalate as sole source of carbon and energy efficiently. On the basis of 16S rDNA sequencing, these strains are identified as Bacillus sonorensis, Pseudomonas guguanensis, Achromobacter xylosoxidens. The optimum pH and temperature were 7 and 30 °C for their growth, respectively. These bacteria were further characterized by KOH test, antibiotics sensitivity test and biochemical characterization. These bacteria also show growth on diethyl phthalate, dioctyl phthalate, and mono-methyl terephthalate as the sole source of carbon and energy which suggested its ability to resist phthalic acid ester toxicities.

Keywords: Biodegradation, Phthalate esters, Plastics

ABSTRACT (PEAM004)

MICROBIAL COMMUNITY DYNAMICS ALTERS WITH TEMPERATURE IN A HIGH ALTITUDE HOT SPRING

Nitish Kumar Mahato1,2, Anukriti Sharma2, Yogendra Singh2 and Rup Lal2,3
**1Department of Zoology, Deen Dayal Upadhyaya College, University of Delhi, India.*
2Department of Zoology, University of Delhi, India
3The Energy and Resources Institute (TERI), New Delhi, India.
*Email *ruplal@gmail.com*

Natural hot springs are extreme habitats where high temperature of surroundings restricts the life only to prokaryotes. Metagenomic analyses can explore diversity of thermophiles growing in these habitats. One such analysis was performed of bubbling water a high altitude hot spring which is rich in arsenic content located at the Himalaya to reveal its microbial diversity. Further, functional analysis was also done to know their adaptations to withstand high temperature. Water samples were collected from two adjacent points having temperatures >96 °C from Manikaran, Parvati Valley, Himachal Pradesh, India (32◦01′34.8″N, 077◦20′50.3″E). eDNA extracted from these samples of water were sequenced using Illumina GAII technology. Quality filtered metagenomic raw reads were used to find out microbial diversity using MetaPhlAn. KAAS and MinPath servers were used to perform the functional analysis. Comparative metagenomic analyses was also done with environmental shotgun data of other samples collected from different habitats (microbial mat and sediment) of same hot spring to discover habitat specific distinctions occurring in the same niche. Bacteria of phyla Actinobacteria, Bacteroidetes, Crenarchaeota, Proteobacteria and Thermi were predominantly reported in the water of hot spring. Functional analyses disclosed enrichment of genes encoding DNA repair system in inhabiting thermophiles highlighting their role in tolerating high temperature. Additionally, a draft genome of a bacterium, namely, Emticicia sp. MM was reconstructed from the metagenomic data of water samples. Comparative metagenomics showed pivotal role of temperature in defining diversity of bacterial community and their metabolic adaptations across different habitats of hot springs. Inter-habitat functional evenness was reported, however microbial diversity fluctuates at different habitats within same environment.

ABSTRACT (PEAM005)

AN ENZYME COCKTAIL FOR GREENER AGRO-PULP BIOBLEACHING IN PAPER INDUSTRY

*Aarjoo Sharma1, Sanjeev Balda1, Naveen Gupta1, Neena Capalash2, Prince Sharma1**
1Department of Microbiology, Panjab University, Chandigarh, 160014, India
2Department of Biotechnology, Panjab University, Chandigarh, 160014, India
Email princess@pu.ac.in

A cocktail from Bacillus halodurans (xylanase-15U, α-amylase-2.5U, protease-2U, pectinase-2U, and lipase-1.8U) was applied for unbleached and ODL (oxygen delignification) agro based pulp biobleaching in the R&D set up of Shreyans Paper Mills Ludhiana, India. Enzyme pre-treatment was upscaled from 5 g (at lab scale) to 100 g odp (oven dried pulp) at temperature and pH optima of 65 °C and 9-9.5 for 90 min followed by reduced chemical treatment. In case of unbleached agro pulp, enzyme cocktail pre-treatment reduced the chemical usage by 50% without compromising brightness and rather with increased tensile strength (23.55%), burst factor (20.3%) and tear factor (3.17%) and reduced kappa number (19.5%) as compared to the total chemical bleaching in mill. While, 40% reduction in the chemical usage with enhanced brightness (2.24%), tensile strength (20.96%) burst factor (5.1%) and tear factor (8.2%) with reduction in kappa number (4.54%) was reported, in case of ODL pulp. The enzyme cocktail thus can make the paper manufacturing process greener, safer, economical and eco-friendly and may replace big budget ODL technologies.
Keywords: Bacillus halodurans, Enzyme cocktail, Biobleaching, ODL pulp, Agro pulp

ABSTRACT (PEAM006)

A BROAD-SPECTRUM ANTIMICROBIAL LIPOPEPTIDE FROM A BACILLUS SP. STRAIN AF2

*Stanzin Choksket, Harshvardhan and Suresh Korpole**
MTCC & Gene Bank, CSIR-Institute of Microbial Technology, Sector -39A, Chandigarh-160039, India.
*Email *suresh@imtech.res.in*

The rapid emergence of drug resistance decreased most conventional antibiotics and resulted in a significant concern of human welfares. Thus, there is a great demand for novel antibiotics' discovery to combat the resistance problem. Bacterial derived antimicrobial peptides, including biosurfactants, have been used as a potential alternative to antibiotics. Various members of the genus Bacillus spp. were used for the production of potential bioactive lipopeptides or biosurfactants. A strain designated as AF2 identified as a member of genus Bacillus was used for the production of potential antimicrobial bioactive compound identified as lipopeptide. It showed activity against gram-positive, gram-negative bacteria as well as phytopathogenic fungi. Different extraction and purification methods were assayed such as ethyl acetate, acid extraction followed by (HPLC) high performance liquid chromatography used to purify the compound. The pure active product was used for Tricine SDS-PAGE, TLC (thin layer chromatography), bioautogram, and MALDI-TOF analysis. The collapse drops assay (CDA) result also confirmed the biosurfactant nature of active compound. The purified peptide inhibited the test strain in the bioautography assay. Tricine SDS-PAGE analysis confirmed the presence of a single band of low molecular weight compound. The MALDI-TOF analysis also revealed the peptide molecular weight as 1060 Dalton. The MIC range of purified peptide was 25 µg/ml against gram-positive and 102 µg/ml against gram-negative indicator strains The MFC (Minimum fungicidal concentration) value was slightly higher against phytopathogenic fungi. The purified peptide was stable at higher temperature, wide pH range, and tolerated different proteolytic enzymes.

ABSTRACT (PEAM007)

ANTIMICROBIAL LIPOPEPTIDE FROM BACILLUS ISOLATES AND THEIR APPLICATIONS

*Urvashi, Stanzin Choksket, Mohini Sharma and Suresh Korpole**
MTCC & Gene bank, CSIR-Institute of Microbial Technology, sector-39 A, Chandigarh-160036, India
*Email *suresh@imtech.res.in*

Antimicrobial resistance is an important concern for the public health with the increasing resistant to antibiotics in pathogens, there is crucial need to develop some alternative antimicrobial compound to antibiotics for the usage in agriculture and food industry. Among the alternative, lipopeptides are one of such potential compounds, which are broad spectrum short peptides containing a fatty acid moiety joined with an acyl bond. Lipopeptides can also be developed as therapeutic agent due to their lesser toxicity towards host and effective killing abilities against the pathogens and opportunistic pathogens. In our study, antimicrobial lipopeptides produced by two bacterial isolates designated as R3140 and SVC were characterized. Strains were identified using 16S rRNA gene sequence assigned both strains to the genus Bacillus. Strains R3140 and SVC showed 100% and 99.48 % similarity with Bacillus subtilis and Bacillus velezensis respectively. The antimicrobial substances were purified from cell free broth (CFB) by solvent extraction and subsequent reverse-phase HPLC. The purified substance was identified as lipopeptide based on drop collapse assay and FTIR. MALDI -TOF analysis confirmed the molecular weight of the peptides from R3140 and SVC as 1060 and 1053 Da, respectively. While lipopeptide from SVC showed broad spectrum, the lipopeptide secreted by strain R3140 inhibited S. aureus, B. subtilis and selected phytopathogenic fungi. Both peptides displayed hemolytic nature, however, they did not show phytotoxic effect in seed germination experiment performed using Vigna radiata (Mung bean). Further they were found to exhibit antibiofilm properties therefore, can have potential applications in agricultural sector. Details of results will be discussed during the poster presentation.

ABSTRACT (PEAM008)

GUESSTIMATION OF AMLA ENDOPHYTES

*Ushma B. Joshi a, Mohammed Faisal Ansari*b and Devayani R. Tipre c*
aMicrobiology Department, Mehsana Urban Institute of Science, Ganpat University,Kherva, Mehsana
bMicrobiology Department, L. J. Institute of Applied Sciences, L. J. Campus,S. G. Highway, Ahmedabad
*cDepartment of Microbiology and Biotechnology, University School of Sciences,Gujarat University, Ahmedabad**
Email faisalansari.ljias@ljinstitutes.edu.in

In search of growth-promoting compounds, fertilizers and pesticides which can enhance plant growth many chemicals have been exposed to soil. Addition of these chemicals in different ecosystems gives spontaneous benefits and a lifelong problem of environmental pollution. There are many microbial alternatives which can be an eco-friendly replacement of this kind of compounds. Some of these kinds of compounds are also produced by endophytes. Endophytes are organisms which reside inside the plant. Many active metabolites have been reported which have been produced by endophytes and showing plant beneficial effects. Phyllathus emblica L. is the scientific name of Indian Gooseberry commonly known as “Amla” is an angiosperm of the order Malpighiales and family Phyllanthaceae. Preliminary research of Phyllathus emblica L. has demonstrated that it has antibacterial, antidiarrhoeal, antidysenteric, antioxidative, antiviral, and resistance building properties. Very few endophytes belonging to Amla plant have been reported till date. So in search of novel endophytes, isolation of bacteria from various parts of amla plant was carried out. Aamla plant parts like root and steam were searched for the presence of endophytes. The plant internal tissue suspension were plated on nutrient media and 7 bacterial isolates from roots, 10 bacterial isolates from the stem and 5 isolates from the fruit were isolated. All endophytic isolates showed different cultural and morphological characters. These isolates will be further checked for beneficial impact on plant growth promotion and different PGPR characterization. Detailed results will be discussed at the time of presentation.

ABSTRACT (PEAM009)

PLANT GROWTH PROMOTING RHIZOBACTEIA FOR SUSTAINABLE AGRICULTURE AND IMPROVED PLANT GROWTH

Deepika Goyal1 and Janmejay Pandey2**
**1 Department of Biotechnology, Central University of Rajasthan, India DST scheme2Department of Biotechnology, Central University of Rajasthan, NH-8, Kishangarh, India.*
*Email *dr.deepika.goyal.22@gmail.com, **janmejay@curaj.ac.in*

Sustainable agricultural practices comprise of scientific and advanced technological principles by which environmental (soil, water, and air) pollution arising from agriculture can be minimized. The goal is to provide food security to all humans without adversely effecting soil health and global climate. Chemical fertilizers and pesticides (adjuvants added to the soil for nutrition and pest control), are causing severe environmental and animal health issues. Two approaches are successful in alleviating the harmful impact of chemicals on soil fertility and pollution, one is the use of soil test crop response correlation (STCR) based fertilizer application (initiated in 2003) and second is the use of biofertilizers and biopesticides. PGPR (Plant Growth Promoting Rhizobacteria) are an attempt to develop green technologies for sustained agriculture and environment. They alleviate many of the deleterious effects of chemical fertilizers, the most important being decreased soil toxicity. That is why studies on the role of biofertilizers in sustainable agriculture are being undertaken globally (Azizoglu, 2019; Castro, Calijuri, Ferreira, Assemany, & Ribeiro, 2020; Tamreihao et al., 2016). This work describes the efforts of our group to isolate and characterize PGP (Plant growth promoting) rhizo-bacteria from arid soils in the interior regions of Rajasthan under Cluster Bean cultivation. By using dilution plating technique and testing on Pikovaskaya phosphate medium, a total of 30 rhizobacterial isolates were obtained. All these were then subjected to a battery of testes namely production of growth hormone (IAA), siderophore production, nitrogen fixation (ammonia production in Nitrogen free medium), ability to grow on ACC as nitrogen source (ACC deaminase production), HCN production (bio-pesticidal action), seed assay (improvement in germination rate) and seedling growth. Selected plant growth promoting rhizobacteria were then subjected to media optimization studies.

ABSTRACT (PEAM10)

PLANT GROWTH PROMOTING BACTERIA (PGPB) AZOSPIRILLUM SPP

*Suresh J Algudkar**
KVK (ICAR) Zonal agriculture research station, Kalaburgi, Karnataka
*Email *sureshalgudkar@gmail.com*

The old genus Azospirillum as a plant associated with bacteria and as a plant growth promoting bacteria (PGPB). Two main characteristics of the genus is fixation of N2 and production of phytoharmones. Azospirillum species include a single phytohormone activity, multiple phytohormone, N2 fixation, assortment of small size molecules, enzymes, enhanced membrane activity, proliferation of root system, enhanced water mineral uptake by xylem, mitigation of environmental stresses. Analyzing all these mechanisms, it was concluded this versatile genus Azospirillum possesses large potential mechanism and proved as “Multiple Mechanism Theory”.Inoculation of Azospirillum brasilence significantly induced root cell membrane to release protons (Proteins) Azospirillum produces lactins which helps in growing cell mitosis. Azospirillum strains produce indole acetic acid (IAA) in vitro form Inoculation of Azospirillum lipoferum and Azospirillum brasilence in paddy crop showed N2 fixation 20% (A. lipoferum) and 19.9% (A. brasilence) in Basmati rice and 58.9% (A. lipoferum) and 47.1% (A. brasilence) in super Basmati rice. Azospirillum halopraferans inoculation under saline stress conditions saline tolerating over 3% NaCl sea water. Inoculation of Azospirillum on wheat plants alleviated water stress under drought hit, rain failure and increased moisture holding in soil. Azospirillum biofertilizer could be stored for 31 weeks without disturbing viability of the organism. Production of Phytoharmones: Azospirillum spp. Are known to produce phytoharmones such as gibberlins (GAs), IAA (Indole Acetic acid), cytokinin’s, Polyamines and ethylene. Azospirillum brasilnese known to enhance seed generation of soya bean and wheat seeds. N2 fixation: most common mechanism fixation of N2 by Azospirillum spp. Contribution of N2 increase in green house plants and enhances nitrogenase enzyme activity in inoculated host plant.“Multiple mechanism theory” of Azospirillum spp. concludes that ecological viability (eco-friendly) and biological feasibility (in general).

Key Words: Azospirillum, N2, Phytohormones

ABSTRACT (PEAM011)

PURIFICATION AND CHARACTERIZATION OF A BIOSURFACTANT PRODUCED FROM A BACTERIUM ISOLATED FROM CRUDE OIL CONTAMINATED SOIL

Jyoti Sharma, Preeti Srivastava and D. Sundar
Department of Biochemical Engineering and Biotechnology, Indian Institute of Technology Delhi-110016
Email jyotisharma18sept@gmail.com

Biosurfactants are surface-active molecules produced from microorganisms either on the cell surface or secreted extracellularly. Several biosurfactant producing microorganisms have been isolated to date but they differ in their efficacy towards different types of hydrocarbons. Here we report the identification and characterization of a biosurfactant produced from a bacterium AS19 isolated from crude oil contaminated soil. The biosurfactant showed very high efficacy towards both aliphatic and aromatic hydrocarbons. The emulsification index was determined with petrol, engine oil and several other oil samples. Biosurfactant production was confirmed by oil spreading and drop collapse assays. The biosurfactant was purified and characterized further by LC-MS and FTIR. Our results suggest that the produced biosurfactant can be used for desludging of oil.

ABSTRACT (PEAM12)

ISOLATION OF PHOSPHATE SOLUBILIZING MICROORGANISMS FROM MANGROVES REGION OF KUTCH

Chinmay Manish Joshi
Email chinmayjoshi1511@gmail.com

The most efficient mineral phosphate solubilization (MPS) in gram negative bacteria occurs through solubilization of insoluble inorganic compounds like tricalcium phosphate, dicalcium phosphate and rock phosphate. Phosphate solubilization by potential nitrogen fixers like rhizobia may prove to be of dual advantage as it can solubilize phosphate as well as fix N for the plants, two of the most important macronutrients vital for plant growth. Many reports have shown ability of rhizobia to solubilize inorganic P Invitro through organic acid production. Gluconic acid production in rhizobia through external PQQ supplementation which results from extracellular oxidation of glucose via the glucose dehydrogenase to gluconic acid. Mungbean (Vigna radiata) nodule isolates solubilized mineral phosphate using glucose and secreting organic acid such as gluconic acid. P solubilization is one of the most important plant growth promoting traits among the others. However, P solubilization and organic acid production was repressed in the presence of succinate resembling the phenomenon of catabolite repression. This study will help to understand organic acid production and succinate mediated repression of organic acid production in this rhizobia. This study will certainly help to understand one of the factors of failure of efficient PSMs in field condition and possibly help in drawing a strategy to overcome it.

ABSTRACT (PEAM013)

STRUCTURAL AND FUNCTIONAL DIVERSITY OF FLUORESCENT PSEUDOMONADS THRIVING IN THE RHIZOSPHERE OF PIGEON PEA GROWN IN PARTS OF EASTERN UTTAR PRADESH

Stanzin Tundup, Amar Prajapati, Shiv Charan Kumar, Pushpendra Tiwari, Murugan Kumar, and Anil Kumar Saxena*
ICAR- National Bureau of Agriculturally Important Microorganisms, Mau Nath Bhanjan, Uttar Pradesh- 275103
*Email *kumarmic84@gmail.com*

Pigeon pea rhizospheric soil samples were collected from different sites of Ballia, Ghazipur and Mau districts of Uttar Pradesh. A total of 76 presumptive fluorescent pseudomonads were isolated from the soil samples employing specific media for isolation of fluorescent pseudomonads. All the 76 isolates were screened for plant growth promoting traits viz., solubilization of phosphorus and zinc, and production of siderophore, HCN, IAA and ammonia and an industrially important trait; lipase production. Among the 76 isolates, four isolates were able to solubilize phosphorus (P), and three were able to solubilize Zinc (Zn), 73 produced IAA and 71 tested positives for ammonia production. All the isolates tested positive for siderophore production and six tested positive for lipase production. Amplified ribosomal DNA restriction analysis was carried out using the restriction enzyme AluI which clustered 76 isolates into ten groups. From among 76 isolates 25 isolates were selected for identification based on the solubilization efficiency (P and Zn) and color intensity in IAA production test. Identification is done on the basis of sequencing 16S rRNA gene followed by BLAST search in EzBiocloud server (https://www.eztaxon.org). The isolates were represented by four species viz., Pseudomona plecoglossicida (9) Pseudomonas guariconensis (8), Pseudomonas monteilii (5) and Pseudomonas taiwanensis (1). These plant growth promoting strains of Pseudomonas spp. can be potential candidates of PGPRs for pigeon pea.

Keywords: Fluorescent pseudomonads, Plant growth promoting traits, Rhizosphere, Pigeon pea

ABSTRACT (PEAM14)

DECIPHERING THE POPULATION STRUCTURE AND DIVERSITY OF CHICKPEA NODULATING BACTERIA IN INDO-GANGETIC PLAINS

*Shiv Charan Kumar1, Rajni Singh2, Murugan Kumar1, and Anil Kumar Saxena*1*
1-ICAR- National Bureau of Agriculturally Important Microorganisms, Mau Nath Bhanjan, Uttar Pradesh- 275103
2-Amity Institute of Microbial Biotechnology, Amity University, Noida, Uttar Pradesh.
*Email *saxena461@yahoo.com*

Soil samples were collected from 16 different sites in Punjab (Districts: Phagwara, Phillaur, Goraya) and 8 different sites in Uttar Pradesh (Districts: Mau, Ballia, Ghazipur, Azamgarh) covering Indo Gangetic Plains (IGP). The population of rhizobia nodulating chickpea was enumerated by Most probable number method using 5-fold dilution and four replications. A range of native population exists in the IGP region. The root nodulating bacteria were isolated by using the plant trapping method from the root nodules of chickpea. More then 100 presumptive rhizobia were isolated from different samples. The rhizobia isolated from the nodules had moderate to fast growth. The analysis of 16s rRNA gene sequences of some of the isolates revealed that the isolates belonged to Mesorhizobium helmanticense and Mesorhizobium ciceri. The plant growth promoting activity was performed for the isolated rhizobia from the IGP region. Among the 46 isolates screened, 12 isolates were able to solubilize P and 14 isolates were able to solubilize Zn in the plate-based assay, as evidenced by the formation of a clear halo zone around the colony. Fifteen isolates were positive for siderophore production showing a yellow zone on the CAS agar medium plate. About 11 isolates recorded positive for K solubilization. A study was conducted in Leonard jar assembly to evaluate 46 strains of chickpea rhizobia for their efficiency in growth enhancement of chickpea (Cultivar: Pusa 362), Nodule number, weight of nodule, shoot and root fresh weight were recorded to select efficient strains for chickpea cultivar. Mesorhizobium cicer Ca7 followed by Mesorhizobium helmanticense Ca2 were identified as efficient strains. The field evaluation of these cultures is in progress.

Keywords: Indo Gangetic Plain, Root nodulating bacteria, PGP traits, Chickpea.

ABSTRACT (PEAM015)

PHYSIOLOGICAL STUDIES OF INDIGENOUS METHANOTROPHS ISOLATED FROM INDIAN RICE FIELDS AND WETLANDS

Jyoti Mohite 1,2, Kumal Khatri1,2, Pranitha S. Pandit1,2, Monali C. Rahalkar1,2***
1 Bioenergy group, MACS-Agharkar Research Institute, Gopal Ganesh Agarkar road, Pune 411004, Maharashtra, India
2 Savitribai Phule Pune University, Ganeshkhind Road, Pune 411007, Maharashtra, India
**jyotimohite@aripune.org, **monalirahalkar@aripune.org*

Methane-oxidizing bacteria (methanotrophs) naturally mitigate methane by oxidizing it. In various natural habitats, methane-oxidizing bacteria (methanotrophs) are present. Methanotrophs oxidize methane under the aerobic environment by utilizing it as a source of carbon and energy. We earlier isolated methanotrophs from many different environments, including freshwater, sediments, rice paddies, soil, wetlands, etc. Five strains of methanotrophs, i.e., Methylolobus strain FWC3, Methylomonas strain WWC4, Methylobacter strain KRF1, Methylomicrobium strain RS1, and Methylomagnum strain KRF4 were evaluated for growth and methane utilization. The effect of temperature on these five cultures of methanotrophs was examined in the range of 15°C to 45°C. All the tested methanotrophs were found to be mesophilic. \Methanotrophs utilize methanol as an interchange carbon and vitality substrate for their growth. As higher concentrations of methanol are toxic, we checked the methanol tolerance level of all the five strains of methanotrophs. The range of methanol concentration from 0.02% to 8% covering 30 different concentrations was chosen. Methylolobus strain FWC3 can grow optimally at a methanol concentration of 2%. Other strains of methanotrophs such as Methylomonas strain WWC4 and Methylocystis strain SnCys could tolerate a methanol concentration of 1.6% and 1% respectively. To regulate the gene expressions of sMMO and pMMO, copper (Cu) being a key regulator involved in the physiological activity of methanotrophs. To assess this circumstance, the copper concentrations in the range between 0.5 to 50 µM were examined. Methylobacter strain KRF1, Methylolobus strain FWC3, Methylomicrobium strain RS1, and Methylomonas strain WWC4 showed maximum growth at copper concentrations from 0.5 to 3µM, whereas, Methylomagnum strain KRF4 could tolerate copper concentration up to 50 µM.

Key words: Methanotrophs; Methanol tolerance; Copper effect; Mesophilic

ABSTRACT (PEAM16)

DECOLOURISATION AND DETOXIFICATION OF RECALCITRANT TEXTILE DYE BY FUNGAL LACCASE AND TOXICOLOGICAL ASSESSMENT OF ITS DEGRADED BIOPRODUCT

*Ashutosh Yadav, Vivek kumar and Abhay Raj **
Environmental Microbiology Laboratory, Environmental Toxicology Group, CSIR-IITR, Lucknow-226001, Uttar Pradesh, India.
Email ashutoshyadav.shalu@gmail.com

Bioremediation of textile wastewater can be enhanced by the use of lignolytic enzymes such as laccase. A robust and efficient treatment process is required to problem of synthetic dyes from textile industries. Due to synthetic dyes released to the environments and their low biodegradability, this work aimed the potential capacity of laccase enzyme was used to optimize the decolourisation process for anthraquinone Remazol Brilliant Blue R dye. In this study, Response Surface Methodology (RSM) using Box-Behnken Designs (BBD) was applied to optimize the decolourisation of recalcitrant RBBR dye treated with laccase produced by (fungal strain). In decolourisation process for RBBR were used the optimum concentration of laccase dose (2IU/ml), neutral pH (6.0), temperature (35 °C) in the reaction mixture, respectively. At the present result, the laccase (2IU/ml) was able to decolourise 93% of 100 mg/L RBBR within 4 h. The dye degradation was confirmed by UV-vis spectrum, ATR-FTIR, HPLC and GC-MS analysis. In addition, toxicological analysis of degraded product of the RBBR dye was evaluated using Allium cepa by determining cell death and metabolic activity. The degraded product after laccase treatment was revealed the non-phytotoxic and non-cytotoxic nature.

Keywords: RBBR, Laccase, Decolourisation, GC-MS, Phytotoxicity, Allium Cepa

ABSTRACT (PEAM017)

EXPLORING STRESS TOLERANT PGPR FOR DROUGHT RESILIENCE IN GREEN GRAM AND CLUSTER BEAN

*Saritha M*1., R.C. Kasana2, Praveen Kumar1, N.R. Panwar1, Uday Burman1*
1Division of Integrated Farming System, ICAR-Central Arid Zone Research Institute, Jodhpur, Rajasthan
2ICAR-Central Institute of Post-Harvest Engineering & Technology, Ludhiana, Punjab
*Email *Saritha.M@icar.gov.in*

Rhizosphere soil samples of mungbean and clusterbean were collected from Jodhpur, Pali, Jalore, Nagaur, Ajmer, Barmer and Jaisalmer districts of Rajasthan and bacterial isolations were done. Isolates were screened for plant growth promoting attributes like phosphate and potassium solubilization, siderophore, ammonia, hydrogen cyanide, indole acetic acid production, phytase and catalase activities. Isolates which possessed three or more PGP attributes and which showed growth at 20% PEG 6000 were used to treat mungbean and clusterbean seeds. Bacterial treatment increased seedling shoot length by 2-32 % in mungbean and 2-8% in clusterbean, and root length by 6-18 % in mungbean and 1-21% in clusterbean. The treatments also increased root and shoot dry weights, with significant increase observed in treated mungbean seeds. The bacterial isolates which showed better results in the lab were used for studies in pots and in field. In pots under drought stress, the isolates G8-7, G10-1 and MPSB2 enhanced mungbean seed weight, significantly. In clusterbean, the isolates G8-7, G10-1, G12-3, G21-9 and MPSB2 significantly enhanced the plant dry weight and seed weight under drought stress. Study on effect of PGPR treatment on the antioxidant status of plants showed that catalase and peroxidase were produced by the plants in less amounts under stress following bacterial treatment. In clusterbean, all the treatments significantly reduced the enzyme levels to 40-80% compared to control under drought stress. The cultures, G8-7, G12-3 and G21-9 also improved the crop physiological parameters, mainly the leaf area, nitrate reductase activity, chlorophyll fluorescence and the relative water content, under drought stress conditions. Under field conditions, the isolates G10-1 and G12-3, followed by G21-9, G8-7 and MPSB2 increased the yield and yield attributes significantly as compared to control. These promising isolates have been identified by 16SrRNA gene sequencing as Rhizobium pusense, Bacillus pseudomycoides, Bacillus subtilis and Acinetobacter baumannii.

ABSTRACT (PEAM18)

EXPLORATION OF METHANE-OXIDIZING BACTERIA FROM RUMINANTSAND HERBIVORES

*Kumal Khatri1,2, Jyoti Mohite1,2, Pranitha S. Pandit1,2, Rahul A. Bahulikar2,3, Sumit S. Dagar1,2, Monali C. Rahalkar1,2,**
1Bioenergy group, MACS-Agharkar Research Institute, Gopal Ganesh Agarkar Road, Pune 411004, Maharashtra, India
2Savitribai Phule Pune University, Ganeshkhind Road, Pune 411007, Maharashtra, India3BAIF Development and Research Foundation, Central Research Station, Pune, India
*Email * monalirahalkar@aripune.org*

Methane is the second most abundant hydrocarbon and a potent greenhouse gas after carbondioxide. Methane emissions from ruminants are one of the important sources of anthropogenic methane and a major by-product of anaerobic digestion. Methanotrophs or methane-oxidizing bacteria use methane as their carbon and energy source. Methanotrophs are almost always oligate, growing only on methane or (sometimes) methanol which is the first intermediate in methane utilization.There has been no concrete evidence of the presence of methanotrophs, unlike methanogenicarchaea, in the rumen gut. However, methanotrophs do exist in the rumen gut as showed inmetagenomic studies of cow rumen studied by a research group in Australia. We present hereone of the first studies on the enrichment and isolation of methanotrophs from fecal samples of various ruminants and herbivores. A total of 13 strains of methanotrophs were isolated in which one of the strains was found to be a novel member of the genus Methylobacter and named strain BlB1. Based on the phylogenetic affiliation the strain BlB1 is found to be putative novel species. Strain BlB1, isolated from the feces of an Indian blackbuck (Antilope sp.) showed aclose phylogenetic affiliation to Methylobacter marinus A45T (98.46% similarity). The strain BlB1 showed the presence of coccoid or diplococcus cells (1.5-2 µm in diameter) and formed yellow colonies on an agarose medium. The draft genome showed 27.4% DDH and 83.07%ANIb values with the same species. While, methanotrophs from cow, horse, spotted deer, showed the phylogenetic affiliation to Methylocaldum species, isolate from camel to Methylocystis.
Keywords: Methane; Methanotrophs; Rumen methanotrophs; Methylobacter

ABSTRACT (PEAM019)

IN SILICO BIOTRANSFORMATION OF EMERGING CONTAMINANTS OF HIGH CONCERN 17SS-ESTRADIOL AND 17A-ETHINYL ESTRADIOL EXPLOITING MICROBIAL BIOCATALYTIC REACTIONS AND BIODEGRADATION PATHWAYS PREDICTION TOOL

Anil Kumar Singh1, 2, Abhay Raj1, 2
1Environmental Microbiology Laboratory, Environmental Toxicology Group, CSIR-IITR, Vishvigyan Bhawan, 31, Mahatma Gandhi Marg, Lucknow-226001, Uttar Pradesh, India
2Academy of Scientific and Innovative Research (AcSIR), Ghaziabad-201002, India
Email phd.anil@yahoo.com

Endocrine-disrupting chemicals (EDCs) are the contaminants of high concern for inducing health hazards in humans. Wastewaters from different industrial sources are the key emerging points and accountable for the significant quantitative contribution of different EDCs. Less effective treatment, partially with flaws and scarce transformed compounds are the major parts of the advanced oxidation process and photocatalysis process. For addressing and quickly solve such concern, herein we evaluated the in silico resource for possible biodegradation/transformation pathways prediction. In the present focus, we selected two potent known human EDCs, most prevalent in wastewater treatment plants (WWTPs) as; 17ß-estradiol and 17a-ethinyl estradiol. Both are contaminants of high concern and required urgent mitigation from different mediums. We convert both compounds in SMILES for molecular descriptor information, and precede it under EAWAG-BBD: Pathway Prediction system for possible bt rule-based transformation in simplest and relatively less hazards form. Transformed results reveal the rule-based transformed compounds in several stages with aerobic likelihood. Such simplicity and hybrid biodegradation can further implement directly at the wet lab level to biodegradation both EDCs at significant quantities.
Keywords: Biodegradation pathways prediction; EDCs; in-silico; biotransformation; biological hazards.

ABSTRACT (PEAM20)

AN OVERVIEW ON FUNGICIDE THIRAM APPLICATION, TOXICITY AND ITS EFFECTS ON ENVIRONMENT WITH THEIR MICROBIAL DEGRADATION BY SOIL ORGANISMS

*Sonalkunwar Chouhan and Dweipayan Goswami**
Department of Microbiology and Biotechnology, University school of sciences, Gujarat University, Ahmedabad – 380009
Email sonal.kunwar85@gmail.com

India is farming based country where 70% of the universe is depending on pesticides yield. The indiscriminate utilization of pesticides in agricultural field has resulted into contamination of soil environment leading to toxicity in the biological diversity. Thiram (tetramethylthiuram disulfide) is carbamate group of fungicides is apply for control the crop, seed treatment, animal repel, rubber accelerator. It has been used in the treatment of human scabies, as a sunscreen and as bactericide medicated soap. It's also effectively used in mice in vitro against Tricophyton and control fungal diseases on safflower (Pythium spp., Fusarium spp.) and damping-off diseases (Phytophthora and Pythium spp.) of maize, ornamentals and vegetables. Increased utilization of pesticides can result in various health and environmental problems like pesticides poisoning in farmers and farm workers, neurological, skin disorders and cardiopulmonary. Pesticides of feet nervous system of target pest and nontarget organism by disrupting acetycholinesterase activity, the enzyme that regulate the acetylcholine. Usually microbial degradation is powerful and active method to degrade and detoxify pesticides pollutants. Thiram could be degraded as a major source of carbon and energy by Pseudomonas Aeruginosa, Bacillus spp., Artrobacter spp., Aspergillus niger and Penicillium steckii. Their repeated application in crop improvement is understood but their toxic nature cause serious environment burden so that this study is necessary.
Keywords: Agriculture, Thiram (TMTD) pesticides, Biodegradation, Soil Organisms

ABSTRACT (PEAM021)

COMPOSTING OF PARTHENIUM HYSTEROPHORUS USING MICROBES

Monika Kayasth and Jagdish Parshad*
Department of Microbiology, COBS & H, CCS HAU, Hisar
Email monakayasth@gmail.com

Parthenium hysterophorus is one of the worst weeds in the world. It spreads rapidly in all regions of the country and adversely affecting crop production, animal husbandry and biodiversity. It is poisonous, allergic and aggressive dominating weed due to its allelopathic properties and fast growth rate, which enables it to compete with other crops. The allelochemicals such as parthenin released from Parthenium affects many plant species. This proves disastrous in terms of space and nutrients at the expense of other vegetation. So options must be sought for management of Parthenium in a sustainable way. One option is utilizing Parthenium as a nutrient source in the form of compost. In the present investigation, composting of uprooted Parthenium before flowering was carried out at pit house located at CCS, HAU, Hisar. Cattle dung was mixed with parthenium and microbial consortia in different ratio. The compost samples were withdrawn at interval of 15 days and analyzed for change in organic carbon, total N and C:N ratio. Organic carbon of compost ranged from 34.97-37.01% and nitrogen content varied between 0.80-0.85%. C/N Ratio at 60 days was found to decrease from 46.26 - 41.14. By using problematic weed Parthenium for preparation of compost, we can avoid environmental hazards of use of chemical herbicides as well as chemical fertilizers. This is environment friendly method to increase soil productivity leading to sustainable agriculture. Utilization of Parthenium for the preparation of compost will provide new perspective in nutrient management of soil.
Keywords: Parthenium, compost, sustainable, weed.

ABSTRACT (PEAM22)

EXPLORING CYANOBACTERIAL AMENDMENT AS AN OPTION TO ENRICH SOIL CARBON AND INCREASED NUTRIENT AVAILABILITY UNDER ELEVATED CO2 ENVIRONMENT

*Kokila V, Nishanth S, Arun Kumar, Lata Nain and Radha Prasanna**
Email kokilavc93@gmail.com

Cyanobacteria are photosynthetic prokaryotes, which can accomplish fixation of C and N, leading to savings of nitrogenous fertilisers, improved crop productivity and soil fertility. Biological-CO2 mitigation triggered through efficient fixation and release of metabolites rich in carbon by cyanobacteria is gaining significance in the climate change scenario for usefully diverting the excess C to useful products or soil biomass carbon. Cyanobacteria possess mechanisms for actively acquiring and transporting C to discrete structures known as carboxysomes in which C-fixing enzymes Rubisco and carbonic anhydrase (CA) are packaged. The focus of the present investigation was to compare the performance of cyanobacterial inoculation in soil, under ambient (aCO2) and elevated (eCO2) environments. Preliminary analyses revealed significant enhancement in chlorophyll accumulation, proteins and C and N assimilating enzyme activities under elevated (eCO2) conditions. Biomass of Anabaena laxa (RPAN8) was added to the soil surface in pots kept under controlled conditions, in the National Phytotron Facility, IARI, New Delhi. The addition of cyanobacteria, when compared with control (uninoculated pots) recorded 48% higher N availability in soil under elevated condition, while only 27% increase was recorded under ambient control pots. Organic C in soil showed an almost 30% increase under eCO2, as compared to ambient conditions vis-à-vis only 15% increase in uninoculated soil. The values of soil polysaccharides and soil chlorophyll showed a two-fold increase while proteins and dehydrogenase activity showed a 10-30% enhancement in the A. laxa-primed treatments, as compared with controls. Soil chlorophyll, available nutrients and soil enzyme activities were correlated positively with one another. The phospholipid fatty acid (PLFA) profiles of soil samples provided interesting results, illustrating the changes in the total biomass and distribution of soil microbial communities. Further experiments are being undertaken to investigate the long-term beneficial effects under elevated CO2 levels for benefitting crop productivity.
Keywords: CO2; chlorophyll; cyanobacteria; nitrogen; PLFA; soil carbon

ABSTRACT (PEAM023)

BIOSORPTION OF CHROMIUM FROM AQUEOUS SOLUTION USING VARIOUS WASTE BIOMASSES

Ankita B. Kheradia1, Devayani R. Tipre2, Shailesh R. Dave3, Viral Y. Shukla1*
1 L.J Institute of Applied Sciences, L.J. Campus, Between Sanand Sarkhej Circle, Ahmedabad, Gujarat.
2Department of Microbiology, School of Sciences, Gujarat University, Ahmedabad, Gujarat.
3Xavier's Research Foundation, St. Xavier's College Campus, Navrangpura, Ahmedabad, 380009, India
*Email *ankitakheradia@gmail.com*

Heavy metals are one of the most serious problem of environmental pollution. Gradual uptake of heavy metals even in low concentration can cause several disorders in human. The effluent of industries like metal mining, electroplating, metal finishing etc. contains high concentration of heavy metals. Chromium are found in various industrial effluents. The use of dead biological material for removal of heavy metal is an alternate to conventional methods. Screening of the biomass for chromium biosorption was conducted using six different waste dead biomasses namely, cabbage leaves waste, lemon peel, groundnut shell, eucalyptus leaves, banana trunk, and pineapple peel. Dry weight and wet weight of all the biomasses was done. Initial chromium ion concentration were checked before and after digestion of biomasses. Efficiency in removal of chromium metal as compared to other tested biomasses and results of sreening showed 80.6%, 47%, and 78% chromium removal by groundnut shell, banana trunk, pineapple peel biomass respectively. The highest Cr biosorption was obtained at pH 6.0 with groundnut shell biomass, banana trunk biomass showed maximum sorption at pH 4.0. While sorption of Cr by pineapple peel biomass was observed highest at pH 3. The optimum contact time for chromium biosorption by banana trunk, pineapple peel, ground nut shell biomass were 120 min, 90 min and 90 min respectively.

ABSTRACT (PEAM24)

STATICALLY PROVEN: QUANTITATIVE RESPONSE OF PHOSHATE SOLUBILIZING BACTERIA ON FOUR WHEAT GENOTYPE IS POSITIVE AND OCCURS IN GENOTYPE SPECIFIC MANNER

Hemant Dasila1, V.K.Sah2, Vandana Jaggi1, Samiksha Joshi1 And Manvika Sahgal1*
1Department of Microbiology, G.B Pant University of Agriculture and Technology, Pantnagar, Udham Singh Nagar, Pantnagar.
2Department of Agronomy, G.B Pant University of Agriculture and Technology, Pantnagar, Udham Singh Nagar, Pantnagar.
*Email *hemantdasila4@gmail.com*

In present study effect of 18 phosphate solubilizing bacteria (PSB) recovered from Dalbergia sissoo Roxb. forest soil on wheat for plant vigor were examined. To evaluate this, four superior wheat genotypes e.g. UP 262, PBW 502, HDV 2329, and CBW 38 were chosen and examined statically whether effect of 18 PSB is genotypes specific or not and for that two hypothesis e.g. null and alternative hypothesis were drawn and analyzed by R-software tool at p-value 0.5 or 50%. To examine soil health, three soil enzyme activities e.g. Fluroscein di acetate hydrolysis (FDA), alkaline phosphates (AP) and urease were monitored. Since FDA is representation of total microbial activity e.g. FDA directly correlates with other two enzyme activities. In FDA, response of L3 and P2 was 333002 and 334002 nmol gm-1 respectively which was significantly higher as compared to uninoculated control (28791 nmol-1gm-1). Similar trend was found in other two soil enzyme activity viz., AP and Urease and these results were further supported by quantifying phosphorous in NBRIP medium. The reflection of soil enzyme activity was seen in plant vigor. Overall impact of 18 PSB on four wheat genotypes was positive but response of two PSB e.g. L3 and P2 was significantly higher in all four wheat genotypes. For example in UP 262 at 90 DPI, shoot length of wheat plants inoculated with the majority of 18 PSBs was higher as compared to untreated control (17.66 cm) but the maximum response was observed in wheat plants inoculated with L3 (28 cm) and P2 (27 cm) respectively but quantitative response of 18 PSBs in all four wheat genotypes is different as concluded upon examining hypothesis by R-software.

Keywords: PSB, Genotypes, R-software, Soil enzymes.

ABSTRACT (PEAM025)

COMPARATIVE EFFICIENCY OF DIFFERENT PLEUROTUS SPECIES FOR THEIR YIELD AND NUTRITIONAL PROPERTIES USING PADDY STRAW AS SUBSTRATE

*Asha Singh Rajavat1, 2, Neeraj Shrivastava2, Neha Pandey2, Samadhan Yuvraj Bagul1, V. Mageshwaran1, Abha Agnihotri2, Anil K. Saxena1, K Pandiyan1,3**
1 ICAR-National Bureau of Agriculturally Important Microorganisms, Mau
2Amity Institute of Microbial Technology, Amity University, Noida
3ICAR-Central Institute for Research on Cotton Technology (CIRCOT), Mumbai
*Email *pandiannkl@gmail.com*

Oyster mushroom (Pleurotus spp.) is second most attractive crops worldwide next to button mushroom (Agaricus bisporus) due to low cost production technology and high nutritional value which provides consistent growth with high biological efficiency. The present work was aimed to evaluate the potential yield, biological efficiencies and nutritional of different Pleurotus species using paddy straw as substrate. The mushrooms were harvested in three flushes and total fresh and dry weight for the Pleurotus species were ranged from 1501.31- 2417.5 and 261.14-353.06 gm/kg dry substrate respectively. The highest yield of 2417.53 gm/kg dry substrate was recorded in Pleurotus ostreatus (DMRP66). The highest (>90%) biological efficiency was recorded in P. ostreatus strains DMRP66 (96.37 %), DMRP122 (91.95%) while the least was observed in P. Pulmonarius (60.05%) and P. flabellatus (72.05%). The highest dry matter loss of 54% was observed in P. ostreatus (DMRP66) and the lowest 30% was recorded in P. Pulmonarius. Nutritional characteristics such as moisture, carbohydrate, protein, fat, crude fiber and ash content of oyster mushroom were studied. The moisture content of oyster mushrooms varied from 80 - 89 %. Total carbohydrate and protein content were found to be varied from 25.12 – 56.87 (g/100g) and 21.14 - 41.03 (%), respectively, among the cultivated strains. P. pulmonarius showed maximum carbohydrate (56.87 g/100g) while highest protein content was recorded in fruiting bodies of P. ostreatus DMRP66 (41.03 %). Total fat content was found to be greater in P. Pulmonarius (1.90) while lowest in P. ostreatus DMRP66 (1.01) and crude fiber was maximum in P. ostreatus DMRP66 (31.04 ± 1.1) as compared to others. The results showed that the oyster mushroom, P. ostreatus is the potential candidate among Pleurotus species cultivated on paddy straw (lignocellulosic) substrate based on yield and nutritional quality properties.
Keywords: Oyster Mushroom; Pleurotus spp.; yield; biological efficiency; nutritional value.

ABSTRACT (PEAM26)

RICE RHIZOSPHERE MICROBIOMES AS INFLUENCED BY REDOX CYCLING OF IRON AND NITROGEN

Elakkya M, Prusty Prashant, Shivay Y.S., Prasanna R., Ramakrishnan B.*
ICAR-Indian Agricultural Research Institute, New Delhi-110012
*Email *elakkya1996@gmail.com*

Iron is the most abundant redox-active metal and has a significant impact on nutrient cycling in rice soils. The agricultural practices such as N fertilizers and microbial inoculants may impact the iron deposition on roots. Frequent high-amplitude redox fluctuations in the rice paddy ecosystem can act as a strong selective force on the rhizosphere microbiome's phylogenetic and physiological composition. As several members of Archaea and Bacteria involved in the nitrogen- and iron cycling processes are challenging to study using the culture-based laboratory methods, the quantification of microbial taxonomic- and functional genes associated with these cycling processes by the qPCR assay was undertaken in field-grown rice plants (cv. Pusa Basmati 1509). The rice plants were cultivated by two methods [conventional flooded (CF) and direct-seeded rice (DSR)] and different nutrient management practices using chemical and biological fertilizers. The composition of microbial communities based on the taxonomic groups using the 16S rRNA gene copies was determined while the functional genes related to N-cycling, iron-oxidation and iron-reduction were quantified at the vegetative and flowering stages from the rice rhizosphere. The potentials for iron reduction, arginine ammonification, and ammonium oxidation activities were more at the vegetative stage than at the flowering stage of rice growth, especially under the CF method. The application of the new consortium with ammonium oxidizers had a distinct effect on β-Proteobacteria, Bacteroidetes, and Acidimicrobium, compared to that of the Anabaena-Nostoc consortium and the biofilm of Anabaena torulosa and Mezorhizobium ciceri. Precise and accurate analysis of microbial community structure and elemental cycling genes are needed to understand better plant-microbe interactions, microbe-microbe interactions, microbial mineral transformation in soil, which are critical for applying chemical- and biological fertilizers.

ABSTRACT (PEAM027)

ISOLATION AND SCREENING OF CADMIUM, LEAD AND NICKEL TOLERANT RHIZOBACTERIA FROM PIRANA LANDFILL SITE, AHMEDABAD, GUJARAT, INDIA

*Sarita Sharma, Ritika Jain, Meenu Saraf**
**Department of Microbiology and Biotechnology, University of School of Sciences,Gujarat University Ahmedabad-380009, Gujarat (India)*
*Email *sarafmeenu@gmail.com*

Soil pollution and Municipal solid waste landfill site contamination due to heavy metals is one of the major environmental problems in many countries and have a dangerous effect on soil environment, quality of ground water, human health over bioaccumulation through the food chain. The Pirana landfill site is a municipal solid waste dumping site, has a multifarious contaminating source which offer an extortion microbial diversity. Bioremediation processes for soil contaminated with heavy metals is an eco-friendly pathway to remediate pollution. For this purpose, the present study represents the isolation and screening of Cadmium, Nickel and Lead tolerant rhizobacteria from the Pirana Landfill Site, Ahmedabad, Gujarat, India. The composite rhizosphere soil samples were collected and enriched in the nutrient broth, which is supplemented with 100 ppm of HMs (Cd^{2+}, Ni^{2+} and Pb^{2+}). Serial dilution tubes were prepared from enriched broth and aliquots of dilution were spread on N-agar plates supplemented with 100 ppm of HMs (Cd^{2+}, Ni^{2+} and Pb^{2+}). Total 40 rhizobacteria were isolated and the morphological and colonies characteristics of isolated rhizobacteria were noted. For Screening of Cd^{2+}, Ni^{2+} and Pb^{2+} tolerate rhizobacteria were carried out by using Minimum Inhibition Concentration (MIC) method – solid agar plate method. The starting concentration of HMs was 100µg/ml. In this method the concentration of heavy metal gradually increasing, 100 µg/ml each time on N- Agar plate having respective heavy metals until the strains failed to give colonies on the plate. Out of 40 isolated rhizobacteria, Four isolates (SPHM4, SPHM17, SPHM18, SPHM38) revealed a very high grade of tolerance from 100 to 1700 µg/ml against Pb^{2+}, Two isolates (SPHM4, SPHM23) revealed a very high grade of tolerance from 100 to 1200 µg/ml against Cd^{2+}, one isolate (SPHM38) revealed a very high grade of tolerance from 100 to 4500 µg/ml against Ni^{2+}. These isolates may be used as prospective agents for plant growth promoting rhizobacteria assist phytoremediation of heavy metals in contaminated soil.

ABSTRACT (PEAM28)

SYNTHETIC PLASTIC BIODEGRADATION BY MICRO-ORGANISMS

*Christian Venisha V1, Makwana Sonal K1 and Thakkar Aarti V.*2*
1Department of Microbiology and Biotechnology, University School of Science, Gujarat University, Ahmedabad380009, Gujarat
2Department of Microbiology, President Science college, Ahmedabad-380061, Gujarat, India.
Email venishachristian.vc@gmail.com

General term used for high molecular weight polymer is “Plastic”. They are light weighted, durable, corrosion resistant materials, strong, inexpensive and the uncontrolled use of plastic has led to various environmental and health problems. Scientists have reported many adverse effects of the plastic in the human health and environment. Plastic causes because of increase in plastic waste disposal and burning of plastic waste causes air pollution due to the release of CO_2 and dioxins. Interest is growing for using microorganisms effectively for biodegradation of synthetic polymers. Biodegradation of plastic is a slow process but refers to change in physical and chemical properties of polymer induced by heat, light, moisture and biological agents such as Bacteria and Fungi. Different strains degrade different types of plastic waste. Various methods are used for evaluation of biodegradation of plastic such as FTIR, Strum Test, etc. Biodegradation of plastic promises a reduction in plastic waste.

ABSTRACT (PEAM029)

IMPACT OF NATURAL INOCULUM ADDITION ON FOOD WASTE COMPOSTING

*Jayanta Andraskar a,b, Shailendra Yadav b, Atya Kapley a,b**
a Academy of Scientific and Innovative Research (AcSIR), Ghaziabad 201002, India
b Director's Research Cell, National Environmental Engineering Research Institute (CSIR-NEERI), Nehru Marg, Nagpur 440020
*Email *a_kapley@neeri.res.in*

Rising food waste (FW) generation puts a substantial load on the municipal waste management systems. Among the different food waste management techniques composting has acquired attention due to its economic feasibility and reliability for food waste recycling. Under natural environmental conditions, the efficiency of the composting process is determined by multiple factors. The addition of inoculum during the composting process increases the biological degradation rate of food waste and improves compost quality. In this study, we have examined the effect of two natural inoculums addition (cow dung and compost made from food waste composting) on the food waste composting. An experiment set consists of food waste mixed with dried leaves as a bulking agent for optimum C/N ratio (mix food waste + 2% cow dung and mix food waste + 2% compost) with control (no added inoculum). A Composting experiment was conducted for 28 days, including initial and final values of physicochemical parameters such as moisture content, C/N ratio, pH, and TOC were determined by standard methods. Although the composting process's efficiency depends on various influential physicochemical parameters, but the C/N ratio is considered as a critical parameter to assess composting efficiency and final compost quality. Results showed that 50.5% and 44.7% C/N ratio reduction was observed in cow dung and compost added food waste, respectively, than in control (37.5%). However, a detailed evaluation is necessary to evaluate this natural inoculum's effect on other physicochemical parameters, composting microbial profile, and final compost quality.

Keywords: Compost, Cow dung, C/N ratio, Food waste, Composting

ABSTRACT (PEAM30)

FUNCTIONAL DIVERSITY OF BACTERIA FROM NEEM (AZADIRACHTA INDICA) GUM

Pragya Saxena1,2, Hillol chakdar1 , Arjun Singh3, K Pandiyan4, M Kumar1, Sheetal shirodkar2, Alok K Srivastava1*
1 ICAR National Bureau of Agriculturally Important Microorganisms (NBAIM), Mau, Uttar Pradesh-275103
2 Amity institute of Biotechnology, Amity University, Uttar Pradesh, Noida-201313
3 ICAR-CSSRI Regional Station, Lucknow, Uttar Pradesh- 2260024ICAR-CIRCOT, GITC, Nagpur, Maharashtra- 440023
*Email *pragya.saxena070988@gmail.com*

Plant parts and secretions are one of the specialized niches that support unique microflora. Neem is one of the most important medicinal plants which has diverse pharmacological applications. Neem gum is produced from wounded stem and is brown viscous water soluble substance. Chemically it contains poly saccharides and carbohydrates. In the present study, we aimed to functionally characterize bacterial population derived from Neem gum. 50 different bacterial isolates were obtained using different media. These isolates were characterized functionally on the basis of their plant growth promoting activity, physiological adaptations and enzyme production. 90% of the isolates were found to be positive for IAA production, 42% were siderogenic, 24% were positive for HCN production. Approximatley 12% isolates were P solubilizers, 36% were Zn solubilizers and 12% K solubilizers. About 26% of the isolates showed amylase activity ,30% showed cellulase activity , 28% showed lipase activity while 62% had pectinase activity. The results indicated that functionally diverse bacteria were present in Neem gum. 56% bacteria tolerated pH ranging from 5-10, 16% bacteria could tolerated salt (NaCl) concentration ranging from 0.5-10%. Predominance of IAA producing bacteria indicated their possible role in healing of the injured part through eliciting cell divisions.

Keywords:-Plant growth promotion, enzymatic activity

ABSTRACT (PEAM031)

AEROBIC AND ANAEROBIC REACTORS APPLIED IN TREATMENT OF SDBS: UNVEILING THE MICROBIAL COMMUNITY BY GENE AND GENOME-CENTRIC APPROACHES

*Upasana Arora1, Himanshu K. Khuntia1,H.N. Chanakya2, Atya Kapley1**
1 Director's Research Cell, National Environmental Engineering Research Institute (CSIR-NEERI), Nehru Marg, Nagpur 440020, India
2 Centre for Sustainable Technologies, Indian Institute of Science, Bangalore 560012, India
*Email *a_kapley@neeri.res.in*

Gene and genome-centered approach were enforced to check the metabolic diversity profiles and microbial taxonomy from lab-scale anoxic, aerobic, and anaerobic reactors. Anionic surfactant wastewater with increasing concentrations of Sodium dodecylbenzene sulphonate (SDBS) was applied. Metagenomic analysis was conducted with samples taken from three reactors, AGN (Anoxic), AGA (Aerobic) & AGAm5 (Anaerobic) fed with synthetic medium and SDBS. Metagenome sequencing was carried out by Illumina Hiseq 2 x 150bp platform. Gene-based analysis at each of the steps for metabolic-pathway (fumarate addition, β-oxidation, desulfonation, and ring cleavage) for degradation exhibited various representative genes in samples, suggesting a core microbial role in SDBS biodegradation. Some genera were recovered through a binning method, depicting sixty-eight bacterial and eight archaeal metagenome-assembled-genomes (MAG's). The degradation pathway reconstruction of SDBS using the various MAGs unveiled the syntrophy for complete degradation of SDBS. MAG's for taxonomic annotation for Enterobacter, Pseudomonas, Sulphospirilum showed genetic context. The current study represents a genome-centric path to study anionic surfactants applied to biological reactors, depicting the metabolic knowledge of the primary organisms involved in SDBS degradation. The outcome of the study will pave the way for aiming biostimulation and bioaugmentation of intrinsic microbial communities.

ABSTRACT (PEAM32)

DECIPHERING THE INTERACTIONS OF CYANOBACTERIUM ANABAENA LAXA WITH PHYTOPATHOGENIC FUNGI

*Udita Gulia, Jyoti Shukla, Lata Nain, Radha Prasanna**
Division of Microbiology, ICAR-IARI New Delhi
Email lostsoul199721@gmail.com

Cyanobacteria are promising candidates as biofertilizers and plant growth promoting agents; however, their role as biocontrol agents against phytopathogenic fungi is less explored. The focus of the present study was to understand the interactions of Anabaena laxa against common soilborne phytopathogenic fungi - Fusarium solani and Rhizoctonia solani which are a major scourge in nursery-raised crops. In vitro experiments using two types of media - BG11 and BG11 + PDB, 1: 1 (BG-PDB), recorded interesting results. A significant increase of 32.2 and 75% was recorded in IAA and CMCase activity respectively, in BG-PDB + A. laxa + F. solani, whereas there was a decrease of 2.88% in IAA in treatment BG-PDB + A. laxa + R. solani. An increase of 46.66% in terms of seed germination of tomato was observed with extract from BG11 grown A. laxa + F. solani. Except for chlorophyll, BG-PDB medium showed an increase in all parameters as compared to BG11 medium. Light and electron microscopic examination illustrated no inhibitory effect of F. solani on the growth of A. laxa and akinetes were observed after 23 days in BG11 + A. laxa + F. solani/ R. solani. However, no akinetes were observed in BG-PDB medium, but the cells of A. laxa contained numerous cyanophycin granules in all treatments with BG-PDB medium, after 6 days of co-inoculation. Interesting results were recorded in terms of siderophore production and volatiles. Comparative analysis of all parameters of different treatments with R. solani and F. solani showed that R. solani is more inhibitory as compared to F. solani and the latter functions more towards growth promotion of A. laxa. Further research is focussed towards understanding the expression of genes involved in plant-cyanobacterium fungal interactions, for developing effective biocontrol strategies.

ABSTRACT (PEAM033)

RECENT DEVELOPMENTS AND APPLICATIONS OF LACCASE IN SYNTHESIS OF NOVEL TEXTILE DYES: A REVIEW

*Makwana Sonal K.1, Christian Venisha V.1, Panchal Rakeshkumar R.1Deshmukh Kiran C.2**
1 Department of Microbiology and Biotechnology, University School of Science, Gujarat University, Ahmedabad Gujarat India.
2 Department of Microbiology, P.H.G Municipal Arts and Science College, Kalol, Gujarat India
Email makwanasonal08@gmail.com

Novel sustainable and cost effective processes involving oxidative enzymes as catalysts are used alternative for classical organic chemistry. Fungal laccase can be used as biocatalyst for the production of novel bio products having bioactive properties. It oxidises substrates belonging to amine and methoxy organic derivatives and synthesis bio-dyes. The synthesis process is occurs in optimised conditions such as temperature, pH, pressure, and in absence of toxic oxidants. On large scale, fungal laccase can be measured on substrates mixture transformation efficiency in terms of antimicrobial dye synthesis. According to research, in presence of fungal laccase, several phenazine dyes are obtained and studied for their structure and properties.10-((2-carboxy-6-methoxyphenyl) amino)-11-methoxybenzo[a]phenazine-8-carboxylic acid is one of the compound from dye synthesis , showing antibacterial activity against the growth of Staphylococcus aureus.These novel biodyes shows excellent dyeing properties with potent antibacterial and anti oxidative activity. The present review shows enzyme-mediated synthesis that is an alternative potent and eco-friendly route for the synthesis that renders the process "green synthesis "of novel antimicrobial compounds with great importance for the medical textile industry.

ABSTRACT (PEAM34)

ISOLATION OF SILICATE SOLUBILIZING BACTERIA FOR USE AS BIOFERTILIZER IN AGRICULTURE

Gourav Chopra, Nandni, Savita Rani and Leela Wati*
Department of Microbiology, Chaudhary Charan Singh Haryana Agricultural University, Hisar, India.
*Email *gouravchopra73@gmail.com*

Nowadays use of biofertilizers for nitrogen and phosphorus is very common, as they efficiently provide nitrogen and phosphorus from soil to plants in eco-friendly manner. Silicon is a micronutrient required in small amount for plant growth. Benefits of silicon fertilization to plant and soil fertility are disclosed in literature over the time. Silicon in plants reduces abiotic and biotic stress. Silica deposition in cell wall reacts with metal ions and reduces metal toxicity by hindering translocation of metal ions. Silica in plant cells reacts and accumulates sodium ions for salt stress tolerance. Plants can take silica in form of monosilicic acid. Enough amount of silicon in form of feldspar, mica, quartz and oxides of metals is present in soil. Silicate solubilizing bacteria can efficiently transform these insoluble silicates to monosilicic acid. Keeping this in view, total 41 bacterial isolates were retrieved from rhizospheric soil of paddy field and garden soil. These isolates were screened for silicate solubilizing activity on Bunt and Rovira medium containing 0.25% magnesium trisilicates. Six isolates (G13, G15, G26, G49, SSB1 and K13) exhibited silicate solubilization index (SSI) of range from 1.58 to 2.66 after 72 h incubation at 30±2°C. Isolate G13 showed maximum 2.66 silicate solubilization index among all the isolates after 72 h incubation at30±2°C. Efficient silicate solubilizing isolates can further be explored as silicon biofertilizers for growth promotion and stress tolerance in different silicate accumulating crops like rice, wheat and barley after assessing other beneficial plant growth promoting activities.
Keywords: Silicate solubilizing bacteria, Silicon Biofertilizer

ABSTRACT (PEAM035)

EFFECTIVE BIOREMEDIATION OF HEXAVALENT CHROMIUM BY BIOFILM FORMING ISOLATES ENTEROBACTER FAECIUM STRAIN ISOLATED FROM TANNERY SLUDGE

*Annapurna Maurya a,b and Abhay Raja, b, **
a Environmental Microbiology Laboratory, Environmental Toxicology Group, CSIR-Indian Institute of Toxicology Research (CSIR-IITR), Vishvigyan Bhavan 31, Mahatma Gandhi Marg, Lucknow-226001, Uttar Pradesh, India.
b Academy of Scientific and Innovative Research (AcSIR), Ghaziabad, Uttar Pradesh, 201002, India
*Email *araj@iitr.res.in*

A biofilm forming strain IITR007 was isolated from tannery sludge and identified as Enterococcus faecium on the basis of morphological and 16S rRNA sequences analysis. E. faecium is coccus shape gram positive bacteria and found to be formed black colour colonies on congo red agar plate. The congo red dye was bound to extracellular polymeric substances (EPS) synthesized by biofilm forming isolates. EPS staining of isolate by ruthenium red dye was showed further confirmation of EPS production by isolate. Scanning electron microscopy study was also confirmed the morphological and EPS production ability of the isolate. The major contaminant of tannery effluent is Cr (VI) which poses severe threat to human and environmental health. Hence, we have investigated the Cr (VI) reduction studies of E. faecium to explore its potential in Cr (VI) removal. The MIC of Cr (VI) for E. faeciumis 500 mg/l and isolate has efficiently removed the 70% of 100 mg/l Cr(VI) within 48 h and further increasing of incubation time to 120 h, the reduction of 100 mg/l Cr (VI) was 96%. However, the maximum bacterial growth was achieved after 24 h of incubation. The result obtained from gram staining of cells grew on 100 mg/l Cr(VI) concentration was demonstrated that the cell shape and size was distorted and elongated, respectively in presence of Cr(VI).The FTIR study was demonstrated that surface functional groups (hydroxyl, carboxyl, phenyl, carbonyl and amide) was actively interacted with Cr(VI) when cells are exposed to 100mg/l Cr(VI) concentration. The effect of different concentration of Cr(VI) (25-400 mg/l) on biofilm formation along with Cr(VI) reduction were also studied. The results indicated that the biofilm formation, bacterial growth and Cr(VI) reduction were negatively correlated with Cr(VI) concentrations (except 25mg/l). The results of the present study indicated that biofilm forming E. faecium could serve as a promising agent for adequate removal of Cr(VI) from tannery effluents.

Keywords: Biofilm forming bacteria, Enterococcus faecium, Congo red agar plate, EPS staining, FTIR analysis,Cr (VI) reduction.

ABSTRACT (PEAM36)

ISOLATION, OPTIMIZATION AND CHARACTERIZATION OF LIGNOLYTIC BACTERIA WITH LIGNIN PEROXIDASE ACTIVITY AND KRAFT LIGNIN DEGRADATION

Rajesh kumar a,b and Abhay Raj a,b
a Environmental Microbiology Laboratory, Environmental Toxicology Group, CSIR-Indian Institute of Toxicology Research (CSIR-IITR), Vishvigyan Bhavan 31, Mahatma Gandhi Marg, Lucknow-226001, Uttar Pradesh, India.
b Academy of Scientific and industrial research (AcSIR)
*Email *araj@iitr.res.in*

The study reports isolation and characterization of ligninolytic bacteria for kraft lignin degradation. Lignin is a major contaminants effluent discharge from pulp and paper industry and poses a serious concern for environmental and public health. Lignin peroxidase enzyme producing bacterium isolated from from activated sludge of pulp and paper mill and they were identified based on biochemical analysis and 16S rRNA gene sequencing. Isolate designated as Bacillus cereus (MW065550) was tolerated and grew well at high concentration of lignin i.e. 15000 mg/l. The time-course of lignin degradation and LiP production were monitored and results were according to incubation. The lignin degradation products were characterized by UV-spectrophotometricaly, SEM, FTIR and GC-MS which revealed degradation of lignin by Bacillus cereus. We conclude that present isolate could be a potential candidate for use in paper mill effluent remediation.

Keywords: Lignin biodegradation, Bacillus cereus, Metabolic products, SEM, FTIR, GC-MS

ABSTRACT (PEAM037)

ALTERNATIVE SOLUTIONS FOR LAKE REMEDIATION

*Sampurna Nandy a,b, Atya Kapley a,b **
a Academy of Science and Innovative Research (AcSIR), Ghaziabad- 201002, India
b Director's Research Cell, CSIR-National Environmental Engineering Research Institute, Nagpur 440020, India
*Email *a_kapley@neeri.res.in*

Conventional floating systems have been introduced for the remediation of polluted water but failed in treatment of highly eutrophic water due to limited stand biomass, lack of the substrate and instability of substrate purification efficiency. Herein, we designed and tested the performance of various modified ecological floating beds for nutrient reduction from synthetic hyper eutrophic water under batch conditions. Purification performance of different ecological beds assembled with straw, plant and aerator were compared to control system (only synthetic water). Under the batch conditions, average removal efficiencies of ecological system assembled with plant and aerator ranges as 91-92%, ⩽99%, 78-86%, 61-69% for CODCr, NH3-N, NO3- and total phosphorus, respectively. The microbial community structure was also analysed from the plant roots and straw samples taken from ecological beds assembled with plant and aerator using 16s amplicon library sequencing. Based on the above results, systems assembled with plant and aerator proved to be proficient for treatment of eutrophic water.

ABSTRACT (PEAM38)

INFLUENCE OF CYANOBACTERIAL INOCULATION AND ITS INTERACTIONS WITH FE-N AMENDMENT IN MAIZE

*Sekar Nishanth a, Udita Gulia a, Jyoti Shukla a, Arun Kumar b, Radha Prasanna a**
a Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi, India-110012
b National Phytotron Facility, ICAR-Indian Agricultural Research Institute, New Delhi, India-110012
Email nishanthseka94@gmail.com

Cyanobacteria and their biofilms are known for their plant benefitting role in several crops, including cereals, flowers, legumes and vegetables. Iron (Fe) is an essential micronutrient, which helps in plant growth and development, and its deficiency leads to growth retardation and crop yield reduction. This study, using a hydroponic setup, focuses on how Anabaena torulosa-Trichoderma viride (An-Tr) biofilm inoculation and its interactions with N-Fe influence root architecture and plant attributes in maize. Seeds of Pusa Vivek QPM 9 Imp, primed with An-Tr showed higher percent seed germination of 90% and seed vigor index of 6.37, as compared to control (73.33%). Root scanner analyses illustrated significantly greater total root length, projected area, surface area and root volume in An-Tr -primed seeds. Significant increase of 40.74% and 10.42% in leaf chlorophyll content was recorded in An-Tr treatment at 15 and 21 DAT (days after transplanting) respectively, over control. This was supported by significant interaction effects among treatment, N and Fe applied. Leaf proteins and carotenoids were significantly higher in An-Tr treatment, and addition of Fe and N stimulated the activity further. Most interestingly, An-Tr treatment showed 1.5-fold increase and 2.0-fold decrease in ferric chelate reductase (FCR) activity over control at 15 DAT and 21 DAT respectively. Interaction of N and Fe with FCR was significant. Leaf PEPcarboxylase activity and root proteins at 21 DAT were positively correlated with leaf pigments, and culture chlorophyll, highlighting the beneficial interplay between the cyanobacterial inoculation and maize seedlings. An-Tr priming of maize seeds helped in improving plant growth, with more distinct response to Fe amendment, than N, thereby leading to better nutrient availability and metabolic activities. Further studies on gene expression relating N and Fe mobilization is in progress to decipher the mechanism underlying the tripartite interaction of Fe and N on An-Tr biofilms.

ABSTRACT (PEAM039)

OPTIMIZATION OF EPS PRODUCTION IN PRESENCE OF DROUGHT STRESS BY BOX BEHNKEN DESIGN

Sheetal Sharma and Meenu Saraf*
Dept. of Microbiology and Biotechnology, School of Sciences, Gujarat University, Ahmedabad 380009, India.
*Email *sheetumsharma2961994@gmail.com*

Environmental changes are strongly influenced by anthropogenic activities, including drought deposition in the soil. Deficiency of precipitation, hike in evaporation and transpiration rate and proliferation of water resources, are the fundamental parameters which lead to drought. EPS play a significant role in maintaining relative water potential, aggregation of soil particles, establishing contact between root architecture and rhizobacteria directly under the abiotic stresses like dry weather and water scarcity condition. Klebsiella spp SSN1, SGM81 and M5a1, isolated from different rhizosphere were selected for EPS production. SSN1 was characterized as a enhance EPS producer rather than SGM81. Whereas M5a1 was unable to produce EPS. The Jensen media was design for EPS production with the addition of peptone as the nitrogen source. The maximum range of precipitation obtained from SSN1 strain, after 72 to 144 hours of incubation period fresh weight of extracted precipitate was recorded 1.98 mg/10ml to 5.81 mg/10ml. The equal observation was recorded in dry weight wherefrom the third to the sixth day, there was a hike in the number of precipitates ranging from 0.86mg/10ml to 3.10mg/ml. An optimization of EPS production by SSN1 was studied with the application of a Box-Behnken design tool by a design expert. To induce drought stress in media, 20% polyethylene glycol was added. With 15 different sets of media maximum EPS was recorded with 1% sucrose, 0.1 % peptone, 0.3% CaCO3 and 20% PEG with 3.65mg /100ml of production media.

ABSTRACT (PEAM40)

BIOCONTROL EFFICACY OF PSEUDOMONAS STRAIN FOR MANAGEMENT OF BANDED LEAF AND SHEATH BLIGHT IN MAIZE

1Manisha Kabdwal, 1Vandana Jaggi, 1Hemant Dasila, 2R.P.Singh and 1Manvika Sahgal*
1Department of Microbiology, G.B Pant University of Agriculture and Technology, Pantnagar, Udham Singh Nagar, Uttarakhand.
2Department of Plant Pathology, G.B Pant University of Agriculture and Technology, Pantnagar, Udham Singh Nagar, Uttarakhand.
*Email *manishamahi.kabdwal26@gmail.com*

For the development of biocontrol agent (BCA), field efficacy is necessary in addition to in vitro and in planta polyhouse studies. Maize is the third most economically significant cereal crop in the world and suffers a huge loss due to biotic stress. Considering that maize Banded Leaf and Sheath Blight disease caused by fungus Rhizoctonia solani results in 10 to 40% yield loss, two Pseudomonas spp. strains AS19 (16S rDNA 89.27% similar) and AS21(16S rDNA 86.62% similar) from the maize rhizosphere of Almora and Pithoragarh district of Uttarakhand were screened for antagonism against Rhizoctonia solani f.sp. sasakii. Both the isolates showed significant mycelia inhibition in vitro with both cell-free supernatant (CFS) and whole-cell culture (WCC).But percent mycelial inhibition in cell-free supernatant of AS19 (58.3) and AS21 (62.56)was higher than observed with whole-cell culture of AS19 (48.43) and AS21 (52.2).Both AS19 and AS21 were positive for hydrolytic enzyme production (chitinase,β1-3 glucanase, protease, amylase, and gelatinase) and PGP traits (siderophore, ammonia, IAA, HCN, and phosphate solubilization). Subsequently, these two strains AS19and AS21 were selected for field trial where 25-34.63% reduction in disease incidence and 31-39.83% reduction in avoidable grain yield loss was observed. Seed plus soil formulation of both the strains AS19 and AS21 resulted in enhanced level of various defense-related enzymes such as superoxide dismutase, phenylalanine ammonia-lyase, peroxidase, polyphenol oxidase and catalase.The results from the present study indicated that the two Pseudomonas strains AS19 and AS21 induced plant immunity against R.solani f.sp. sasakii and thus can be used as effective BCA against Banded Leaf and Sheath Blight.
Keywords: Biocontrol agent, phytopathogen, polyhouse, catalase.

ABSTRACT (PEAM041)

GENOME ANNOTATION AND COMPARATIVE GENOMIC ANALYSIS OF STRAIN BREVIBACTERIM SP. LS14 WITH BIOSURFACTANT PRODUCING CAPABILITY

*Khushbu Kumari, Sudhanshu K Gouda, Ananta N. Panda1, Dinabandhu Sahu2, Vishakha Raina1**
1School of Biotechnology, Campus-11, Kalinga Institute of Industrial Technology-KIIT (Deemed University), Bhubaneswar
2Institute of Bioresource & Sustainable development, Imphal, Manipur- 795004
Email Indiavraina@kiitbiotech.ac.in

Microbially derived surfactants (biosurfactants) with surface activity and emulsification properties are considered as a good candidate to replace synthetic surfactants due to their low toxicity and biodegradability. However, past few decades the bioprospecting of natural resources and microbial isolates has increased tremendously, but the leads transformed to products are few. Perhaps this trend has led to the exploration of unexplored bioresources. Also, In the recent years, the advent in genome sequencing has provided us with deeper insights into biosynthetic gene clusters of diverse bacterial communities, residing in various environmental niches, which might encode compounds with valuable industrial, agricultural, and environmental values. This study, reports the whole genome sequence analysis of Brevibacterium sp.LS14, isolated from Loktak Lake, Imphal, India. Loktak lake is a unique environment known for floating mats (Phumdi), being made up of heterogeneous mass of soil and vegetation located in northeastern region of India, an endemic region and a hot spot for new microbial biodiversity, offering potential in the search for new molecules of commercially importance. An integration of both genomics and chemical approach was employed to explore the genomic insight of the strain LS14 and displayed the presence of biosurfactant biosynthesis gene. The genome analysis revealed this biosurfactant potential gene to be intrinsic to the strain. Preliminary screening techniques viz., drop collapse (DC), oil displacement (OD) and emulsification index (E24) showed strain LS14 as a potent biosurfactant producer. Subsequent investigation on chemical characterization using FTIR and LC/MS revealed surfactin and terpene containing biosurfactant having sugar and lipid moieties.

ABSTRACT (PEAM42)

NOVEL BIOSYNTHETIC SECONDARY METABOLITES FROM STREPTOMYCES SP.ITACT2: POTENTIAL ANTIMICROBIAL AGENTS FOR HEALTHCARE MANAGEMENT

Sudhanshu K Gouda, Khushbu Kumari, Ananta N. Panda1, Dinabandhu Sahu2, Vishakha Raina1
1School of Biotechnology, Campus-11, Kalinga Institute of Industrial Technology-KIIT (Deemed University), Bhubaneswar, Odisha, India
2Institute of Bioresource & Sustainable development, Imphal, Manipur- 795004, India
*Email *sudhansukugouda@gmail.com*

The advent of antibiotics for treating the bacterial infection is considered to be one of the major advances in modern medicine. However, in recent years as antibiotic use is increasing, untreatable infectious diseases by resistant strains of pathogenic bacteria are also evolving at a higher rate. Bacteria maintain a large number of antibiotic resistance genes (ARGs), that is overtime mobilized and transferred to other species by horizontal gene transfer. Natural products(NPs) extracted from bacteria are the prime source of antibiotics which are being used successfully in the last century. Bacteriocins are a class of secondary metabolites and are ribosomally synthesized toxic peptides having antimicrobial potential. Out of the four classes of bacteriocins i.e., Class 1- Lantibiotics, Class 2- The small heat-stable non-lantibiotics, Class 3- Large heat-labile proteins, Class 4- Complex protein carrying lipid and carbohydrate Class 1 and 2 are majorly present in most microorganisms. Bacteriocin and antibiotics in the combinatorial approach have lots of potential in healthcare management because of the different mode of action of both compounds, the likelihood of developing resistance against such an approach is very low. This study, reports the analysis of secondary metabolites of Streptomyces sp. ITAct 2 by whole-genome analysis isolated from Loktak Lake, Imphal, India. Loktak lake is a unique environment located in the north-eastern region of India, an endemic region and a hot spot for new microbial biodiversity, offering potential in the search for new molecules of commercial importance. In this proposed work, the bacteria which have been isolated from the different aquatic ecosystem and screened for the presence of bioactive compounds against multiple pathogens. A genomic approach was taken for the identification of the secondary metabolite gene cluster and the pathways responsible for the production of different bioactive compounds.

ABSTRACT (PEAM043)

EXPLORING THE CHEMOLITHOTROPHIC AND CHEMOORGANOTROPHIC MICROORGANISMS FROM DEEP GRANITIC CRUSTS UNDERNEATH THE DECCAN TRAPS AT KOYNA-WARNA REGION, INDIA

*Sunanda Mandal1, Rajendra Prasad Sahu2, Anumeha Saha2, Himadri Bose2, Sukanta Roy3, Pinaki Sar2 and Sufia K. Kazy1**
1Department of Biotechnology, National Institute of Technology Durgapur, Durgapur 713209, West Bengal, India
2Department of Biotechnology, Indian Institute of Technology Kharagpur, Kharagpur 721302, West Bengal, India
3Borehole Geophysics Research Laboratory, Ministry of Earth Sciences, Karad 415114, Maharashtra, India
*Email *sufia.kazy@bt.nitdgp.ac.in*

Microorganisms residing in deep subterranean oligotrophic, polyextremophilic habitats have remained mostly unexplored. The aphotic deep dark microbial realm that has evolved possibly billions of years ago has developed unique metabolic repertoire for their survival. To get an insight about the inhabitant microbial diversity, their cultivability, their metabolic preference and probable mechanism behind these preferences, granitic rock samples obtained via scientific drilling from different depths of the Deccan traps were cultivated using a variety of electron donors, electron acceptors, and carbon sources (both organic and inorganic). Chemolithoautotrophic (hydrogen + carbon dioxide, bicarbonate metabolizing) and chemoorganoheterotrophic (CH4 and other organic carbons metabolizing) microorganisms were enriched under hot, anaerobic conditions. 16S rRNA gene amplicon sequencing of metagenome of the enrichments revealed the ubiquitous dominance of Burkholderiaceae members in all sets except the one enriched with a mix of organic carbon compounds where Bacillaceae was found to be the dominant group. Other groups found in the inorganic sets included Enterobacteriaceae, Rhodocyclaceae, Sphingomonadaceae, Pseudomonadaceae members, etc. many of which are known to oxidize H2 and produce methane. Methane enriched culture sets showed the abundance of (other than Burkholderiaceae) Pseudonocardiaceae, Bacillaceae members etc. Anaerobic, thermophilic, fermentative members of Thermoactinomycetaceae, Nocardiaceae, etc. were found in mixed organic carbon enrichment along with Bacillaceae members. Sphingomonadaceae, Moraxellaceae members, etc. could be found in polymeric carbon enrichments. Studies suggests that deep biosphere species play a significant role in carbon and energy exchange between one another and other bacterial groups in these environments. The metabolic flexibility of Burkholderiaceae Pseudomonadaceae and Bacillaceae members is beneficial in the deep habitats where availability of carbon substrates is scarce and varies under different environmental conditions and with time.

Keywords: deep biosphere, chemolithotrophic, chemoorganotrophic, enrichment, granitic rock, microbial diversity

ABSTRACT (PEAM44)

SCREENING OF ZINC TOLERANCE FUNGI AND THEIR USE FOR THE SYNTHESIS OF ZINC NANOPARTICLES

Ajay Kumar, Anuj Rana, Rajesh Gera*
Department of Microbiology, COBS&H, Chaudhary Charan Singh Haryana Agricultural University Hisar-125004, India
*Email *akjiari@gmail.com*

Fungal strains were isolated on potato dextrose medium from the metal contaminated site of hisar district. Twelve fungal cultures F1-F12 were isolated on the basis of their phenotypic characterization and screened for zinc tolerance up to 6000 PPM ZnSO4. Four fungal isolates have shown to be highly zinc tolerant and grow at 6000 ppm in plate assay. Among all tested fungi F8 had shown the highest growth with zinc salt and further used for the synthesis of zinc nanoparticles. F8 fungi were grown in specific medium and extracellular enzymes in filtrate were used for zinc nanoparticles synthesis with addition of ZnSO4. The colour change in the reaction from brown to white confirms the synthesis of the zinc oxide nanoparticles. Synthesized nanoparticles were characterized by UV spectroscopy and FTIR while observing sharp peaks and presence of metal oxide functional groups respectively. This study shows the potential of fungi for synthesis of environmental friendly zinc oxide nanoparticles and it could be safely used for the development of the nanofertilizer and nanobiofertilizer to increase nutritional content and crop productivity.

Keywords: Fungi, zinc sulphate, nanoparticles, nanofertilizer, Nanobiofertilizer

ABSTRACT (PEAM045)

ISOLATION OF SULPHUR OXIDISING BACTERIA FOR USE AS BIOFERTILIZER FOR MUSTARD CROP

Nandni, Savita Rani, Gourav Chopra and Leela Wati*
Department of Microbiology, Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana, India
*Email *nandininagar94@gmail.com*

Sulphur (S) is the 13th most abundant element in the earth crust and fourth major plant nutrient after nitrogen (N), phosphorus (P) and potassium (K). Sulphur uptake by plant roots occurs preferentially in the form of sulfate (SO42-), S can also be absorbed as thiosulfate (S2O32-). Oxidation of sulphur is the most important step of S cycle which improves soil fertility. Sulphur oxidizing bacteria oxidize sulphur as the principal metabolic process and play an important role in the conversion of reduced sulphur (sulfide) and partially reduced sulphur (thiosulphate, sulphite) into sulphate. Microbial sulphur oxidation is beneficial to soil fertility, resulting the formation of SO42-, which can be used by the plants, while the acidity produced by process of oxidation is used to solubilize other plant nutrients especially that of phosphorous and improve the alkaline soils. In the present study, five sulphur oxidising bacterial isolates (SOB1, SOB2, SOB3, SOB4, SOB5) were retrieved from soil by enrichment culture using modified thiosulphate medium. Among these two isolates namely SOB1 and SOB5 exhibited zones of clearance on modified thiosulphate medium after 5 days of incubation at 300C. Maximum solubilisation index (SI) observed for SOB1 was 1.91 after 1st day of incubation and 1.89 for SOB5 after 3rd day of incubation at 300C. These isolates after assessing other plant growth promoting beneficial traits could be explored as biofertilizer for mustard crop.

ABSTRACT (PEAM46)

SYNTHESIS OF SILVER NANOPARTICLES FROM FRESH OYSTER MUSHROOMS

Rajni Gupta, Yamal Gupta, Aditya Kiran*
Department of Botany, Kirori Mal College, University of Delhi, Delhi 110007, India
*Email *rajniguptakmc5@gmail.com*

Nanoparticles have been incorporated into the consumer products and have thus moved from the laboratory to store shelves. Nanoparticles possess unique properties that make them suitable for specific purposes. For instance, the silver nanoparticles are reported to show anti-microbial properties, and find application in medical devices, dressings, prostheses, contraceptives, water purification systems, electric generation and etc. It has been extensively discussed that biological methods for synthesis of silver nanoparticles are advantageous over the chemical methods. The present work highlights the use of fresh oyster mushroom (Pleurotus sp.) for the synthesis of silver nanoparticles. The mushroom was grown under controlled conditions in the mushroom house. Here we report an aseptic method for synthesis of silver nanoparticles using oyster mushroom. In the present investigations the freshly harvested mushroom was incubated in the 1ml of AgNO3 salt solution and autoclaved for 15 min. at 121oC and 15 psi. The color of the AgNO3 salt solution incubated with Pleurotus sp. changed from colourless to brown. This indicates the extracellular formation of silver nanoparticles. The formation of silver nanoparticles was confirmed by the UV-Vis spectrophotometry.

ABSTRACT (PEAM047)

MICROBIAL PHA PRODUCTION FROM BIOWASTE, OPTIMIZATION AND BIOPROCESS MODELING

Rukhsar Afreen, Mamtesh Singh, Shivani Tyagi and Gajendra Pratap Singh*
Department of Zoology, Gargi College, University of Delhi, Delhi, India
*Email *s.mamtesh@yahoo.com*

Raw waste is easily available, low cost feed for polyhydroxyalkanoate (PHA) producing Bacteria. Optimization for different concentration and incubation time was carried out. In the present study 4% and 6% Total solids (TS) sweet lime waste (peel, pomace, peel+pomace) was hydrolysed by a mixed bacterial consortium. Hydrolysate was supplemented with Peptone, ammonium chloride Glucose and sodium propionate for further optimization of PHA yield. We can use a mixed slurry of raw waste as a carbon source to avoid synthetic carbon sources. Hydrolytic products from sweet lime fruit waste were analysed for sugar content and volatile fatty acids which provided a definite pattern of different volatile fatty acids (VFAs). The production of propionic acid was maximum after 4 days of incubation i.e. up to 3000 mg/L. Hydrolysate was utilized by Bacillus sp. for production of PHA. Maximum yield of PHA was observed in 6% of TS on the 4th day. Bacillus sp. was shown to produce 470 mg PHA /L from 6% TS. Sugar production was maximum up to 9500mg/l. Mathematical modelling in form of Petri net software is used for efficient optimisation of this bioprocess. Plant based biomass can be best utilized for automated bacterial PHA production by this approach.
Keywords: Bacillus, bio-waste, hydrolysis, polyhydroxyalkanoate

ABSTRACT (PEAM48)

EVALUATING BIOGAS PRODUCTION BY CO-DIGESTION OF CATTLE DUNG AND WATER HYACINTH

Shikha Mehta and Kamla Malik*
Department of Microbiology, COBS&H, CCS HAU, Hisar, Haryana, India
*Email *shikhamehta@hau.ac.in, *shikhamicrobio@gmail.com*

Water hyacinth is an invasive water weed that thrives in water bodies (rivers and lakes) and can form thick mats. These mats cover the entire surface of ponds and cause oxygen depletion as well as various environmental problems. It is therefore necessary to develop economic exploitation strategies. The production of bio-energy from water hyacinth can be a solution as there is never-ending rise in demand for fossil fuels. Water hyacinth leaves can be harvested and used for biogas production due to high hemicellulose content and other nutrients. The present study investigates the effect of digestion of cattle dung using different concentrations of water hyacinth under laboratory conditions. Chemical analysis of substrates such as cattle dung and water hyacinth was carried out. Biogas production was determined by water displacement method. Cellulose content of cattle dung was found to be higher than that of water hyacinth whereas hemicellulose was lesser in case of cattle dung. Biogas production in all the treatments increased upto 4 weeks and maximum was observed in treatment containing cattle dung (75%) and water hyacinth (25%). The study recommends that water hyacinth can be a great alternative to produce renewable energy and biogas production using its biomass is an appropriate way of managing waste.
Keywords: Biogas, renewable, co-digestion, water hyacinth

ABSTRACT (PEAM049)

BIOREMEDIATION OF AZO DYE BY MICROBES RETRIEVED FROM CONTAMINATED SOIL

Poonam Ranga, Baljeet Singh Saharan, Jagdish Parshad*
Department of Microbiology, COBS&H, CCS HAU, Hisar, Haryana, India
*Email *rangamicro@yahoo.co.in*

In present time increasing demand for water is the main problem in front of us due to the excessive use of water by various industries. Principal water polluters are textile industries because their effluent contains a large number of colorful dyes and chemicals. This highly colored untreated effluent pollutes the receiving water bodies. Textile effluent adversely affects aquatic organisms by interfering in sunlight penetration. The physicochemical characteristics of the effluent do not permit its disposal directly into inland water or on agricultural fields for irrigation. Physiochemical methods for effluent treatment are very costly as compared to Biological methods. In this study, decolourization of textile dye (Coractive Blue) was accessed by using bacterial strains isolated from textile effluent contaminated soil samples. An bacterial isolate TCB17 was able to decolourize Corractive Blue (an azo dye) at a concentration of 10 mg/l upto 41% within 72 hrs at 37OC. Bacterial isolate can be effective for the bioremediation of pollutants present in textile effluent.

Keywords: azo dye, textile effluent, bioremediation, coractive blue

ABSTRACT (PEAM50)

FUNGAL PATHOGENS ASSOCIATED WITH FRUIT ROT OF SOLANUM MELONGENA L. IN PANTNAGAR (UTTARAKHAND)

Damini Maithani, Anita Sharma*
Department of Microbiology, College of Basic Science and Humanities, Govind Ballabh Pant University of Agriculture & Technology, Pantnagar (263145), India
*Email *daminimaithani27@gmail.com*

Solanum melongena L.(brinjal), an important vegetable crop in India is prone to fungal attacks that are responsible for decay and reduction in its yield. Present study was conducted for isolation, characterization and identification of the fungi associated with diseased fruits of the mature eggplant in Pantnagar (Uttarakhand). Characterization of the recovered isolates was done on the basis of morphological characters, staining properties and molecular techniques. Fungi were identified using the rDNA-ITS region as Diaporthe vexans (MW425838) and Alternaria alternata (MW425839). Bioassay conducted on detached fruits to test pathogenicity of the fungal isolates showed that both the pathogens were able to cause rot on detached mature eggplant fruits. Pathogenic variation among the isolates was ascertained via a pattern of lesion formation on inoculated fruits. Although both the fungi were pathogenic to eggplant fruits but, fruit rot pattern observed for both the pathogens was different and A.alternata (MW425839) was found to be an aggressive colonizer of fruit tissue in comparison to D.vexans (MW425838) .

ABSTRACT (PEAM051)

DISSEMINATING INFORMATION ON MICROBIAL GENETICS RESOURCE THROUGH INFORMATION AND COMMUNICATION TECHNOLOGY

Dhiraj Kumar Verma, Renu, Arvind Gupta, Khan Mohd Sarim, Hillol Chakdar, Udai Bhan Singh, K. Pandeyan, Arjun Singh, Manish Roy, Anil K. Saxena*
ICAR-National Bureau of Agriculturally Important Microorganisms, Mau (U.P) 275103, India
*Email *renuiari@rediffmail.com*

Information and Communication Technology is the most user friendly and effective way of sharing information. In this line of research ICAR- National Bureau of Agriculturally Important Microorganisms has developed two web-based databases on microbial genetics resource. These two web-portals can be easily accessed by user at the following web address viz. www.mgrportal.org.in and www.microveda.org.in freely. The methodology used to develop both the web-portals is to first design database structures and field through MySql programming database, followed by selection of programming language (php, java script) and web page designing by (html, CSS and Bootstrap). Next step is to run all the designed pages and database on the apache server. Microbial Genetic Resource Portal (www.mgrportal.org,in) contains information pertaining to conservation of microbial genetic resource with special reference to agriculturally important microbes in National Agriculturally Important Microbial Culture Collection (NAIMCC), an IDA on microbial germplasm, at NBAIM, Mau, Uttar Pradesh. The portal is informative in various aspects of microbial conservation, microbial diversity with special reference to India, need for microbial genetic resources conservation and International and National status of conservation of microbial genetic resources. Latest listings on different federations, societies and networks of Microbial Resource Centers in the world, some leading culture collections in the world, some important microbial culture collections in India and microbial repositories in India recognized by National Biodiversity Authority (NBA), India are available. Besides this, the portal gives various services offered by NAIMCC, dynamic database search engine, and accessibility to catalogue, microbial registration facility, easily downloadable forms for various purposes and linkages to important sites. Microveda (www.microveda.org.in) is first of its kind digitized attempt from India which provides comprehensive information about AIM w.r.t. characteristics and importance. The database is based on the primary passport data of microbial cultures at NAIMCC. Its unique database defining geo-locations of isolated AIM strains; Knowledge models of microbes and Microbial Database Search (MIDAS) giving concise information on particular agriculturally important microbe. Besides this there is provision for trait wise listing of elite microbes at NAIMCC. The information available in the database will be useful to the researchers, students and academia pertinent to their research related to agricultural microbiology covering important aspects like taxonomy, ecology and their importance in agriculture and especially on the availability of specific microbe from particular location.

ABSTRACT (PEAM52)

STRUCTURAL AND FUNCTIONAL ANALYSIS OF ACC DEAMINASE PRODUCED BY ROOT-NODULATING ENSIFER ADHAERENS: AN IN SILICO APPROACH

Prashant Katiyar, D K Maheshwari*
Gurukula Kangri (Deemed to be) University, Haridwar- 249404, Uttarakhand (India)
*Email *prashant22021994@gmail.com*

Nodulation can be assimilated as one of the most important aspects in leguminous plants. However, several growth hormones such as ethylene have an essential role to play in plant metabolism, but it may also act as a harmful factor for plant growth, mainly pertaining to nodule formation in leguminous plants. Ethylene is also produced while a number of biotic and abiotic stresses are upon plants. 1-aminocyclopropane-1-carboxylic acid (ACC) deaminase cleaves ACC that is an immediate precursor of ethylene and mainly converting it into α-ketobutyrate and ammonia ultimately reducing the levels of ethylene and delaying the plant senescence. The capability to produce ACC deaminase has been widely studied in PGPRs including root nodulating genera. In this study, root nodulating Ensifer adhaerens KS23 was chosen for ACC deaminase secondary structure prediction and characterisation of enzyme. The present study concludes into an in silico structural (secondary structure prediction and homology modelling) and functional analysis of ACC deaminase from E. adhaerens in order to explore its physico-chemical properties using a wide array of bio-informatics tools. E. adhaerens KS23 was selected as a concurrent species of Ensifer genera for 3D modelling of ACC deaminase protein.
Keywords: Ensifer adhaerens, ACC deaminase, abiotic stress, in silico structures, rhizobia

ABSTRACT (PEAM053)

EVALUATING THE EFFECT OF PROMISING CYANOBACTERIAL STRAINS ON PLANT GROWTH, PHOTOSYNTHETIC EFFICIENCY AND N ASSIMILATORY PARAMETERS IN RICE CROP

Premsing Shivsing Marag1, Dolly Wattal Dhar2 and Archna Suman3
1Centre for Conservation and Utilisation of Blue Green Algae, Division of Microbiology,ICAR-Indian Agricultural Research Institute, New Delhi-110012, India,
2 School of Agricultural Sciences, Sharda University, Knowledge Park III, Greater Noida, UP
3Division of Microbiology,ICAR-Indian Agricultural Research Institute,New Delhi-110012, India
*Email *premsingmarag19@gmail.com*

Cyanobacteria comprise a large group of structurally complex, photosynthetic, gram-negative prokaryotes, which flourish in rice fields and play a major role in maintaining the fertility of its ecosystem. In present study, the effect of promising cyanobacterial strains namely Anabaena cylindrospermoides (D3), Nostoc carneum (P12), Anabaena kashiensis (K16) and Nostoc carneum (M10) was studied on growth, root architecture, photosynthetic efficiency, N assimilatory parameters along with yield and its attributes in rice crop (Variety: Basmati, PB-1121). The experiment was undertaken in pots with soil as rooting medium under natural conditions at ICAR-IARI, New Delhi. The treatments used were as T1: 100% N, T2: 75% N, T3: 75% N + D3, T4: 75% N + P12, T5: 75% N + K16 and T6: 75% N + M10. Observations were recorded at 30, 60, 90 days after transplantation (DAT) and at harvest stage.The effect of treatments was significant on root length and total plant length with highest mean observed under treatment T3 for root length and T1 for total length. The treatment effect on shoot length was, however, non-significant.The effect of treatments on dry weight of roots, shoots and total was significant with highest mean observed under treatment T4 for these parameters. The treatment effect on number of tillers and leaves was non-significant.The root scanning results in terms of total length, diameter and root volume were significantly influenced by the treatments, while surface area remained uninfluenced. The highest values for roots were observed under T1 for total length, T4 for diameter and T3 for root volume, whereas, these observations were lowest under treatment T2.The effect of treatments on chlorophyll a was significant and ranged from highest under T3 and lowest under T2. The treatment effect on chlorophyll b and carotenoids was non-significant. Photosynthetic rate, stomatal conductance and transpiration rate were significantly affected by treatments and these ranged between highest under T4 to the lowest under T2.The treatment effect on N-assimilatory enzymes namely Nitrate Reductase and Glutamine Synthetase in leaves was significant at all sampling occasions. There was a significant treatment effect on % N in shoot and seeds, which ranged between lowest under T2 to the highest under T3. The observations on grain yield and its attributes showed significant treatment effect on panicle length per plant and % filled grains per panicle. Thus, observations revealed that the treatments with cyanobacterial inoculant can save about 20% to 25% of nitrogenous fertilizers.
Keywords: Cyanobacteria, Plant growth, Photosynthesis, N assimilation, Yield

ABSTRACT (PEAM54)

STUDY THE TOLERANCE OF RHIZOSPHERIC BACTERIA ISOLATED FROM CYAMOPSIS UNDER ABIOTIC & BIOTIC STRESS

*Ritika Jain, Sarita Sharma, Meenu Saraf**
Department of Microbiology and Biotechnology, Gujarat University, India
*Email *smile_gudiya03@yahoo.co.in*

Agriculture plays a vital role for any economy primarily for developing and under developed economy. Increasing abiotic as well as biotic stresses adversely affects crop productivity across the world. Microorganisms inhabiting the Rhizospheric region of plant soil are known to play an important role in alleviating these stresses, thus enhancing crop productivity and yield. The present study was carried out to isolate the rhizospheric bacteria from Cyamopsis showing potential for biotic and abiotic stress tolerance. To carry out this, bacteria were isolated from the rhizospheric soil of Cyamopsis which were collected from different regions of Gujarat. These isolates were screened for tolerance to different abiotic stresses such as temperature, pH, salt and drought. Highly abiotic stress tolerant isolates were further tested for biotic stress against pathogenic bacteria and fungi. Among the 80 bacterial isolates, best grown 30 cultures were tested for different abiotic stress. Four cultures i.e MN40, KM1, KM6 and AK17 showing high tolerance to abiotic stresses were further investigated for Biotic stress tolerance. Biotic stress tolerance were tested against bacteria Salmonella typhi, Staphylococcus aureus, Bacillus subtilis, Micrococcus luteus and Fungi Macrophomina phaseolina, Fusarium oxysporium, Sclerotinum rolfissii & Trichoderma spp using Agar diffusion method. Amongst the 4 selected bacterial strains, KM6 showed high tolerance to Biotic stress.

ABSTRACT (PEAM055)

AN ENVIROSAFE FUNGICIDE FOR PLANT DISEASES CONTROL

*Kruti Dave**
Department of Biotechnology, Mehsana Urban Institute of Sciences, Faculty of Science, Ganpat University, Gujarat, India
*Email *davekruti2@gmail.com*

Plants are assaulted by different phytopathogenic organisms. The utilization of synthetic pesticides for controlling different plant infections is as yet a typical practice particularly in non-industrial nations. In spite of the fact that with the utilization of substance fungicides, plant sicknesses can be controlled yet the risky effects of such items in human wellbeing and climate are notable. In addition, with their abundance applications bug obstruction may exist. Characteristic items have been discovered successful in plant sickness administrations and could be securely consolidated as appropriate choices for manufactured fungicides. Bioactive compounds of plants and a few fungi can repress the development of pathogenic growths. So by separating bioactive compounds from common sources and applying in the yield field we can improve crop creation. This will be a protected choice to protect plants from pathogenic organisms.

ABSTRACT (PEAM56)

ISOLATION, CHARACTERIZATION AND IN-VTRO ANALYSIS OF SALT TOLERANT HALOMONAS SULFAEDRIS MV-19 FROM MUD-VOLCANO ANDAMAN-NICOBAR ISLAND

Ees Ahmad, Pawan K. Sharma, Rakhi Dhyani, Anil K. Saxena*
ICAR-National Bureau of Agriculturally Important Microorganisms, Kushmaur, Maunath Bhanjan, 275103, Uttar Pradesh
*Email *eesahmad@gmail.com*

Agronomically salinity is the major challenge for cultivation of different crops in sustainable agriculture. The diverse microorganisms that inhabit the extreme niches like hot springs, salt lake and mud volcano may yield direct economic benefits through their exploitation for conferring salt tolerance. Therefore, the present study was undertaken to isolate salt tolerant bacteria from extreme niches. We isolated salt tolerant bacterial strain MV-19 which can grow on nutrient agar supplemented with 18% sodium chloride (NaCl). This bacterial strain was identified as Halomonas sulfaedris MV-19 after biochemical assay, FAME analysis and 16S rRNA characterization. Interestingly the carbohydrate utilization test reveals that the Halomonas sulfaedris MV-19 utilizes only three sugars namely dextrose, fructose and mannose out of twenty one tested sugars as carbon source. The growth kinetics assay was done and best growth of Halomonas sulfaedris MV-19 was observed in nutrient broth supplemented with 8% NaCl. When different sugars (dextrose, fructose and mannose) were supplemented, the Halomonas sulfaedris MV-19 grew maximally in nutrient broth supplemented with 8% NaCl and 5% mannose. The strain also produced exopolysaccharides in nutrient broth supplemented with 8% NaCl and sugars (dextrose, fructose and mannose). The EPS production was increased by 450% after addition of 5% mannose in nutrient broth. The Halomonas sulfaedris MV-19 strain can, thus be useful in alleviation of salinity stress in different crops cultivated in saline soils. It is also expected that the results of this investigation would further contribute towards effective abiotic stress management.

ABSTRACT (PEAM057)

BIOSURFACTANTS FROM BACILLUS SP. A5F AS BIOCONTROL AGENT

Apekcha Bajpai, Anil Prakash*
Department of Microbiology, Barkatullah University, Bhopal 462 026, India
*Email *apekshabajpai@gmail.com*

Bacillus sp. A5F possesses the potential to produce biosurfactants under in-vitro conditions. Glucose, soybean oil and incubation time were identified as significant variables affecting the production of cell density and biosurfactants in terms of emulsification index (EI %). The selected ingredients were optimized using response surface methodology (RSM) that resulted in 2.14-folds increase in emulsification index (E24%) with optimal values of 3.5 %, 3.5 % and 78 h for glucose, soybean oil, and incubation time, respectively. Production of biosurfactant was scaled up in a 5 L fermentor with an improved yield of 29 µgmL-1 in 78 hrs under optimized culture conditions. Gel exclusion chromatography using sephadex G50 purified factions were subjected to LCMS analysis resulted in iturin and surfactin type of biosurfactant. Further QTOF analysis revealed several other lipopeptides possessing antimicrobial property. The purified biosurfactants showed significant antifungal activity against phytopathogens Sclerotinia sclerotiorum 7889, Macrophomina phaseolina 7893 and Fusarium oxysorum 7883 of soybean plants.
Keywords: Bacillus sp., response surface methodology, biocontrol.

ABSTRACT (PEAM58)

RESPONSE OF AZOSPIRILLUM FORMOSENSE STRAINS TO MOISTURE DEFICIT STRESS CONDITIONS

*Jayasurya Anegundi, Minakshi Grover**
Division of Microbiology, Indian Agricultural Research Institute, Pusa, New Delhi-12, India
*Email *minigt3@yahoo.co.in*

Microbial mitigation of abiotic stresses in crop plants is gaining importance in the present times. In the present study, five strains of Azospirillum formosense namely AIM3, AIM19, AIM38, AIM57 and AIM82 were evaluated for their morphological, physiological and PGP traits under moisture deficit condition induced by different levels of PEG (Polyethylene glycol) 6000. Increasing concentrations of PEG 6000 had a negative effect on bacterial growth as indicated by cfu counts and absorbance at 600nm. At 30% PEG concentration growth was significantly inhibited. Under stress conditions, bacterial cells showed change in shape from spiral to round and increase in size for all the strain. Under stress conditions bacterial cells accumulated higher concentration of proline and also exhibited biofilm formation. Seed germination test revealed the potential of the Azospirillum sp. strains to promote root hair density and lateral branching in Pearl millet. The strains can be potential candidates for application as bioinoculants under abiotic stress conditions.

ABSTRACT (PEAM059)

EVALUATION OF GROWTH ENHANCING EFFECT OF PLANT GROWTH PROMOTING HALOARCHAEA IN WHEAT THROUGH NUTRIENT MANAGEMENT AND SALINITY STRESS ALLEVIATION

*Mayur G Naitam, K. Annapurna, B. Ramakrishna and Rajeev Kaushik**
Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi-12, India
*Email *mayur.naitam70@gmail.com*

Forty-five halophilic archaea, previously isolated from Rann of Kutch Gujrat, India, were screened for PGP attributes (solubilisation of P, K and Zn) and traits responsible for imparting salinity stress tolerance. Out of forty-five, 17, 21 and 6 haloarchaea were found to solubilize phosphorus (14-61 ppm), potassium (37-78 ppm) and zinc (8-17ppm) respectively. Haloarchaea showing maximum growth and solubilisation of P, K and Zn, was selected for pot experimental studies to evaluate its effect on growth and salinity stress alleviation. Five different cultivars of wheat (two salinity tolerant, K65 and KRL210, and three salinity susceptible, HD2687, HD3086 and HD2380) were grown in triplicates in pots containing 10 kg of soil with EC maintained at 8 dsm-1. Inoculated pots with selected haloarchaea (Halogeometricum borinquense Arch27) were taken as treatment and uninoculated ones were maintained as control. Observations were recorded after 45 days of sowing (DAS) and at the time of harvest. Total protein, sugar and chlorophyll in inoculated treatments increased significantly by 43-46%, 5-27%, and 12-17%, respectively over un-inoculated control. Inoculation significantly reduced the level of proline and antioxidant enzymes (SOD, catalase and peroxidase) by 18 to 26%. Plant vegetative growth parameters also showed significant increase as a result of inoculation over un-inoculated treatments. The overall effect of haloarchaeal treatment was found to be more in susceptible cultivars (28- 42%) as compared to tolerant ones (9- 15%). The findings of the study suggest that inoculation of halophilic Halogeometricum borinquense Arch27 not only promotes the growth but also alleviate the harmful effects of salinity. Hence, this halophilic archaeon can be evaluated further in field condition for its further exploitation in biofertilizer development programs.

ABSTRACT (PEAM60)

AN EFFECTIVE FUNGAL CONSORTIUM FOR COMPOSTING OF AGRICULTURAL RESIDUES IN EXTREME COLD AND ARID ECOSYSTEM OF NORTHERN HIMALAYAS

Udita Pushpad1, Govind Singh Tomar1, Tsering Stopden2, Rajeev Kaushik1*
1Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi, India
2Defence Institute of High-Altitude Research (DIHAR), Leh, Ladakh, India
*Email *pushpad1995@gmail.com*

Traditionally, Ladakh region has been growing barley and wheat. The cropping period in Ladakh is very short (April to October) and farmers tend to use high amounts of chemical fertilizers to gain maximum crop yield. The Government has proposed to certify Ladakh as an organic district by 2025. Hence, emphasis is being given for increased use of organic amendments like compost and biofertilizers to achieve this target. The process of composting in Ladakh is hampered significantly due to harsh winters. In present study, a fungal consortium comprising of native psychrophilic (Geomyces sp RF02 and Mucorplumbeus LF09) and procured mesophilic (Trichodermaviride ITCC 2211 and Phanerochaete chrysosporium NCIM 1073) lignocellulolytic fungal isolates was developed and evaluated for the composting of wheat straw in pits (1 m3) during winter season (-15 to 5°C) at DIHR, Leh, in the month of November, using standard composting procedure. C: N ratio was kept at 60:1 using poultry droppings.The inoculum of consortium was added in different treatments along with an un-uninoculated control in triplicates. The samples were drawn at the 0, 30 and 60 d interval and analysed for different parameters. Significant reduction in the EC (<1.2 dSm-1), C: N ratio (18.4 to 21.3), total carbon content was observed in treatment inoculated with consortium over other treatments. Similarly, consortium significant increase in available N and P in finished compost over other treatments. The FT-IR spectra of finished compost showed no or smaller peaks of lignocellulose spectra in treated substrate as compared to untreated control. Hence, the consortium of psychrophilic and mesophilic fungal isolates was found effective in degrading the biomass in a shorter period of 60 d at extremely low temperature and can be further evaluated for composting in a natural cold environment at multi-locations.

ABSTRACT (PEAM061)

BIOREMEDIATION OF HEAVY METALS THROUGH THE POTENTIAL BACTERIA ISOLATED FROM THE YAMUNA RIVER WATER

*Jagjot Arora1, Simran Madaan1, Divisha Shukla1, Aman Kumar1, Anushka Rao1, Avinash Kumar1, Nishi Kumari1, Santosh Kumari2, Mohit Kumar1, Sudershan Kumar2, Varunendra Singh Rawat1**
1Department of Zoology, Hindu College, University of Delhi, Delhi-110007, India
2Department of Chemistry, Hindu College, University of Delhi, Delhi-110007, India
*Email *vsrawat@hindu.du.ac.in*

Heavy metals have been polluting the water bodies for several years and are of great environmental concern because of their bioaccumulation and non-biodegradability in nature. Yamuna, the lifeline of Delhi, is severely affected by untreated domestic and industrial effluents. Heavy metals viz., Lead (Pb), Copper (Cu), Cadmium (Cd), Chromium (Cr), Zinc (Zn), Nickel (Ni), and Arsenic (As) on bioaccumulation have adverse effects on human metabolism and health.The potential heavy metal tolerant bacterial strain W4 was isolated from the Yamuna river water (Wazirabad stretch, 28°42'28.0"N 77°13'55.8"E). At this point, the polluted Najafgarh drain meets the river. The bacteria also showed cross-resistance with antibiotic, ciprofloxacin. The physiochemical properties of contaminated water were checked and isolated bacteria was also characterized by antibiotic test and biochemical tests. The isolated bacteria will then be tested for their respective metal degradation properties. A possible bioremediation pathway will be elucidated by utilizing in-silico tools.

Keywords: Bioremediation, Heavy metal degradation, bacteria, in-silico tools.

ABSTRACT (PEAM62)

BIOREMEDIATION POTENTIAL OF XYLANIMONAS OLIETROPHICA SP. NOV. PW21: GENOMIC INSIGHTS

*Pradnya Nagkirti1, 2 Prashant K. Dhakephalkar1, 2**
1Bioenergy Group, MACS Agharkar Research Institute, G.G. Agarkar Road, Pune-411004, India
2Savitribai Phule Pune University, Ganeshkhind, Pune-411007, India
*Email *pradnyanagkirti@aripune.org, *pkdhakephalkar@aripune.org*

Petroleum hydrocarbons and their products lead to severe environmental problems because of their carcinogenic nature. Studies of genetic potential of bacterial species gave insights into development of bioremediation strategies to clean up petroleum hydrocarbon contaminated sites. Present work focuses on the whole genome sequencing of novel Xylanimonas olietrophica PW21, isolated from Indian oil reservoirs. Draft genome of PW21 was sequenced by using Illumina NextSeq next generation sequencer revealed its genome size of 3.4 Mb with 73.8% G+C content. It harbors the genes responsible for biosurfactant synthesis and degradation of alkanes and aromatic hydrocarbons. Cytochrome P450 monooxygenase along with ferredoxin reductase mainly involved in degradation of alkanes. Aromatic hydrocarbon degradation primarily takes place by both para- and meta- type of cleavage. Presence of several genes in degradation of crude oil components revealed efficiency of PW21 in utilization of diverse petroleum hydrocarbons. Genetic basis also revealed presence of genes involved in membrane transport and stress response such as heavy metal resistant, heat shock proteins, osmotic stress and oxidative stress. Versatile genes, flexible stress response systems and well developed transport system help PW21 for survival under harsh oil contaminated region. These results gave insight into exploring the role of novel Xylanimonas sp. PW21 to develop a successful bioremediation strategy to clean oil contaminated regions.

ABSTRACT (PEAM063)

ISOLATION, CHARACTERIZATION AND PLANT GROWTH PROMOTING ATTRIBUTES OF ENDOPHYTIC BACTERIA ENTEROBACTER ROGENKAMPII BLS02 ISOLATED FROM BARLERIA LUPULINA LINDL

Nikhil Kumar, R. C. Dubey*
Gurukula Kangri Deemed to be University, Haridwar-249404, Uttarakhand (India)
*Email *loashyan.nk358@gmail.com*

Endophytes are microorganisms which live symbiotically with almost all varieties of plant. Future studies required to determine the antimicrobial susceptibility profile and potential application of these isolates in biological control, microbial biofertilizers and degradative enzyme production. The aim of this study was to isolate and identify putative endophytes from vegetative parts of Barleria lupulina viz. root and stem grown in the Botanical garden at Department of Botany and Microbiology, Gurukul kangri deemed to be University,Haridwar,-249404 Uttarakhand (India). These isolates were also morphologically and biochemically characterized for enumeration of desired traits. Further, the bacterial isolates were evaluated for their plant growth promoting traits. Many of these bacteria were able to solubilize inorganic phosphate, produce Indole-3-acetic acid, Siderophore as well as Hydrogen cyanide production. A total of 40 isolates were isolated from (25) stem and (15) roots of B. lupulina. Furthermore, putative isolates were identified as the ones with maximum IAA production i.e. by isolate BLS02 after 72 hours of incubation. Maximum solubilization of phosphate was showed in BLS02, BLS07, BLR19 and BLR27 via halo zone formation. Qualitative results of siderophore production reveal that maximum production occurred in isolates BLS02 and BLR25 after 72 hours of incubation. Exponentially grown cultures were used for volatile production of HCN (hydrogen cyanide) and after complete incubation at 28±1°C, positive HCN production was recorded in BLS02 and BLR21. The most effective endophytic bacteria BLS02 was identified as Enterobacter roggenkampii, by 16S rRNA sequencing analysis. This work for the first time, reports the isolation of endophytic bacteria from the selected plant, B. lupulina Lindl.
Keywords: Endophytic bacteria, Barleria lupulina, Phosphate solubilization, Enterobacter roggenkampii, 16S rRNA.

ABSTRACT (PEAM64)

BIO-DECOLOURIZATION OF SYNTHETIC DYE METHYL ORANGE BY NEWLY ISOLATED BACILLUS SP.

*Ankita Vinayak, Gajendra B. Singh**
University Institute of Biotechnology, Chandigarh University, Mohali (140413), Punjab, India
*Email *gajendra.singh@cumail.in, gajendrabiotech@gmail.com*

Azo dyes represent the largest class of synthetic dyes known with a range of colours and numerous applications. However, their complex chemical structure and recalcitrant nature have a detrimental effect on the environment and human health. The tonnes of coloured effluent discharged from textile mills into water bodies. The coloured water damages aesthetic value of water, affects aquatic flora and fauna. Problems associated with the textile industry's contamination highlight the need for efficient treatment methods. Microbial degradation and decolourization of azo dyes has gained importance for the removal of synthetic colours, as it is an eco-friendly and economical method. Microbes have developed various enzyme systems to degrade the synthetic dyes. The present study deals with the bio-decolourization of sulfonated azo dye, methyl orange, using newly isolated bacterial strain. Approximately, complete decolourization of 100 ppm dye was observed in 18 hours of incubation at 37 ˚C and 150 rpm. UV-Vis spectroscopic analysis of dye samples, before and after bacterial treatment, confirmed the complete dye decolourization. The optimum temperature, pH and rpm for bacterium was found to be 37˚C, 7.0 and 150 rpm, respectively. Bacterial strain was also able to decolorize a wide range of dye i.e. 50-500 ppm just in 100 hrs. Further, the effect of untreated and microbially treated dye samples on agriculturally important seeds was examined. There was significant reduction in the germination and root, shoot length of seeds watered with treated dye and original dye samples. Thus, findings suggest that isolated bacterial strain has potential to decolorize dye contaminated water enabling environmental remediation, water treatment and its reuse for industrial purposes.
Keywords: Bio-decolourization, Azo dyes, Recalcitrant, Methyl orange, Bacillus sp.

ABSTRACT (PEAM065)

BIOREMEDIATION OF HEXAVALENT CHROMIUM BY USING BACTERIAL CONSORTIUM

*Sakale Sagar Subhashrao**
Department of Microbiology, N.S.B. College, Nanded, Maharashtra, India
*Email *sagar_sakle@yahoo.com*

Heavy metals especially hexavalent chromium have become a serious threat to the biosphere, due to natural and anthropogenic causes. Accumulation of hexavalent chromium in the aquatic ecosystem, agricultural soil leads to serious environmental issues due to their persistent and biomagnifications in the food cycle and food web. Bioremediation can be used as an alternative to overcome the limitations of the conventional methods. The present study emphasized the use of an indigenous consortium developed by using chromium resistant bacteria. Among sixty heavy metal resistant bacteria screened from metal contaminated effluents, five isolates showed higher MIC values for Cr (VI). These five isolates were identified by 16s rRNA sequencing and used in different combinations for development of eight bacterial consortia. Among eight consortia, Consortium M (C. amylolyticum, B. cereus, S. arlettae, and C. funkei) showed a complete reduction of 10µg/ml Cr (VI) in 6 h of the incubation period. The effects of various temperature, pH, and concentrations of Cr (VI) and heavy metals on chromium reduction efficiency of selected consortium showed that at pH 7.0, and 30◦C, Cr reduction efficiency of Consortium was optimum. In the presence of Cu, Ni, and Zn, Cr reduction efficiency of Consortium was activated whereas Cd, Co, Pd, and Hg showed an inhibitory effect on Cr reduction efficiency. The bacterial consortium showed complete reduction of Cr (VI) present in electroplating industrial effluent sample. The phytotoxic study by pot assay showed that, in comparison with the untreated electroplating sample, the treated effluent sample was found to be plant (V. radiata) growth supportive. In the SEM-EDS analysis of the consortium showed that slight changes occurred in surface morphology due to the presence of Cr (VI). The bioremediation process is a cost-effective, environmental friendly process for removal of hexavalent chromium from the environment.

ABSTRACT (PEAM66)

METAGENOMIC DIVERSITY AMONG THE PHENANTHRENE DEGRADING CONSORTIA IN THE REGION OF HARYANA, INDIA

*Suryakant Panchal, Manju Bala Bishnoi, Taruna Sheoran, Mandeep Kumar, Namita Singh**
Department of Bio and Nano Technology, Guru Jambheshwar University of Science and Technology, Hisar, Haryana – 125001
*Email *namitasingh71@gmail.com*

Polycyclic aromatic hydrocarbons (PAHs) are cyclic aromatic hydrocarbons having two or more fused benzene rings and have different structural arrangements. Phenanthrene is a three ring PAH having K and Bay-region in its structure. It is predominantly found around coal gasification sites and thermal power stations. It is an environmental hazardous compound and also acts as mild photosensitizer as well as skin irritant/allergen. Bioremediation of phenanthrene and other PAHs contaminated sites using naturally isolated bacteria strains or mixed bacterial culture (i.e., consortium) is a safe, economic and efficient way. In the present study two different consortia were collected from Hisar and Panipat districts of the Haryana region. The collected microbial consortia were enriched and maintained at 500 ppm MS phenanthrene media. The 16S rRNA genes of the V3- V4 specific region of the bacteria were targeted, amplified, sequenced using Illumina based MiSeq technology and analyzed using the bioinformatics tools for the identification of metagenomic diversity among the two consortia. The results showed that in both consortia, the phylum proteobacteria dominate at phylum level diversity with an abundance of >99%. In the Hisar region consortium, the class gammaproteobacteria (53.15%), alphaproteobacteria (31.77%) and betaproteobacteria (15.04%) were the dominating taxa, whereas the class gammaproteobacteria (47.58%), betaproteobacteria (34.49%) and alphaproteobacteria (17.21%) were the dominating taxa in the Panipat region consortium. The results of gas chromatography analysis showed that both consortia have efficient phenanthrene biodegradation potential. This study pleads the use of a natural picked and enriched consortium for the bioremediation of phenanthrene and other PAHs contaminated sites.
Keywords: Phenanthrene, consortium, biodegradation, metagenome and bioremediation.

ABSTRACT (PEAM067)

TRACKING OF HEXACHLOROCYCLOHEXANE (HCH) - DEGRADING SPHINGOBIUM INDICUM B90A INOCULUM DURING BIOAUGMENTATION OF HCH CONTAMINATED SOILS

Sonika Phian1, Durgesh Narain Singh2, Helianthous Verma1, Yogendra Singh2, Rup Lal3, Charu Dogra Rawat1***
1 Molecular Biology and Genomics Research Laboratory, Ramjas College, University of Delhi, Delhi 110007, India
2 Department of Zoology, University of Delhi, Delhi 110007, India3 The Energy and Resources Institute, Darbari Seth Block, IHC Complex, Lodhi Road, New Delhi 110003, India
*Email *sonikaphian@gmail.com, **cdrawat@ramjas.du.ac.in*

Tracking of bioinoculant to ensure its survival, performance and specific distinction from the indigenous microflora during the remediation of contaminated sites is one of the challenging and necessary tasks. Here, we use specific primers to amplify a unique gene (B90A.285 that encodes for NAD (P)-binding protein) of Hexachlorocyclohexane (HCH)-degrader Sphingobium indicum B90A to detect its presence during bioaugmentation of the contaminated soils. The primer set did not give amplification with the closest neighbours of S. indicum B90A, such as, S. lucknowense F2, Sphingobium sp. HDIPO4, S. chinhatense IP26, and S. japonicum UT26. No amplification was observed with the metagenomic DNA isolated from the HCH dumpsite soil. Microcosms containing contaminated dumpsite soil (strained environment) and autoclaved garden soil (conducive environment) were inoculated with S. indicum B90A. Appropriate control microcosms without addition of S. indicum B90A were also kept. Periodic mixing and watering of the soil was done to maintain aeration and humidity in the microcosms. Soil samples were periodically drawn from the test and control microcosms up to a period of 9 days. PCR amplification of the metagenomic DNA isolated from the microcosm soil samples collected at different time points revealed amplification of the unique gene of S. indicum B90A for up to 4 days of bioinoculation in both the dumpsite and garden soil. Colonies of S. indicum B90A (yellow in color and producing brown pigment) on culturing of the samples on culture plates could be observed in autoclaved garden soil samples (until 4 days of bioinoculation), however, no colonies of S. indicum B90A could be observed or distinguished in the culture plates of contaminated soil drawn samples.

ABSTRACT (PEAM68)

ESTABLISHMENT OF POLYMERASE SPIRAL REACTION FOR THE DETECTION OF LEPTOSPIRA INTERROGANS

Archana Vishwakarma, J. Punith Chowdary, Mohandass Ramya*
Department of Genetic Engineering, School of Bioengineering,SRM Institute of Science and Technology, SRM Nagar, Kattankulathur 603203,Kanchipuram, Chennai, TN, India
*Email *Vishwakarma.archana2018@gmail.com*

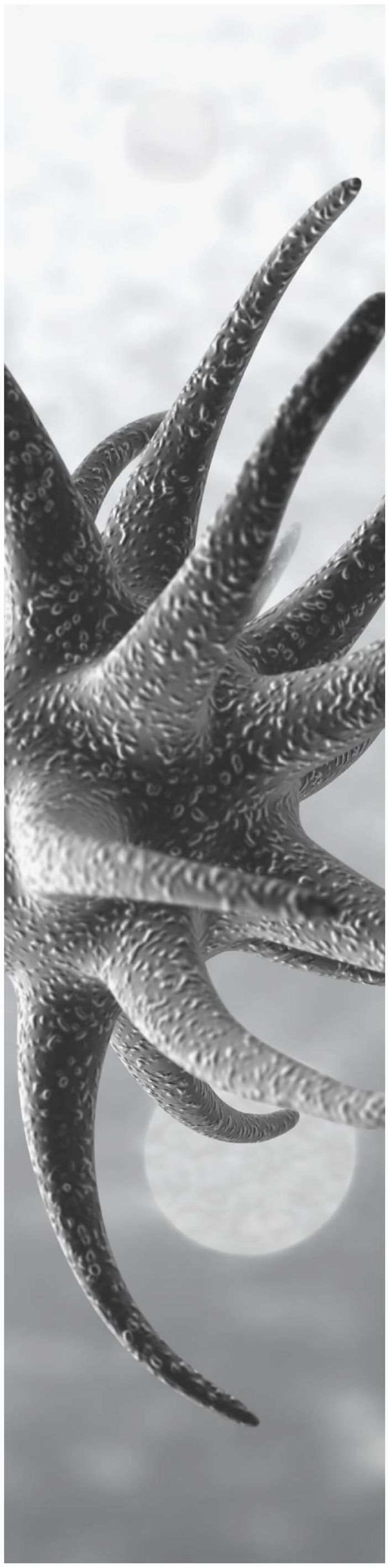
Leptospirosis is a waterborne zoonosis. It is a significant but neglected disease and a cause of mortality both in animals and humans. Leptospira interrogans, the causative organism, is a Gram-negative spirochete. In this study, we report the first Polymerase Spiral Reaction (PSR) assay for the rapid detection of Leptospira interrogans. Lipl32, a highly conserved gene among pathogenic Leptospira, was used as a target. Two primers were designed to amplify the Lipl32 gene, and the PSR assay was evaluated by visual detection using a colorimetric dye and a nucleic acid stain. The assay was optimized for reaction time, temperature, and template concentration. The detection limit of the PSR assay was 100 ag/µl in 1 hour. L. interrogans serovar Canicola was used as the positive control, while one non-pathogenic Leptospira along with nine non-leptospiral strains were used as negative controls to check the specificity of the assay. Artificial contamination study using tap water established the limit of detection of the assay at 16 GEq/mL. The assay showed high specificity and sensitivity in comparison to Loop-based isothermal amplification (LAMP) while using only a single primer pair in contrast to the six primers required for LAMP. The assay shows the potential to be used as the method of choice for Leptospira detection.
Keywords: Leptospirosis, zoonosis, isothermal amplification, PSR, visual detection.

ABSTRACT (PEAM069)

HARNESSING THE POWER OF THE MICROBIAL STRUCTURE OF HERMETIA ILLUCENS FOR THE BENEFIT OF WASTE MANAGEMENT PROCESS

Punita Sharma1, Namita Singh2***
1National Institute of Malaria Research, Indian Council of Medical Research, Sector-9, Dwarka, New Delhi-110077, India
2Bio and Nano technology department, Guru Jambheshwar University of Science and Technology, Hisar, Haryana-125001
*Email *sharma.punita86@gmail.com, **namitasingh71@gmail.com*

The largest population of the world that exists on earth is of the insects which comprises around more than 97% beneficial or harmless to human existence among which a wonder insect has come to light very recently in the late 19th century: Hermetia illucens also known commonly as Black soldier Fly (BSF). It is well known and highly studied for its voracious eating capabilities and in turn giving the proteinaceous biomass for use in the animal feed industry, frass as the biofertilizer and soil improvement agent. Decomposition of waste with Black Soldier Fly Larvae (BSFL) is an emerging treatment technology that would have a noticeable impact on the economics of the waste treatment field. Although the power of BSFL is being recognized by western countries like USA, Canada, Europe, African and some Asian countries where governmental permissions have been given for waste treatment and use of BSFL in animal feed, but in India this is still at a nascent stage and requires recognition, attention and implementation. The processes for BSFL waste treatment are in a nascent stage and optimization is being done for a self sustainable system. Process improvement involves maximization of the waste treatment in the least time frame. So, at least the larval stage which is the main biological compost reactor needs to be carefully monitored. One of the concepts is the knowledge of residing bacteria of this insect gut may prove to be beneficial for the life cycle improvement or an efficient process development as it is evident that digestibility, metabolic functions, ecological adaptations and even survival for few is shown to be influenced by the insect gut bacterial communities. Microbiome structure of an insect depends on their diet, environment they thrive in and their evolutionary history. Therefore, study needs to be conducted for the population of BSF found in India for their gut symbionts, so that their beneficial properties can be utilized for the reduction of biological food waste heaps at the local level, to deter the toxic leachate reaching the water table and lower the emission of Greenhouse gases to the atmosphere.



THEME 3

Industrial Microbial Biotechnology

ABSTRACT (PIMB001)

PURIFICATION AND CHARACTERIZATION OF PHARMACEUTICAL GRADE PHYCOCYANIN AND PHYCOERYTHRIN FROM CYANOBACTERIA

Samadhan Yuvraj Bagul, Ritu Vishwakarma, Shaloo Verma, Hillol Chakdar, Anil Kumar Saxena*
ICAR- National Bureau of Agriculturally Important Microorganisms, Kushmaur, Maunath Bhanjan Mau-275103
*Email *samadhanbagul@gmail.com*

Phycocyanin (PC) and phycoerythrin (PE) are natural colorants found in cyanobacteria have wide applications in food, beverages and pharmaceutical industries. In the present study, PC and PE were extracted from Pseudoanabaena RD1 and Nostoc BG1 respectively by freezing and thawing method. Purification was achieved by ammonium sulphate precipitation followed by ion exchange chromatography using DEAE cellulose. Purity of PC and PE obtained after ammonium sulphate precipitation was 2.08 and 3.87 respectively, however, after ion exchange chromatography purity was achieved 5.16 (pH 5.10) and 6.28 (pH 7.0) respectively. Absorption maxima of purified PC and PE were shown at 620 nm and 562 nm respectively. SDS-PAGE analysis showed presence of two subunits (α,β) of pchycocyanin 16 kDa and 18 kDa. Two subunits (α,β) of phycoerythrin also showed at 13 and 15 kDa. Purity of the pigments obtained was pharmaceutical grade hence, these pigments could have potential applications in food and pharmaceutical industries.

ABSTRACT (PIMB002)

SUSTAINABLE BIOMETHANATION OF RICE STRAW WITHOUT THERMOCHEMICAL PRETREATMENT

*Payal Deshpande, Deepa Shetty, Pranav Kshirsagar, S.S. Dagar, P. K.Dhakephalkar**
Bioenergy Group, MACS- Agharkar Research Institute, G.G. Agarkar Road, Pune-411004, India
*E-mail *pkdhakephalkar@aripune.org*

Rice straw is one of the most abundant lignocellulosic agro-waste in India. Each year, million tons of rice straw is burned in northern parts of India creating heavy smog in and around the area. The present investigation was undertaken to convert the rice straw to biomethane by anaerobic digestion without any thermo-chemical pretreatment. The optimized methane yield (274 L/kg Volatile Solids) was obtained at 1 L scale from particulate rice straw (~1 mm size, 7.5% total solids) supplemented with zinc and urea (C/N ratio of 25) and inoculated with cattle dung (Substrate/inoculum ratio of 1 in terms of VS) at 37°C, pH-7 and 21 days hydraulic retention time. At 30 L scale, the optimized methane yield of 246 L/kg VS was obtained which was ~75% of the theoretical maximum yield. The process reported here is an energy-efficient, cost-effective and environmentally benign method for efficient extraction of energy from rice straw bypassing the need of any polluting pretreatments.

Key words: rice straw, anaerobic digestion, biogas.

ABSTRACT (PIMB003)

MICROBIAL ENHANCED OIL RECOVERY (MEOR) POTENTIAL OF BIOSURFACTANTS IN WASTE OILY SLUDGE

*Ayushi Chafale 1,2, Atya Kapley 1,2**
1 Academy Of Scientific And Innovative Research (AcSIR) Ghaziabad 20100, India
2 Directors' Research Cell, CSIR-National Environmental Engineering Research Institute (CSIR-NEERI), Nehru Marg, Nagpur
*Email *a_kapley@neeri.res.in*

Refining and processing of crude oil often results in inevitable accumulation of waste in the form of oily sludge. Bioremediation methods such as landfarming and landfilling are recently ruled as inappropriate methods due to the concern associated with it such as length of time it takes for bioremediation, occupying large valuable surface area and release of harmful contaminants into the soil. Considering that oily sludge contains a relatively acceptable amount of oil, the present study is focused on a biological treatment method for recovery of oil from the oily sludge known as microbial enhanced oil recovery method (MEOR). MEOR biologically allows the recovery of residual oil fractions from the oily sludge by the action of microbes producing surface active metabolites. A series of screening tests, DNA isolation and 60S RAPD-PCR of isolates assisted in identification of unique and distantly related strains having biosurfactant property. Biosurfactant producing isolates Pseudomonas sp. and Acinetobacter sp. were selected based on screening tests for biosurfactant production. The qualitative analysis of hydrocarbons in the oil recovered through the protocols performed in this study showed that the hydrocarbons detected in the oil samples extracted from recovered oil layer have most of the hydrocarbons that were present in oil extracted from untreated sludge resulting in confirmation of recovery of oil from oily sludge using these strains. These isolates were found to have high biosurfactant production ability suggesting that these protocols can be used for oil recovery from oily sludge.

ABSTRACT (PIMB004)

GENOME MINING FOR BIOSYNTHETIC GENE CLUSTERS IN STREPTOMYCES CHRESTOMYCETICUS ADP4

Varsha Verma1, M. Krishna Mohan2, Ashok K Dubey1*
1Department of Biological Sciences and Engineering, Netaji Subhas Institute of Technology, Dwarka, New Delhi, 110078, India
2Birla Institute of Scientific Research, Jaipur, India
*Email *varsha92igib@gmail.com*

Natural product biosynthesis is undergoing an extensive transformation, driven by the technological advancements in genomics, bioinformatics, analytical chemistry and synthetic biology. Exploration of the genome provides insight of the genes, which are present for metabolic network, metabolite synthesis and utilization, regulatory elements and other associated genetic elements. Biosynthetic gene clusters (BGCs) in actinobacteria have proven to be goldmines for drug discovery. However, their full potential largely remains unexplored as only a few of them get expressed under laboratory conditions. Genome mining for exploring BGCs has become a powerful means for characterization of their regulatory networks with an aim to maximize their exploitation for drug discovery purposes. We have been investigating Streptomyces chrestomyceticus ADP4 for antimicrobial and therapeutic metabolites. In the present work, we report identification of 46 BGC-containing regions in the genome sequences of S. chrestomyceticus strain ADP4. Further analysis of predicted BGCs has revealed a T2PKS Polyketide lysolipin-I biosynthetic gene cluster, which contains 69 ORFs and includes putative regulator which encode proteins of the SARP, sensor histidine kinase, LuxR and MarR transcriptional regulator families. Lysolipin-I is a broad spectrum antibacterial compound which is known to interfere with bacterial cell wall biosynthesis. Comparative analysis of BGC profiling reveals strain ADP4 as first with lysolipin I biosynthetic gene cluster described to date in S. chrestomyceticus and other related species. Further, strain improvement and antimicrobial discovery can lead to understanding the role of regulator for the antimicrobial biosynthesis.
Keywords: Streptomyces chrestomyceticus strain ADP4, CSRs, BGC, T2PKS, and antimicrobial discovery

ABSTRACT (PIMB005)

IN SILICO CHARACTERIZATION OF B-GLUCOSIDASE OF MYCELIOPHTHORA THERMOPHILA (MTBGL3C) AND ITS SUITABILITY IN LIGNOCELLULOSE BIOCONVERSION

Anica Dadwal1, Shilpa Sharma1,2, Tulasi Satyanarayana1,2*
1Department of Biological Sciences and Engineering, 1 Netaji Subhas Institute of Technology
2Netaji Subhas University of Technology, Sector-3 Dwarka, New Delhi-110078, India
*Email *anicadadwal@gmail.com*

Lignocellulosic biomass is a renewable energy source comprising mainly of cellulose, hemicellulose and lignin. Cellulases are the third largest industrial enzymes with a great potential in bioethanol production, which degrade cellulose into monomeric glucose units by cleaving β-1,4-glycosidic linkages. Cellulases consist of three main enzymes: endoglucanase, exoglucanase and β-glucosidase. Three enzymes act synergistically in cellulose bioconversion. In this investigation, a β-glucosidase of a thermophilic mould from Myceliophthora thermophila (MtBgl3c) was structurally analysed and characterized using various in silico approaches. Since the protein structure of MtBgl3c is not known, an attempt has been made in modelling 3D structure using homology modelling approach. The generated protein model of MtBgl3c was validated from Verify 3D and ERRAT scores derived from SAVES. The Ramachandran plot generated using RAMPAGE also confirmed the accuracy of the 3D model. The ion binding and N-glycosylation sites were predicted. The generated model, by docking to cellobiose, predicted the most favourable substrate binding sites of MtBgl3c. The catalytically important amino acid residues involved in cellobiose binding are Asp287 and Glu514. MD simulations performed for analysing MtBgl3c indicated structural stability and protein-ligand interaction analysis. The docking studies suggested the tolerance of MtBgl3c to glucose that makes MtBgl3c useful in cellulose hydrolysis.
Keywords: Cellulases; β-glucosidase; cellobiose; homology modelling; molecular docking.

ABSTRACT (PIMB006)

EVALUATION OF FUNGI FOR PRODUCTION OF INDUSTRIALLY IMPORTANT ITACONIC ACID

Meena Sindhu, Seema Sangwan*
Department of Microbiology, COBS&H, CCSHAU Hisar, Haryana, India
*Email *meenasindhu20@gmail.com*

Organic acid such as citric acid, lactic acid, malic acid and itaconic acid has huge demand in polymer, food and medical industries. It has been estimated that by 2022 market value for these acids will be more than 10 billion dollars. Among them the importance of itaconic acid has been increased because it can be used for production of biopolymers and can act as replacement of petroleum derived chemicals. It will reduce our dependence on fossil fuels and will help in environmental protection and sustainability. In this study, thirty-five fungal Isolates were retrieved from soil samples collected from various sites. Screening of these fungi for production of organic acid was done on potato dextrose agar plates amended with bromophenol blue. Six isolates ITA5, ITA8, ITA15, ITA22, ITA27 and ITA34 produced yellow colour zones on the plates amended with bromocresol green indicating their potential for production of itaconic acids. Further purification will be done using high performance liquid chromatography. Solid-state fermentation using agricultural wastes could help in reduction of production cost for industry. Production of itaconic acid using these fungi can be a robust approach for industries as it will be a less costly and environmentally friendly approach.
Keywords: Fungi, Itaconic acid, Organic acid, Industry, Fermentation

ABSTRACT (PIMB007)

ANTIMICROBIAL ACTIVITY OF POTENTIAL LACTIC ACID BACTERIA DERIVED FROM PLANTS

Mausamy Nandha1 and Rachana Shukla2*
1Department of Microbiology and Biotechnology, School of Science, Gujarat University, Ahmedabad-380009, Gujarat, India
2Department of Microbiology, President Science College, Ghatlodiya, Ahmedabad-380061, Gujarat, India
*Email *mausamycn28@gmail.com*

The probiotics are one of the fastest growing categories within food for which scientific researchers have demonstrated therapeutic evidence. Lactic acid bacteria (LAB) isolated from unconventional sources are often attractive targets in the quest for obtaining better probiotics. The aims of this study were to isolate and select an appropriate probiotic LAB from plant source to use as a starter culture. Owing to their unique probiotic activities LAB derived from plant sources are considered to be a promising source of novel microorganisms. Total 11 isolates were isolated from various plants of Cocoa criollo, Cocoa forastero, Saccharum officinarum, Fragaria ananassa and Opuntia ficus indica from various locations of Gujarat. They were withstanding broad spectrum antibiotics so it should be safe for the followers of antibiotics. The antimicrobial spectrum of selected isolates was investigated against a range of Gram-Negative and Gram-Positive amongst them 3 isolates showed antagonistic effects against the pathogens. Gujarat is at the forefront of pharmaceutical companies, where this data will surely be a valuable addition. Further, the relatively less explored group of organisms from an equally rare habitat would be an added attraction.

Key words: Lactic acid bacteria, Antimicrobial activity

ABSTRACT (PIMB008)

ISOLATION OF HALOPHILIC BACTERIA PRODUCING IMPORTANT INDUSTRIAL ENZYMES

Deepa Yadav, Dr. Anuradha Singh, Dr. Nupur Mathur, Dr Jyoti Sharma, Dr Aditi Agarwal*
Environmental Molecular Microbiology Laboratory, Department of Zoology, University of Rajasthan, Jaipur, India
*Email *89deepayadav@gmail.com*

Halophilic microorganisms are those which are found at high salt concentrations. These microorganisms produce a wide range of bioactive compounds such as enzymes, antibiotics, pigments etc. Enzymes derived from halophiles can function under different harsh conditions and have different properties of conventional enzymes, therefore they offer many different applications in various industries. For the isolation of halophilic bacteria, samples were collected from different places in Rajasthan. Total forty- five halophilic bacteria were isolated at different salt (10%-30%) concentrations. These isolated halophilic bacteria were then screened for production of different enzymes (amylase, lipase and cellulase). It was found that many of the isolated bacterial strains were able to produce different enzymes and many of them were found to be producers of multiple enzymes.

ABSTRACT (PIMB009)

ENDOPHYTIC FUNGI ASSOCIATED WITH MANGROVE ECOSYSTEM OF KUTCH, WESTERN INDIA: A POTENT SOURCE OF ANTIMICROBIAL METABOLITES

Nidhi Trivedi1 and Jignasha Thumar2*
1Department of Microbiology and Biotechnology, School of Science, Gujarat University, Ahmedabad 380009, Gujarat, India
2Department of Microbiology, Government Science College, Gandhinagar-382015, Gujarat, India
*Email *nidhitrivedi4030@gmail.com*

Mangroves are considered as one of the most productive ecosystems. Mangrove harbors a large number of unique fungal communities known as manglicolous fungi. Fungal endophytes are attracting much attention and are increasingly renowned, as their host plants are traditionally used for medicinal purposes. With the increase in microbial disease and increase in drug resistant microorganisms, the need for novel as well as more potent antimicrobial compounds remains constant. In this context, our study was aimed at exploration of mangrove endophytic fungi as a potent source of antimicrobial compounds. Total 13 halophilic fungal isolates were isolated from the root sample of Avicenia marina collected from Kutch, Gujarat. They were able to grow in the range of 5-15% W/V NaCl. An antimicrobial spectrum of selected isolates was investigated against a range of Gram negative and Gram-Positive bacteria. Three of the fungal isolates showed broad spectrum activity against the pathogens. The antimicrobial metabolites were further extracted using Ethyl acetate. The DNA was isolated from the fungi and the ITS region of 18S rRNA was sequenced and sequence similarities were observed by phylogenetic analysis. These preliminary findings of endophytic fungi showed their ability to produce potent bioactive metabolites for drug discovery.

Key words: Mangrove endophytic Fungi, Antimicrobial activity, Halophilic Fungi

ABSTRACT (PIMB010)

CLONING AND HETEROLOGOUS EXPRESSION OF GH43 B-XYLOSIDASEGENE (TTBXS) OF THERMOTHELOMYCEST HERMOPHILES

Ravi Kumar1, Shilpa Sharma1,2 and Tulasi Satyanarayana1,2*
1Division of Biological Science and Engineering, Netaji Subhas Institute of Technology, Azad Hind Fauz Marg, Dwarka, New Delhi-110078, India
2Department of Biological science and Engineering, Netaji Subhas University of Technology, Azad Hind Fauz Marg, Dwarka, New Delhi-110078, India
*Email *bimaldevravi@gmail.com*

Xylan is a heterogeneous polysaccharidemade of a backbone of β-1,4-xylose units with a variety of side chains. Complete degradation of xylan requires an array of enzymatic actions for liberating reducing sugars. The conversion of xylan to xylose is mainly dependent on endo-β-xylanases (EC 3.2.1.8) and β-D-xylosidases (EC 3.2.1.37). Endo-β-xylanases break the main chain of xylan and release xylo-oligosaccharides of varied degree of polymerization, and xylo-oligosaccharides are further hydrolyzed to xylose by β-D-xylosidases. Advancements in molecular biology renewed interest in the mining of β-xylosidases to assess their potential applicability in commercial lignocellulose saccharifying enzyme cocktails in the production of bioethanol. Fungal β-xylosidases are known to display transxylosylation activity which make them attractive in producing xylooligosaccharides for use as prebiotics. Thetransxylosylation activity of β-xylosidases allows the addition of xylose units to lower xylooligosaccharides in increasing their chain length to the desired level for prebiotic application. The present investigation describes cloning and expression of a gene that encodes β-xylosidase from the thermophilic Ascomycete Thermothelomyces thermophilus. Due to a wide variation in codon usage in T. thermophilus and Escherichia coli, the synthetic gene for expression in E. coli was heterologously expressed in E. coli. The molecular mass of expressed protein is 61 kDa with an acidic pI (5.86). Its kinetics, using 4-nitrophenylβ-D-xylopyranoside as the substrate, are underway. Comparison with other β-xylosidases suggested that it belongs to Glycoside Hydrolase (GH) Family 43. These and other aspects of the recombinant Ttbxs will be presented.

ABSTRACT (PIMB011)

EXPLORATION OF OLEAGINOUS FUNGI IN TRADITIONALLY FERMENTED FISH FOOD 'NAFAM'

Avra Pratim Chowdhury and Diganta Narzary*
Department of Botany, Gauhati University, Guwahati, Assam, India
*Email *avranu132@gmail.com*

Non-salted fermented fish food 'Nafam' is a unique traditional food of the Bodos of north east India. Small smoked or sun-dried local fishes are generally pounded together with either alocasia or colocasia petioles. The mixture is then put inside a bamboo container or any plastic container sealing the mouth of the container. Nafam becomes ready for consumption after fermenting about one month and can be preserved for 6–12 months. It has a unique taste and flavor which is much liked by the tribal peoples of the region. Total 36 fungal isolates including 28 aerobic and 08 facultative anaerobic fungi were obtained from a Nafam sample using Potato Dextrose Agar media. Morphological study after lactophenol cotton blue staining of the isolates revealed that most of the isolates were unicellular yeasts or yeast-like with pseudohyphae, except one which showed hyphal cells. The Sudan Black B Staining Test (Lison, 1934), Translucent Test (Williams, 1947), Lipid Solubility Test (Ralston, 1942), and Chloroform (Confirmatory) Test (Hoerr, 1947) were performed to identify the oleaginous fungal isolates. Out of 36 isolates, only 19 isolates including all the facultative anaerobic were found oleaginous in the present study. Distribution of oil droplets were observed mostly in the cytoplasmic regions except a few where it was observed both in the cytoplasm and the nuclear regions. Of course, the oil content greatly varied among the fungal isolates. We explored the oleaginous fungi from the fermented fish food 'Nafam' for the first time, and to record ~53% oleaginous fungal isolates in Nafam is quite interesting. Further study on oil production physiology and oil extraction from the isolates could unravel the scope of bioprospection in the field of biodiesel production from those fungi.

ABSTRACT (PIMB012)

BIOFUEL AND BIOCOMMODITIES PRODUCTION IN MARINE MICROALGAE DUNALIELLA TERTIOLECTA USING COMMERCIAL FERTILIZER AS CHEAP NUTRIENT SOURCE

Alka Devi, Charu Singh, Sunil Pabbi*
Centre for Conservation and Utilisation of Blue Green Algae (CCUBGA), Division of Microbiology, ICAR. Indian Agricultural Research Institute. New Delhi, India
*Email *alkamondela@gmail.com*

In recent years, marine microalgae are considered as promising feedstock for research in the fields of nutraceuticals, pharmaceuticals, cosmeceuticals and production of biofuels. Microalgae are the light driven small bioreactors that convert vital nutrients and carbon compounds to biofuels and high-valued byproducts. Higher accumulation of lipids and other photosynthetic pigments are the considerable factors to make microalgae a promising host. Dunaliella tertiolecta, a marine microalga known to have the ability to synthesize lipids in a prominent amount has the potential to be used for biodiesel production.Various methodologies have been employed to reduce the biomass production cost and one of the best ways is to lower down the media cost. In present study, a commercial low cost fertilizer, suphala was used as alternative source of media components such as nitrogen, phosphorous and potassium (N:P:K in 19:19:19 ratio).The results indicated that various concentrations of NPK fertilizer have significantly impacted the growth, photosynthetic pigment compositions, as well as lipid content and lipid profile of the organism. Where a concentration of 0.225 g/l resulted into the maximum growth (530µg/ml as cell dry weight) as well as chlorophyll (6.815µg/ml) and carotenoids (1.107µg/ml) after 21 days. The lipid content also increased by 7% compared to control. Hence, optimization of cultivation parameters by using alternative nutrient source to produce specific products is a promising technique.

ABSTRACT (PIMB013)

MICROBIAL CONVERSION OF FERULIC ACID TO BIOVANILLIN

Abha Sharma1, Jyoti Singh1, Minakshi Grover1, Surender Singh2, Lata Nain1*
1Division of Microbiology, ICAR-Indian agricultural research institute, New Delhi, India
2Department on Microbiology, Central University of Haryana, Mahendargarh, Haryana, India
*Email *tauras.abha@gmail.com*

Vanilla flavor is mainly composed of the organoleptic compound, vanillin. It is naturally extracted from the pod, Vanilla planifolia. However, the natural production of the compound is cost-intensive as well as cumbersome. Due to the growing consumer interest in natural flavor compounds and chemical synthesis being considered as synthetic by the European Guidelines on flavor compounds, alternative natural production routes are being searched. In this regard, the production of flavors via microbial biotransformation process provides a feasible option to the natural and chemical routes. In the present study, an attempt has been made for the bio-production of vanillin from ferulic acid (precursor of vanillin) using Streptomyces sp. C-99. After growth in glucose media, cells of Streptomyces sp. C-99 were harvested and inoculated into production media containing ferulic acid as the carbon source. The products formed were analyzed after regular intervals by high performance liquid chromatography and the results showed that the strain produces significant amounts of vanillin with small quantities of vanillic acid. The maximum vanillin yield (678. 15 ± 22.34 mg/L) was obtained after 12 h in production media containing 1g/L ferulic acid at 37°C and 150 rpm.

ABSTRACT (PIMB014)

SEQUESTRATION OF HEAVY METALS FROM AQUEOUS SOLUTIONS BY BIOSURFACTANT PRODUCED BY MARINE BACTERIA ISOLATED FROM OIL CONTAMINATED SITE

Shruti Mathur, Abhipsa Pani, Shreya Singh, Surbhi Agarwal, Sandhya Menon*
Amity University, Jaipur, Rajasthan, India
*Email *smathur1@jpr.amity.edu*

Surfactants and emulsifiers are widely used in the pharmaceutical sector, cosmetics industry, soap and detergent industry, textile industry, oilfield chemicals, agrochemicals, food industry, and others. About 54% of the total surfactant output is utilized in household/laundry detergents, with only 32% for industrial use. Biosurfactants are environmentally friendly options produced by microbial fermentation processes .Surfactant properties enable emulsifying, foaming, detergency and dispersing properties The facts that only small amounts are needed to reduce surface tension coupled with their little or no toxicity and higher biodegradability makes them environmentally friendly comparing with chemical surfactants. Additionally, their stability at extreme environmental conditions and their variety in structural and chemical composition makes them versatile in terms of applicability. The present work studies yet another potential of biosurfactants produced from four different bacteria by analysing their ability to remove heavy metal Chromium (VI). Growth of these bacteria in media containing 10 ppm of hexavalent chromium resulted in sequestration of the metal from the medium into the EPS as revealed by analysis in an Atomic Absorption Spectrophotometer. These results point to potential for development of zero liquid discharge technologies (ZLD)for industries whose effluents have a heavy load of heavy metals like chromium e.g. electroplating , leather tanning industries etc.The above work would draw the interest of entrepreneurs with enterprises generating heavy metal containing effluents.

ABSTRACT (PIMB015)

IDENTIFYING BACTERIAL L-ASPARAGINASE FOR ITS APPLICATIONS IN ACUTE LYMPHOBLASTIC LEUKEMIA AND ACRYLAMIDE DEGRADATION

Vinay Kumar and Digvijay Verma*
Department of Microbiology, Babasaheb Bhimrao Ambedkar University, Lucknow, Uttar Pradesh-226025, India
Email: vkvinayak.1992@gmail.com

L-Asparaginase (EC 3.5.1.1) belongs to a group of homologous amido hydrolases family that catalyzes the hydrolysis of the amino acid L-asparagine to L-aspartate and ammonia. The enzyme finds significant applications in treating acute lymphoblastic leukemia (ALL) and in acrylamide degradation. We have merely two L-asparaginases from E. coli and Erwinia lacking glutaminase activity which is a prerequisite of its therapeutic use for treating ALL. However, the problems associated with these L-Asparaginases such as toxicity and immunosuppression suggest us to discover more potential candidates.In the present investigation, we have isolated several bacteria exhibiting L-asparaginase activity from various environmental samples such as soil, effluent, compost soil, cow dung, and sewage water. A modified Czapek-Dox (C-Dox) Agar- medium having phenol red was used to observe the color change (yellow to red) around the bacterial cultures. Of the twenty-seven isolates, two potential isolates of cow's dung were discovered that do not exhibit any glutaminase activity. Preliminary characterization of these isolates revealed that these are Gram-negative Proteobacteria. Molecular characterization of these isolates using 16S rDNA is under progress. Besides, we have also identified two thermophilic L-asparaginases having a role in the degradation of acrylamide in the food processing industry. We are in the process of extensive characterization of these thermophilic enzymes.

ABSTRACT (PIMB016)

PRODUCTION OF TANNASE FROM A NOVEL TANNASE PRODUCER AND ITS APPLICATION IN PROPYL GALLATE SYNTHESIS

*Dhruvil N. Brahmbhatt**
Department of Microbiology, L. J. Institute of Applied Sciences, L.J. Campus, S. G. Highway, Ahmedabad, India
*Email *dhruvilbram@gmail.com*

Tannase (3.1.1.20.) catalyses hydrolysable tannins into glucose, gallic acid, and galloyl esters by cleaving ester and depside bonds. A novel tannase producer, identified as Bacillus timonensis DB 21, was isolated from tea waste dump sites after primary and secondary screening. The isolate was able to produce 3.4 U/mL of tannase under unoptimized conditions. Tannase biosynthesis was optimized by one factor at a time which resulted in the production of 4.56 U/mL of tannase within 48 hours. Additionally, a statistical approach using response surface methodology (RSM) was applied to optimize tannase production which yielded a 3.26-fold increase. This increase corresponded to a production level of 11.08 U/mL in medium containing 2.25% (w/v) tannic acid, 1.25% (w/v) glucose, 1.25% (w/v) ammonium chloride, and 0.01% (w/v) MgSO4 having pH 7.0 incubated at 35°C for 48 hours at 120 rpm with a 2.0% (v/v) inoculum level. Furthermore, tannase was partially purified using salting-in (ammonium sulphate precipitation) and salting-out (dialysis bag) approach. Partially purified tannase was utilised for synthesizing propyl gallate from gallic acid through transesterification reaction using n-propanol. The propyl gallate synthesized was analysed by TLC and FTIR analysis.

ABSTRACT (PIMB017)

UPSCALING THE PRODUCTION OF POLYHYDROXYALKANOATE BIOPOLYMER: BATCH AND FED-BATCH APPROACH

Govind Singh Tomar, Udita Pushpad, Lata and Rajeev Kaushik*
Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi, India
*Email *govind07@outlook.com*

Polyhydroxyalkanoates (PHA) serve as an essential substitute for petroleum-derived plastics because of their close functional analogy and biodegradation quality. The most commonly occurring PHA is poly-β-hydroxybutyrate (PHB), a linear, unbranched homopolymer composed of (R)-3-hydroxybutyric acid (3HB) units.. The process parameters for upscaling the production of PHB by Halomonas sp. LB7 was optimised in the present study. Using optimized growth media having sucrose as a C source, the batch and repeated-batch cultivation of Halomonas sp LB7 was carried out in a 7-L bioreactor. When the concentration of sugar within the bioreactor was reduced to a low concentrations (below 10 mg mL-1), the batch cultivation was transferred to the mode of the nutrient feed cycle in which 80% (v/v) of the culture broth was collected from the reactor and refilled at 48h, 70h and 95h with a fresh medium. During the first cycle of batch cultivation peaked at 48 h of growth, i.e., the late exponential phase and 10.36 g L-1 CDB and 7.08 g L-1 PHB with a volumetric productivity of 0.142 g L-1 h-1. At the end of the second cycle (at 70 h), a significantly high CDB and PHB concentration of 28.68 g L-1 and 21.32 g L-1 was obtained. The overall productivity of PHB with fed-batch in 95 h was 0.54 g L-1 h-1, which was significantly higher than the batch fermentation (0.14 g L-1h-1). The harvested broth yielded 11.4 gL-1 CDM (cell dry mass) and 7.68 gL-1 PHB in the first cycle. At the end of the 5th cycle, 6 and 11% increase in cell dry biomass and PHB productivity. Repeated fed-batch cultivation has benefited from avoiding the non-productive time needed during a batch for the washing, refilling and sterilization of bioreactors, thus increasing the process's overall volumetric efficiency and industrial significance.

ABSTRACT (PIMB018)

EVALUATING ISOTONIC AQUEOUS FORMULATION OF CHAETOMIUM GLOBOSUM KUNZE FOR THE MANAGEMENT OF POTATO BLACK SCURF CAUSED BY RHIZOCTONIA SOLANI IN INDIA

S. Parthasarathy1,2, K. Arunkumar, L. Rajendran and T. Raguchander*
1Department of Plant Pathology, Centre for Plant Protection Studies, Tamil Nadu Agricultural University, Coimbatore - 641 003,
2Department of Plant Pathology, Amrita School of Agricultural Sciences, Amrita Vishwa Vidyapeetham, Coimbatore - 641 032,
*Email *spsarathyagri@gmail.com*

Black scurf of potato caused by Rhizoctonia solani has become a serious disease and causes both quantitative and qualitative damages in most potato producing areas of the world. In order to manage, isotonic aqueous formulation of Chaetomium globosum has been developed and its efficacy was tested under glasshouse and field conditions. In total, forty isolates were tested in vitro, among C. globosum Cg-6 showed maximum R. solani inhibition (60%) and increased the vigour index of potato under roll towel method. Among the various preservatives tested (glycerol, glycine, trehalose and polyvinylpyrollidine), isotonic solution amended with glycerol maintained maximum population up to six months and retained the antagonistic activity. Further, the effect of the isotonic aqueous formulation was evaluated under glasshouse and field conditions as soil, tuber and foliar application alone or in combination. The growth and yield attributes of potato plants were higher when applied with Cg-6 either combined or individually as compared to control with the reduced disease incidence of black scurf.
Keywords: Black scurf; Chaetomium globosum; Formulation; Isotonic; Potato, Survivability

ABSTRACT (PIMB019)

COMPARATIVE INVESTIGATION OF RSM AND GA-FUZZY LOGIC FOR OPTIMIZATION OF PHYCOBILIPROTEINS PRODUCTION FROM ANABAENA VARIABILIS CCC- 421

*Dinesh Kumar Saini1,2, Diya Roy2, Dinesh Yadav3, Deepak Chhabra3 , Pratyoosh Shukla1,4 Sunil Pabbi2**
1Enzyme Technology and Protein Bioinformatics Laboratory, Department of Microbiology, Maharshi Dayanand University, Rohtak-124001, Haryana, India.
2Centre for Conservation and Utilisation of Blue Green Algae (CCUBGA), Division of Microbiology, ICAR - Indian Agricultural Research Institute, New Delhi- 110 012. India.
3Department of Mechanical Engineering, University Institute of Engineering & Technology, Maharshi Dayanand University, Rohtak-124001, Haryana, India.
4School of Biotechnology, Institute of Science, Banaras Hindu University, Varanasi-221005, India
*Email *sunil.pabbi@gmail.com*

Cyanobacteria are promising source of biopigments as they are fast growing and have the ability to synthesize a high amount of valuable biopigments especially phycobiliproteins (PBPs). PBPs are well known for their antioxidant, anti-cancerous, anti-viral properties, etc. These are environment-friendly, non-toxic, and non-carcinogenic in nature and thus gaining importance as natural colorants over synthetic colors in food and cosmetics industries as well. In this study, a comparative investigation was performed between Response Surface Methodology (RSM) and GA-Fuzzy logic to optimize three components Ferric ammonium citrate, K2HPO4 and Trace metal of BG 11 medium for the maximum PBPs production from Anabaena variabilis CCC 421. The stat ease design expert (version 12.0) was used to design matrix of experiment for RSM and similar data was used as a knowledge base for fuzzy algorithms. An evolutionary algorithm comprising Genetic-Algorithm (GA) and Fuzzy-logic-methodology (FLM), i.e., GA-Fuzzy, was used for the optimization of input factors for the response function. Comparatively, higher PBPs production was obtained from GA-Fuzzy (408.5 mg/L) compared to RSM (390mg/L) under their respective optimum combination of input factors. Moreover, the value of regression coefficient was found highest in the GA-Fuzzy approach. The objective of work underlines the significance of new optimization tools for enhanced production of PBPs beside RSM techniques.
Keywords: Phycobiliproteins, Anabaena variabilis; Genetic-Algorithm (GA); Fuzzy-logic-methodology.

ABSTRACT (PIMB020)

INCREASED BIOETHANOL YIELD FROM AGRORESIDUES USING PENTOSE AND HEXOSE CO-FERMENTING YEASTS

*Jyoti Singh1, Abha Sharma1, Govind Singh Tomar1, Surender Singh2, Lata Nain1**
1Division of Microbiology, ICAR- Indian Agricultural Research Institute, New Delhi, India
2Department of Microbiology, Central University of Haryana, Mahendargarh, Haryana-123031, India
*Email *latarajat@yahoo.co.in*

Lignocellulosic biomass, due to its enormous availability, is a potential renewable feedstock for the continuous supply of second-generation bioethanol. In the present study, mixed substrate (paddy straw and jute sticks in 3:1 ratio) was explored for its potential to produce bioethanol. Saccharification parameters viz. reaction time (72 h), substrate loading (10%) and enzyme dose (cellulase 25FPU/gds, cellobiase 15 IU/gds) were optimized for maximum release of reducing sugar (747. 64 mg/gds) at 50˚C from the pre-treated substrate (2% alkali treated). Further, fermentation of the obtained enzymatic hydrolysate with hexose fermenting yeast (S. cerevisiae JRC 6) followed by pentose fermenting yeast (Trichosporon mycotoxinivorons S2) sequentially resulted in production of 10.36 g/L bioethanol compared to 8.4 g/L of ethanol produced when only S. cerevisiae JRC 6 was used for the fermentation process as estimated by HPLC.

ABSTRACT (PIMB021)

IMMOBILIZATION OF MICROBIAL PHENYLALANINE AMMONIA LYASE: RECENT ADVANCES AND PERSPECTIVES

*Anubhuti Kawatra, Rakhi Dhankhar, Pooja Gulati**
Department of Microbiology, Maharshi Dayanand University, Rohtak, Haryana, India
*Email *gulatipooja1@gmail.com, *pooja.micro@mdurohtak.ac.in*

Phenylalanine ammonia lyase (PAL) is a promising biomedical enzyme that catabolizes the non-hydrolytic and reversible deamination of L-phenylalanine to trans-cinnamate. Extensive research on this enzyme over the decades has decoded its potential in diverse agricultural, industrial and clinical applications viz. biosynthesis of arylalanines, phenolics, antibiotics, dietary supplements, and treatment of metabolic disorders like tyrosinemia and carcinomas. Also, its PEGylated formulation 'PalynziqTM' has been approved recently for curing phenylketonurics. However, the reduced operational stability, shelf-life, and rapid turnover of PAL during bioprocessing often impedes its catalytic efficacy. Besides, genetic manipulation and chemical modification, immobilization is a highly promising and cost-effective tool to improve the biophysical properties of the enzyme. Interestingly, several immobilization approaches like multi-tubular enzyme reactors, entrapment, physical adsorption, covalent linking, etc. have been employed to date to immobilize PAL for different biomedical applications. Specifically, the employment of novel carrier-free enzyme linking technique 'cross-linked enzyme aggregates' (CLEAs) and 'nanostructures' have broadened the versatility of PAL as a targeted enzyme therapy against different metabolic disorders. Herein, we highlight the recent advances in immobilization techniques and compare them with respect to improving pharmacodynamics of PAL. Furthermore, a brief insight on the role of template-synthesis and nanotechnology in the development of highly robust and recyclable PAL is also discussed.

ABSTRACT (PIMB022)

ASSESSING THE ANTI-CANCER POTENTIAL AND IMMUNOGENICITY OF RECOMBINANT ARGININE DEIMINASE FROM PSEUDOMONAS FURUKAWAII RS3

*Rakhi Dhankhar, Pooja Gulati**
Department of Microbiology, MDU Rohtak, India
*Email *gulatipooja1@gmail.com*

Amino acid deprivation therapy (AADT) for cancer treatment has gained momentum in the recent years after the successful application of microbial L-asparaginase in the treatment of leukemia. Arginine deiminase (ADI) is another therapeutic microbial enzyme that can be employed in AADT for the treatment of arginine auxotrophic tumors. The present study was undertaken to isolate a potent ADI producer. The arcA gene (gene coding ADI) from the selected producer was cloned and expressed in Escherichia coli. The recombinant ADI was purified and its in vitro anticancer activity was assessed. With this aim, a total of 143 ADI producers were isolated from soil and water samples of Delhi and Haryana, India. Pseudomonas furukawaii RS3 was found to be the highest ADI yielding bacterium among all the isolates. A 1251 bp long arcA gene from P. furukawaii was cloned in pET-28a (+) vector and expressed in E coli. The rADI was overexpressed as inclusion bodies in the E coli BL21 cells. The rADI was purified using affinity chromatography and its molecular mass was estimated to be ~46KDa. The in vitro anticancer efficacy of the purified enzyme was assessed on hepatocellular carcinoma cell lines, HepG2. Recombinant P. furukawaii ADI (PfADI) effectively inhibited the HepG2 cells with an IC50 value of 0.1950 IU/ml which is lower than the IC50 value of ADI from Mycoplasma hominis (MhADI) which is in the clinical trials. Furthermore, in silico analysis was carried out to compare the immunogenicity of PfADI with MhADI. The immunoinformatics analysis revealed that PfADI is less immunogenic as compared to MhADI in terms of number of linear and conformational B cell epitopes, T cell epitope density and overall antigenicity and allergenicity.

ABSTRACT (PIMB023)

STUDY THE EFFECT OF PIGMENT PRECURSOR AS SUBSTRATE FOR MASS PRODUCTION AND PIGMENT ACCUMULATION IN CYANOBACTERIAL ISOLATE 13MNS2014

*Manju Bala Bishnoi, Suryakant Panchal, Renuka Sharma, Monika Verma, Namita Singh**
Microbial Biotechnology Laboratory-202, Department of Bio & Nano Technology, Guru Jambheshwer University Science & Technology, Hisar, 125001, India
*Email *namitasingh71@gmail.com*

Cyanobacteria are oxygenic photoautotrophic prokaryotic organisms and highly dependent on effective utilization of light and nutrients for their survival and accumulation of pigment and other bioactive compounds which have extensive applications in many industries and research fields. Phycobiliproteins, natural colorants, are water soluble derived from cyanobacteria and have a huge impact on health and industrial role. The present work evaluated the effect of phycobiliprotein pigment precursor (Succinic acid and α- Levulinic Acid) by nutrient enrichment of cyanobacterial isolate 13MNS2014, for boosting of biomass growth and higher accumulation of phycobiliproteins. The result showed that 7.5mM Succinic acid and 5mM α-amino levulinic acid enhanced the biomass yield as well as phycobiliproteins accumulation as compared to the control group. We conclude that by addition of substrate (Succinic acid & -amino Levulinic Acid) in culture media, It stimulate the metabolic rate of phycobiliproteins accumulation in the phototrophic culture of cyanobacteria.

Keywords: Cyanobacteria, phycobiliproteins, Succinic acid, α-amino levulinic acid,Biomass

ABSTRACT (PIMB024)

KINETICS OF BACTERIAL EXTRACELLULAR POLYMERIC SUBSTANCE (EPS) MEDIATED DECOLORISATION OF TEXTILE DYE-MALACHITE GREEN

Baby Sharma, Vinay Sharma, Shruti Mathur, Nilima Kumari*
AIB, Amity University Rajasthan, India
*Email *babysharma8742@gmail.com*

Bacteria produce a wide range of extracellular polymeric substances (EPS) which have been reported for its use in cleanup of various environmental pollutants including heavy metals, hydrocarbons and dyes. This is attributed by the biosurfactant and bio-adsorbent nature of bacterial EPS. The current study is an attempt to culture and extract EPS from a potential strain isolated from oil contaminated water from Navi Mumbai Port and to apply it successfully for removal of Malachite Green dye from the aqueous solution as it is a very commonly used dye in traditional textile dying and printing industries of Rajasthan. It is also a major cause for contamination of waterways all across the state. The produced EPS was able to decolorize a maximum of 61.32% of the selected dye within 4 min without the use of any adjuvant and/or alteration in reaction conditions. The reaction kinetics for the decolorisation process was observed to be first order kinetics. Thus, the EPS produced could be a suitable agent for bioremediation of textile dyes from textile industry effluent.

THEME 4

Advances in microbial systematics

ABSTRACT (PAMS001)

UNIQUE SEQUENTIAL UTILIZATION OF SUGARS ENHANCE PHOSPHATE ACQUISITION IN RHIZOBIUM SP. RM

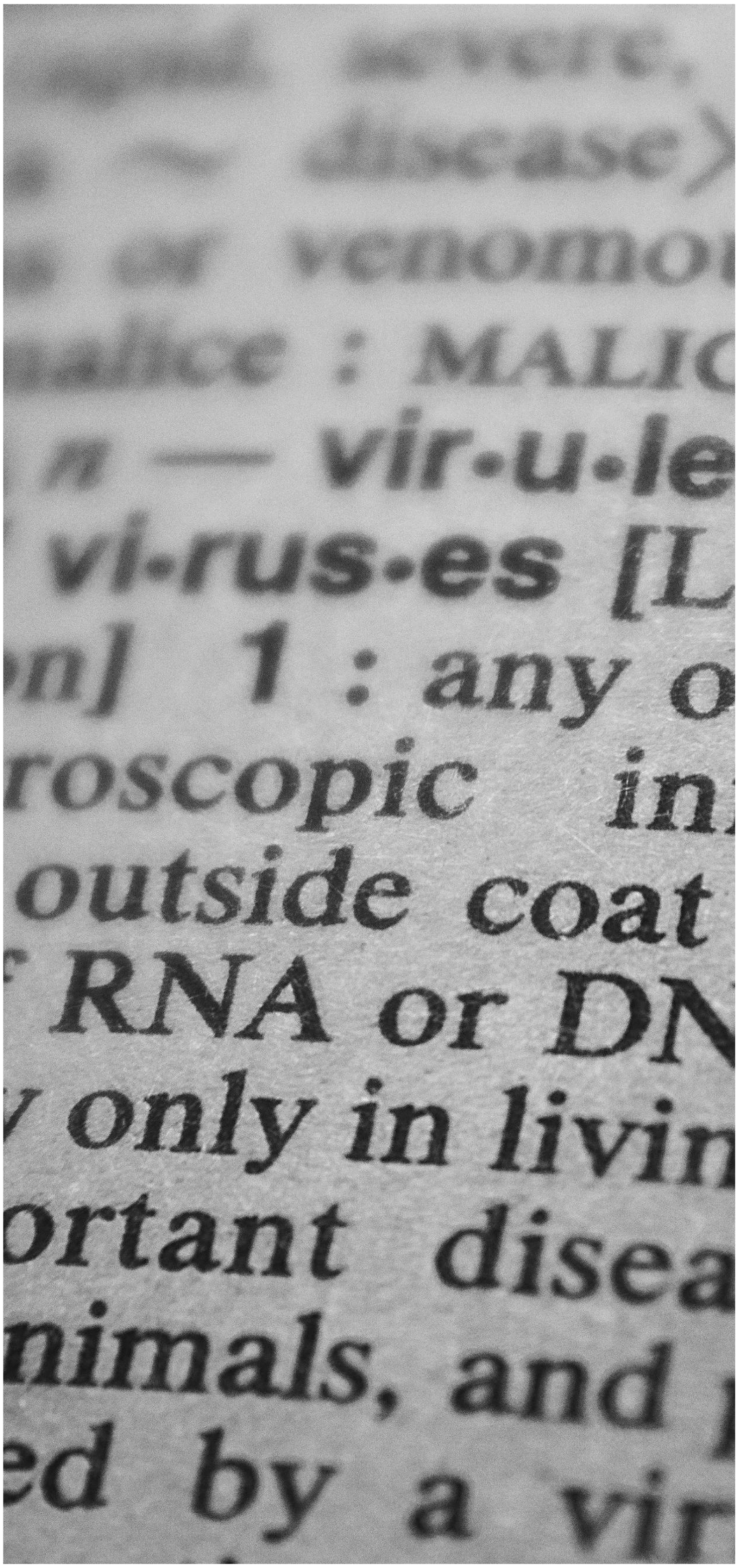
*Akshita A. Champaneria, Shalini Rajkumar**
Institute of Science, Nirma University, Sarkhej-Gandhinagar Highway, Ahmedabad – 382481, Gujarat, India
*Email *shalini.rjk@nirmauni.ac.in*

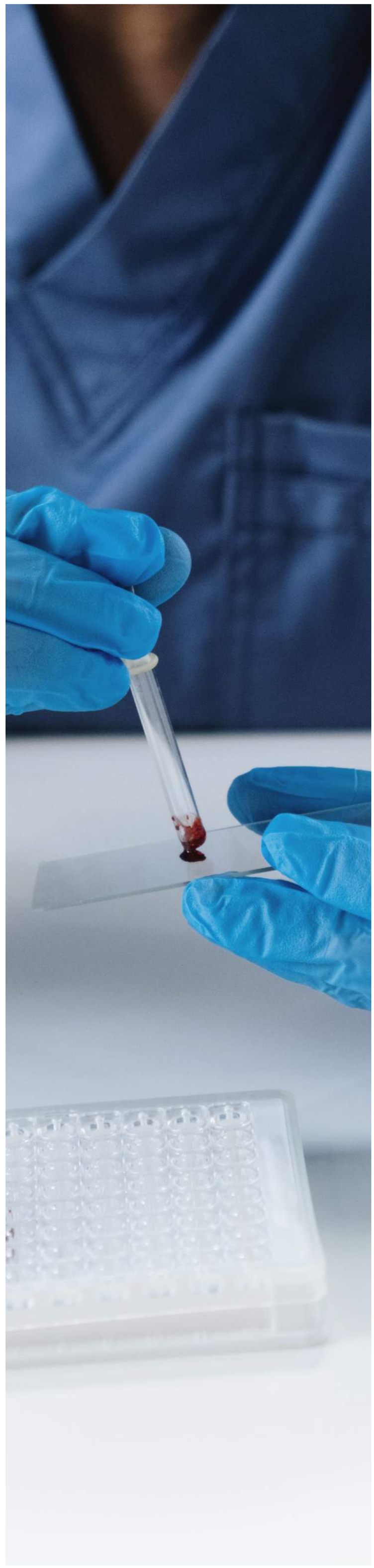
In Rhizobium sp. RM, fructose uptake was prevented in presence of aldoses- glucose, arabinose and xylose, which was evident from the diauxic growth curve with distinct 30min mid-lag when fructose was supplemented with each of the aldoses. It was found that the isolated RM cells gave almost equal glucose dehydrogenase enzyme activity in presence of glucose, arabinose and xylose although fructose grown cells were found negative. This affected the mineral phosphate solubilization trait wherein fructose grown cells could not solubilize the complex rock phosphate in buffered conditions but surprisingly solubilized tricalcium phosphate. Glucose, arabinose and xylose grown cells solubilized both the bound phosphate forms. Qualitative analysis on Tris Rock Phosphate (pH 8.0) agar plate and HPLC profile showed organic acid production to be responsible for phosphate solubilization and helped propose a model of pathways involved. With the aid of whole genome sequencing, fructose metabolic genes showed the presence of EIIC components of fructose specific PTS and ABC transporters however, qRT-PCR data revealed the presence of active sugar transport via ABC. Also, expression profile disclosed two probable pathways of fructose metabolism which might be responsible for its repression in presence of aldoses. This finding of sequential uptake of carbon sources among same group, sugars, is unique and rare where we report that the secondary carbon source, sugar (fructose), might be prevented for its uptake at the transporter level or at the initial steps of its catabolism affecting mineral phosphate solubilization.

Keywords: Unique Rhizobium sp. RM, fructose repression, sequential sugar utilization, HPLC, qRT-PCR

THEME 5

Viruses and vaccines





ABSTRACT (PVVS001)

PROPHYLACTIC POTENTIAL OF CYTOLETHAL DISTENDING TOXIN B (CDTB) SUBUNIT OF TYPHOID TOXIN AGAINST TYPHOID FEVER

*Reena Thakur1, Preeti Pathania1, Navneet Kaur1, Vattan Joshi1, Kanthi Kiran Kondepudi2, Chander Raman Suri3 and Praveen Rishi1**
1Department of Microbiology, Panjab University, Chandigarh, India
2 National Agri-Food Biotechnology Institute, Mohali, Punjab, India
3Indian Institute of Technology Ropar, Rupnagar, Punjab, India
Email reenathakur700@gmail.com, praveenrishi@yahoo.com

Typhoid fever caused by S. Typhi continues to be a major health concern, especially in developing nations. Due to the emergence of multi-drug-resistant (MDR) strains, which renders conventional antibiotics ineffective as well as the limited efficacy of available vaccines, efforts are being made to develop effective prophylactic agents. CdtB, typhoid toxin's subunit has been selected for evaluating its vaccine potential due to its high conservation throughout the Typhi strains. Toxicity studies of cloned and purified CdtB protein performed on cell lines indicated no significant toxicity. The results were further strengthened by cell cycle analysis, assessed by flow cytometry. Keeping these observations in mind, the immunoprotective potential of CdtB was assessed using S. Typhi induced mouse peritonitis model. A significant titer of anti-CdtB antibodies (IgG) was recorded in the mice (immunized with CdtB protein) and sera obtained from typhoid fever positive patients, which was also validated by immunoblotting. Active immunization with the protein protected 75% of mice against a lethal dose of S. Typhi Ty2 with significant (up to 5 log) reduction in the bacterial load in the liver and spleen of immunized-infected mice compared to control (unimmunized-infected) mice. Moreover, the gradual restoration of histoarchitecture of the spleen and liver with modulation in the levels of cytokines (IL-6, TNF-α and IL-10) production indicated the effectiveness of the subunit. The observations deduced from the present study give the proof of concept of the immunogenic and prophylactic potential of the CdtB protein.

ABSTRACT (PVVS002)

IMMUNOINFORMATICS STUDY OF DNA BINDING PROTEINS IN MYCOBACTERIUM TUBERCULOSIS

*Sunita a, Nirjara Singhvi b, Yogendra Singh b, Pratyoosh Shukla ac**
a Enzyme Technology and Protein Bioinformatics Laboratory, Department of Microbiology, Maharshi Dayanand University, Rohtak 124001, Haryana, India
b Bacterial Pathogenesis Laboratory, Department of Zoology, University of Delhi, Delhi 110007, India
cSchool of Biotechnology, Institute of Science, Banaras Hindu University, Varanasi-221005, India
Email pratyoosh.shukla@gmail.com

Tuberculosis (TB) is caused by Mycobacterium tuberculosis (Mtb) which kills more than a million people every year. Currently, there is no effective TB vaccine and a safe and efficacious vaccine is required to reduce the mortality and morbidity. DNA binding proteins (DBPs) are known to regulate gene expression including genes associated with virulence. In this study, we identified 1453 DBPs while screening the 4173 genes of Mtb by the DNABIND tool. Moreover, further screening was performed by using different in silico tools. Eighteen DBPs were selected for the prediction of epitopes. B-cell epitope possesses the antigenic and non- allergenic characters were applied for T-cell epitope prediction using ProPredI, and ProPred server. Using these tools, VQPSGKGGL(Rv2871), IRALPSSRH (Rv3923c), LTISPIANS (Rv3235), VPRPGPRPG (Rv2731), VGQKINPHG (Rv0707), and DGIGSAVSV (Rv1088) were identified as potential T-cell epitopes. The epitopes and DBPs were further analysed by structural modelling to confirm the epitope localization on the respective proteins. The validation of the epitopes was ensured by studying the interactions of these epitopes with human HLA. Significantly, our studies suggest that Rv2731, Rv3235, Rv1088, Rv0707, Rv3923c and Rv2871 are the most suitable vaccine candidates.This study gives an evidence to use DBPs as the peptide-based vaccine candidates for the treatment of TB.

ABSTRACT (PVVS003)

COMPARATIVE GENOMIC AND PHYLOGENETIC ANALYSIS OF SPIKE AND NUCLEOCAPSID PROTEINS OF SEVERE ACUTE RESPIRATORY SYNDROME CORONAVIRUS 2 (SARS-COV-2) AND 10 OTHER TAXONOMICALLY RELATED CORONAVIRUSES USING IN-SILICO TOOLS

*Srishti, Shubhangi Sharma, Jaspreet Kaur**
Department of Zoology, Maitreyi College, University of Delhi
*Email *jkaur@maitreyi.du.ac.in*

The outbreak of Covid-19, caused by the novel coronavirus Severe Acute Respiratory Syndrome Coronavirus Isolate 2 has caused a serious global pandemic. SARS-CoV-2, a single stranded, enveloped RNA virus that first emerged in Wuhan, China; belongs to the family Coronaviridae. The structural proteins present in SARS-CoV-2: Spike protein (S) and Nucleocapsid protein (N) are crucial in the process of binding to the host, morphogenesis and regeneration inside the host. Thus, in order to gain an insight into the evolution, selective pressures and adaptation of SARS-CoV-2, we carried out a comprehensive analysis of genome composition, codon usage as well as physico-chemical properties & post-translational modifications (PTMs) of these 2 important genes in SARS-CoV-2 and 10 other taxonomically related coronaviruses using in-silico tools. We have also focussed on coiled coil regions of spike protein because coiled-coil domains are known for their characteristic heptad repeat and stability, thus making them excellent choices for vaccine development. The phylogenetic analyses confirmed the close genetic relationship of SARS CoV-2 with SARS CoV, Bat CoV RaTG13 and Pangolin CoV. Using the codon adaptation index score, we found that the nucleoprotein and spike encoding genes are more adapted to humans. In addition, we also found evidence for negative pervasive selection at various sites in N & S genes. Thus, the preliminary research conducted in this study shall lead to a deeper understanding of SARS-CoV-2 and its function in Covid-19 pathogenesis. The results obtained from these studied parameters may act as primer for further studies related to development of vaccine targets against SARS-CoV-2.

ABSTRACT (PVVS004)

A HYPOTHETICAL STUDY ON IMMUNOGENESIS OF NOVEL CORONA VACCINES

a Deepanwita Deka, b Avra Pratim Chowdhury
a S. B. Deorah College, Assam
b Division: Microbiology, Dept. of Botany, Gauhati University
Email avranu132@gmail.com, deepanwita87@gmail.com

Immunization on chronological boosted therapy against SARS-CoV2 is now already been certified to progress for implementation to humans all around the world. The physiological response of human cells is now presenting as omnipotent characters for their autoimmune criteria against a viral antigen, types, subtypes, strains, and modified strains. The molecular genesis of viral epitopes and their surface protein is concerned with the activation of monoclonal antibodies by the artificial secondary immune response. Analytical research is developed for the study of artificial immunogenesis to clarify the presence of surface antigens in plasma. RNA extracted immunogens in live or attenuated form is examined to initiate the secondary immune response in the body of the carrier host or patient following the evaluation of three stages of progressive reports. The accuracy of antigen-antibody titer is determined on the efficacy margin of an implemented vaccine in a mass population formulating the reports and outcomes. In these circumstances, the conceptual model on immunogenesis of vaccines is required to study the SARS-CoV2 prone regions by the statistical alignments of the affected population during the pandemic.

ABSTRACT (PVVS005)

A FACT FINDING STUDY ON DIFFERENCES IN FATALITIES DUE TO COVID-19 BETWEEN EAST AND WEST

Shashi Chawla & Shubhaa Chawla
Gargi College, New Delhi, India
Email HAHC Hospital, New Delhi

COVID-19 is a disease caused by SARS-CoV-2, a virus belonging to family coronaviridae. The virus is thought to be a zoonotic virus which jumped from animals to humans. This happens because the viruses have the ability to undergo mutations and adapt to newer biological systems. The disease, COVID-19, spread so fast across the world that it was declared a pandemic by WHO in March, 2020. It has not behaved like a typical respiratory disease caused by a virus. The symptoms vary with age, presence of comorbidities and even geography. It has been observed that the disease has much higher mortality in Western world as compared to East. The plausible reasons for these differences could be many like stricter lockdown, cultural and socioeconomic differences, vaccination policies of East, presence of trained immunity in East, different mutations in different geographical areas (appearance of new variants), genetic differences in populations of the two regions w.r.t ACE receptors and MHC, etc. These facts will be presented and discussed in detail. The disease has proved that our understanding of viral diseases is very limited and there is a need to undertake research in this area.

ABSTRACT (PVVS006)

NEXT-GENERATION RAPID ADVANCED MOLECULAR DIAGNOSTICS BY CRISPR-CAS

Taruna Gupta1, Ashish Srivastava1**, S.K Raj2, Narayan Rishi1*
1Amity Institute of Virology & Immunology, Amity University Uttar Pradesh, Noida
2CSIR-National Botanical Research Institute, Lucknow
Email tarunagupta67@gmail.com, asrivastava10@amity.edu***

The emergence of Coronavirus disease-2019 caused by SARS-CoV-2 has also bought new challenges to the researchers to develop novel therapeutic and diagnostic methods for the pathogen. The preventive vaccines are approved for the public but their role in the development of herd immunity is not clear due to the emergence of new variants of SARS-CoV-2. The prime requirement to cope up with the current situation is to develop early diagnostics of the pathogen to restrict its spread among the human population and the therapeutics to treat serious patients. CRISPR/ Cas is a talk of the town technique for the prevention of the COVID-19 disease through its role in diagnostics as well as in therapeutics. The world is looking towards the development of early diagnosis, treatment, and prevention of Coronavirus disease (COVID-19) caused by SARS-CoV-2 in order to restrict its rapid transmission and mortality among the human population. An outbreak of coronavirus severe acute respiratory syndrome (SARS)-CoV-2 began in Wuhan, China in December 2019. COVID-19, the disease associated with SARS-CoV-2 infection, rapidly spread to produce a global pandemic. Globally, more than 880 million cases have been reported with 1.9 million deaths by the end of December 2020. Currently, the World Health Organization (WHO) adopted the screening and diagnosis of SARS-CoV-2 infection with quantitative RT-PCR (qRT-PCR)-based kits; however, the suitability of such kits is restricted due to the requirement of specialized instruments, well-trained personnel, and unavailability in resource-limited areas. CRISPR/Cas nuclease-based nucleic acid detection has exposed great potential for the development of next-generation molecular diagnostics technology due to its high reliability. The CRISPR-Cas system has recently emerged as a versatile tool for medical research for gene editing, epigenetic control, and disease diagnosis by using several Cas nucleases, such as Cas9, Cas12a, Cas12b, and Cas13a. The use of CRISPR-Cas-based detection of SARS-CoV- 2 infection may results in the development of rapid, affordable, and multiplexed point-of-care diagnostic system. In this article, we have covered the CRISPR-Cas-based efficient techniques developed for the diagnosis of the SARS-CoV-2 and their suitability for COVID-19 surveillance. Advancement in the current researches on CRISPR-Cas technique shows its potential to become the next-generation diagnostic tool for early, rapid, and reliable nucleic acid-based diagnostics. Here, we discussed for the CRISPR techniques which are being used for developing detection kit which included but not limited to SHERLOCK (Specific High-sensitivity Enzymatic Reporter unLOCKing), DETECTR (DNA Endonuclease Targeted CRISPR Trans Reporter), AIOD-CRISPR (All In One Dual - CRISPR), FELUDA (FnCas9 Editor Linked Uniform Detection Assay).

ABSTRACT (PVVS007)

MOLECULAR CHARACTERIZATION OF SUB-GENOMIC RNA PROMOTER OF COAT PROTEIN GENE ENCODED BY APPLE STEM GROOVING VIRUS

Asha Rani1, Sunny Dhir1, Narayan Rishi*
1Amity Institute of Virology & Immunology, Amity University Uttar Pradesh- Noida
Email arani@amity.edu, sdhir1@amity.edu

Molecular and functional characterization of sub-genomic RNA promoter of coat protein gene of a plant virus will have broad implications including foreign gene expression and also for the development of a viral vector system expressing any gene of interest. Apple stem grooving virus, a 6.5 kb long RNA virus, belongs to the family Betaflexiviridae and genus Capillovirus. The virus possesses ORF 1 and ORF 2 in its genome that codes for replicase and movement protein, respectively. The coat protein is expressed via sub-genomic RNA, sgRNA2. However, molecular and functional features of promoter are still elusive. The virus has a unique way of generating two sub-genomic RNAs out of single strand of which one encodes for movement protein and coat protein together and another encodes for coat protein only. Here, we have amplified and cloned eight different sequences from tentative promoter region to check the expression of β-Glucuronidase (GUS) on N. benthamiana and for later confirmation using Quantitative PCR analysis of the GUS expression. The smallest sequence out of these eight sequences from promoter region that has shown maximum expression of GUS which is -70 to + 15 from transcription initiation site of coat protein region in ASGV genome. This will be considered for the further expression of endogenous and exogenous genes in the suitable plants. Our work will not only be helpful in characterization of sub-genomic promoter region and for functional genomics but also its application in the construction of virus induced gene silencing vector construction.

ABSTRACT (PVVS008)

MOLECULAR DETECTION AND HETEROLOGOUS EXPRESSION OF RECOMBINANT COAT PROTEIN OF ASGV AND ASPV FROM KASHMIR APPLE ISOLATES

Rashmi Suman1, Vanita Chandel, Narayan Rishi**
1 Amity Institute of Virology & Immunology, Amity University Uttar Pradesh- Noida
Email arani@amity.edu, sdhir1@amity.edu

Apple is the major commercial horticulture crop of India contributing 24% of total fruit produced. India ranks 5th in the World by producing 1915.3 thousand MT of apples per year from an area of 311.4 thousand hectares. According to the reports, the most devastating viral pathogens infecting apple trees are Apple Stem Grooving Virus(ASGV), Apple Stem Pitting Virus(ASPV), Apple Mosaic Virus(ApMV) and Apple Chlorotic Leaf Spot Virus(ACLSV). Mixed infections by these viruses cause significant decrease in quality and quantity of fruits. This often leads to huge economic losses, hence the management of apple viruses is very important. Use of certified virus-free plants is currently considered to be the most effective way to manage viral diseases of apple. Indexing using ELISA is convenient, relatively cheap and reliable.

ABSTRACT (PVVS009)

CAN HOST GENES EXPLAIN HIGH POPULATION SPECIFIC DIFFERENCES IN CLINICAL OUTCOMES OF COVID-19

Swarkar Sharma1, Inderpal Singh2, Shazia Haider3, Md. Zubbair Malik4, Kalaiarasan Ponnusamy5, Ekta Rai1
1.Human Genetics Research Group, School of Biotechnology, Shri Mata Vaishno Devi University, Katra, Jammu and Kashmir
2. Bioinfores Pvt. Ltd., R. S. Pura, Jammu, Jammu and Kashmir, India.
3. Jaypee Institute of Information Technology, Noida, sector-62, Uttar Pradesh
4. School of Computational and Integrative Sciences, Jawaharlal Nehru University, New Delhi, India.
5. School of Biotechnology, Jawaharlal Nehru University, New Delhi, India.

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a positive single stranded RNA virus that causes a highly contagious Corona Virus Disease (COVID19). Entry of SARS-CoV-2 in human cells depends on binding of the viral spike (S) proteins to cellular receptor Angiotensin-converting enzyme 2 (ACE2) and on S protein priming by host cell serine protease TMPRSS2. Recently COVID19 has been declared pandemic by World Health Organization yet high differences in disease outcomes across countries have been seen. We provide evidences based on analyses of existing public datasets and by using various in-silico approaches to explain some of these as factors that may explain population level differences. One of the key
factors might be entry of virus in host cells due to differential interaction of viral proteins with host cell proteins due to different genetic backgrounds. Based on our findings, we conclude that higher expression of ACE2 facilitated by natural variations, acting as Expression quantitative trait loci (eQTLs) and with different frequencies in different populations, results in ACE2 homo-dimerization which is disadvantageous for TMPRSS2 mediated cleavage of ACE2 and becomes more difficult in presence of broad neutral amino acid transporter, B0AT1 (coded by SLC6A19), that usually does not express in Lungs. We also propose that the monomeric ACE2 has higher preferential binding with SARS-CoV-2 S-Protein vis-a-vis its dimerized counterpart. Further, eQTLs in TMPRSS2 and natural structural variations in the gene may also result in differential outcomes towards priming of viral S-protein, a critical step for entry of Virus in host cells. In addition, we suggest some other potential key host genes like ADAM17, RPS6, HNRNPA1, SUMO1, NACA, BTF3 and some other proteases as Cathepsins, that might have a critical role. Understanding these population specific differences may help in developing appropriate management strategies.

THEME 7

Microbial pathogenesis and AMR

ABSTRACT (PMP001)

MOLECULAR INSIGHTS ON THE PERSISTENCE OF MYCOBACTERIA

*Joshi Hemant, Banerjee Nirupma, Bhatnagar Rakesh **
Laboratory of Molecular Biology and Genetic engineering, School of Biotechnology, Jawaharlal Nehru University, New Delhi, Delhi, 110067, India
*Email *rakeshbhatnagar@jnu.ac.in*

To control M. tuberculosis infection prolonged chemotherapy is recommended. A small population of cells escape from the lethal effects of the drugs either by acquiring drug resistance or by switching to a quiescent state with low metabolic activity. The latter population is antibiotic tolerant and remains dormant in the host. These are termed as persisters and are responsible for reactivation of the disease under conditions conducive for their growth. New approaches are required to understand and kill the persisters for effective eradication of the bacilli from the host. M. tuberculosis has evolved to endure intracellular as well as extracellular hostile environments such as antibiotics, oxidative stress, pH stress and nutrient starvation etc. The underlying mechanisms of bacterial persistence are poorly understood and the key determinants are also not well defined. Therefore, we have undertaken this study to elucidate the molecular basis of persistence. Using transposon mutagenesis as a tool, we have identified mutants defective in parameters likely to be involved in the epigenetic regulation of persistence. We present data using different antibiotic screens for the isolation of mutants of M. smegmatis as model, in this study. In conclusion, we hypothesize that our approach will provide novel insights into the mechanisms of persister formation and survival of mycobacteria, revealing new target for the development of persister directed antibiotics.

Keywords: Tuberculosis; Persistence; Mycobacteria; Transposon mutagenesis

ABSTRACT (PMP002)

DELINEATING RESIDUES OF BACILLUS ANTHRACIS ZINC UPTAKE REGULATOR (ZUR) DIRECTLY INVOLVED IN ITS INTERACTION WITH THE COGNATE DNA

*Divya Kandari a, Rakesh Bhatnagar a **
a Laboratory of Molecular Biology and Genetic Engineering, School of Biotechnology, Jawaharlal Nehru University, New Delhi, Delhi - 110067, India.
*Email * rakeshbhatnagar@jnu.ac.in*

Zinc plays paramount roles including catalytic, structural, and regulatory. Some zinc-dependent proteins are also known to manifest virulence in pathogenic bacteria. Successful survival of pathogen within the host requires zinc homeostasis. Zinc uptake regulator (Zur) is a negative transcriptional regulator of the FUR superfamily of proteins connoted in maintaining Zinc homeostasis. Zinc homeostasis is marginally scrutinized in Bacillus anthracis, a bioterror agent causing the fatal disease anthrax, with no decipherment of Zur. BAS4181 annotated as Zinc-specific transcriptional regulator, substantiated by computational and experimental analyses. BAS4181 gene (bazur) lies in a three-gene operon. The DNA binding helix predicted by homology modelling and sequence/structure analysis, further, confirmed through site-directed mutagenesis and Isothermal titration calorimetry. Recombinant BaZur prodigiously exists in dimeric form, indicated by Size-exclusion chromatography and Blue Native-PAGE. Computational and manual strategies employed to decipher the putative regulon of bazur resulted in the identification of 11 genes. The DNA binding ability of BaZur to the promoter regions of the regulon candidates was ascertained by Electrophoretic Mobility Shift Assays. Most regulon genes lacked functional annotation, however in silico analysis predicted their role in zinc uptake, mobilization and as zinc chaperones. BaZur exerts negative regulation on most of the regulon genes. A downregulation was observed in the expression of bazur under zinc-excess and marked upregulation under zinc-depleted environment, adding credence to its negative autoregulation. Moreover, an increase in the transcript levels of the regulon genes upon zinc-depletion connoted their role in combating hypo-zincemic conditions. It's proposed that under zinc feast conditions, the BaZur represses expression of its regulon genes and, under zinc famine condition, BaZur (in the non-zinc bound form) derepresses it. Taken together, this in-depth study provides an insightful investigation of Zur and zinc homeostasis in B. anthracis and reveals the essential residues of the protein crucial for recognition of the cognate DNA.

Keywords: Zinc homeostasis; Bacillus anthracis; Zinc uptake regulator; Regulon; Transcriptional regulator

ABSTRACT (PMP003)

DEVELOPMENT OF MULTIPLEX HRM BASED LOOP-MEDIATED ISOTHERMAL AMPLIFICATION METHOD FOR SPECIFIC AND SENSITIVE DETECTION OF TREPONEMA PALLIDUM

*Krishnamoorthy Priya1, Pasupathi Rathinasabapathi1, Sugapriya Dhanasekaran2, Mohandass Ramya1**
1Molecular Genetics Laboratory, Department of Genetic Engineering, College of Engineering and Technology, SRM Institute of Science and Technology, SRM Nagar, Kattankulathur 603203, Kanchipuram, Chennai, Tamil Nadu, India.
2 Department of Medical Laboratory (Pathology), College of Applied Medical Sciences, Prince Sattam Bin Abdulaziz University, Wadi-Al Dawaser, Riyadh 11451, Saudi Arabia
Email priyaselvi199624@gmail.com

Syphilis is a sexually transmitted disease caused by Treponema pallidum. Currently, the diagnosis of the disease is based on serological methods like fluorescent Treponemal antibody absorption test (FTA-Abs), T. pallidum hemagglutination assay (TPHA), T. pallidum particle agglutination assay (TPPA), rapid plasma reagin (RPR) test, and venereal disease research laboratory (VDRL) test. However, these serological methods are less effective to detect T. pallidum during the early stages of infection. In our study, we have developed a multiplex High-Resolution Melt curve (HRM) LAMP assay targeting polA and tprL marker genes of T. pallidum. The multiplex HRM-LAMP reaction conditions were optimized at 65°C for 45 minutes. Real-time melt curve analysis of multiplex HRM-LAMP showed two melt curve peaks for polA and tprL genes with a Tm value of 80 ± 0.5°C and 87 ± 0.5°C, respectively. The detection limit of this assay was found to be 120 fg/µL of T. pallidum DNA. The specificity was evaluated using five different bacterial species and the developed method was found to be 100 % specific in detecting T. pallidum. A total of 64 blood samples were collected from T. pallidum suspected cases to test the developed assay. The clinical validation showed that the assay had 96.43 % sensitivity and a 100 % specificity on detection of Syphilis. The developed method is more rapid, sensitive than the available methods, and also provides a multigene based specific diagnostic approach for T. pallidum.
Keywords: Treponema pallidum, Serological methods, LAMP, polA, tprL, Multiplex HRM-LAMP

ABSTRACT (PMP004)

ROLE OF INFLAMMASOME IN HELICOBACTER PYLORI SECRETORY PROTEINS INDUCED OXIDATIVE STRESS

Sandeep Kumar1 and Monisha Dhiman2
1Department of Biochemistry and Microbial Sciences, Central University of Punjab, Bathinda
2Department of Microbiology, Central University of Punjab, Bathinda.
Email sandeep.kumar665@gmail.com,

Gastric carcinoma is a major outcome of prolonged infection caused by gastric pathogen Helicobacter pylori. Inflammation due to infection leads to oxidative stress via reactive oxygen species (ROS) and reactive nitrogen species (RNS) by associated epithelial and immune cells. ROS and RNS are host immune response to overcome bacterial infection but bacteria have evolved to prevent killing from these reactive species and simultaneously modifying immune cells for its survival. Bacterial pathogen associated molecular patterns (PAMPs) such as lipopolysaccharide and secreted toxins induced ROS activates procaspase-1 cleavage, inflammasome formation and secretion of pro-inflammatory cytokine IL-1β. Present study evaluate role of H. pylori secreted concentrated protein (HPSCP) in THP -1 macrophages and gastric epithelial cell lines AGS for ROS and NOS production. Oxidative stress inhibitors, inflammasome activators and inhibitors were used to evaluate the role of ROS, NOS and inflammasome. AGS cell line produced significantly higher level of ROS than THP-1 macrophages while NO production was significantly high in THP-1 macrophages than AGS. THP-1 showed significantly higher level of IL-1β and TNF-α cytokines AGS. Overall lipid peroxidation was high in THP-1 macrophages than AGS cell line. THP-1 showed no significant difference in ROS, NO and lipid peroxidation level among untreated and HPSCP treatments. Study conclude that AGS produced oxidative stress may stimulate THP-1 macrophages for pro-inflammatory responses during HPSCP.
Keywords: H. pylori, Oxidative stress, Inflammasome, ROS, Macrophage differentiation

ABSTRACT (PMP005)

USE OF CRISPR/CAS SYSTEMS IN UNDERSTANDING MICROBIAL PATHOGENESIS AND AMR

*Aashlesha Pathak, Mihir Phadke, Sunita bundale**
Hislop school of biotechnology, Hislop college, Nagpur, Maharashtra, India-440001
*Email *sbundale@gmail.com*

The development of antibiotics and vaccines, has been accompanied by the emergence of new strains of anti-biotic resistant bacteria. With this rapid emergence of anti-biotic resistance bacteria, researchers are facing difficulties to combat infectious diseases and to find new and more effective anti-biotics. Understanding host-pathogen interactions that govern microbial pathogenesis is essential to understand potential targets for drug discovery and vaccine development. The discovery of clustered regularly interspaced short palindromic repeats abbreviated as Crispr, a bacterial adaptive immune system has led to some advances towards methods of combating against such infectious pathogens. Crispr/Cas is recognized as one of the new strategies to deal with anti-biotic resistant bacteria. Besides, Crispr/Cas9 genome wide screening has been employed on a variety of pathogens in order to determine the dynamic molecular pathways that drive microbial pathogenesis. Some examples of this include, understanding the molecular mechanism of how the alpha-hemolysin virulence factor results in cytotoxicity in S. aureus infection. Specifically programmed Crispr/cas systems are used to target and cleave any DNA in vivo, based on information provided by the Crispr array, which has been exploited to target the bacterial population that carry specific genes encoding for anti-biotic resistance. Crispr based platforms have also shown tremendous potential in identifying and eradicating bacterial resistance genes, which allow the pathogen to evade or neutralize anti-biotics. Crispr has made it easier to treat drug resistant bacterial infections. Researchers have also shown promising results of Crispr based techniques to treat Mycobacterium abscessus infections. Further, transcriptional repression of specific TB genes has also been achieved. This can be a potential therapeutic in Mycobacterium tuberculosis infections. Crispr/cas system has also been beneficial in treating and combatting viral infections and can be a tool for controlling genetic disorders like cancer. Hence Crispr is a boon in research related to microbial pathogenesis and AMR. Keywords: Crispr/Cas, microbial pathogenesis, Anti-biotic resistant bacteria, Therapeutics

ABSTRACT (PMP006)

IN SILICO STUDIES FOR THE IDENTIFICATION OF NOVEL ANTIMICROBIAL PEPTIDES (AMPS) FOR THE BIOCONTROL OF URINARY TRACT INFECTIONS

Sonia Goel and Kiran Nehra***
Department of Biotechnology, Deenbandhu Chhotu Ram University of Science and Technology (DCRUST), Murthal, Sonepat
*Email *nehrakiran@gmail.com, **soniagoel6408@gamil.com*

Nowadays, urinary tract infections (UTIs) have become a serious health problem in humans due to the development and a rapid spread of antibiotic-resistant bacteria all over the world. The common causative bacteria for UTIs include E.coli, Proteus species, Pseudomonas aeruginosa, Klebsiella species, Acinetobacter species etc. More recently, it has been observed that these causative agents are turning resistant to most of the antibiotics being commonly used for the treatment of UTIs, hence there is an urgent need for the search for an alternative approach to combat against such antibiotic-resistant uropathogens. In this direction, Antimicrobial peptides (AMPs) having a broad spectrum antimicrobial activity and low resistance make them a potential better therapeutic agents for treatment of UTIs. Many different AMPs have been identified from different sources of living organisms and have shown different antimicrobial activity like anticancer, antibacterial, antifungal, antiviral, antiparasitic. Experimentally, the isolation and purification of AMPs are very costly and time consuming. Therefore, to reduce the cost and time, the present study involves in silico methods for identification of novel AMP/s against antibiotic-resistant uropathogens. For this, experimentally validated AMP/s against uropathogens will be retrieved from different databases of AMP and Profile Hidden Markov Models (HMMER) will be used to align the sequences, build profiles and to scan the queried random peptide sequences against created profiles with cutoff E value 0.01 to identify novel AMP/s. 3-D structure of identified novel AMP/s will be predicted by I-TSSSER. Subsequently molecular methods will be used to validate the antibacterial activity of identified novel AMP/s against antibiotic-resistant uropathogens.

ABSTRACT (PMP007)

MITOCHONDRIAL DYSFUNCTION FROM A NOVEL MECHANISM IN FUNGI, AFFECTING DRUG RESPONSE

Ritu Pasrija1, Deepika Kundu1*1Department of Biochemistry, Maharshi Dayanand University, Rohtak, Haryana*
Email ritupasrija@yahoo.com

Candida albicans is the most common fungal pathogen causing Candidiasis in humans. Like other eukaryotic organisms, it offers limited drug targets, and situation further worsens with the emergence of drug resistance. This is due to either one or multiple mechanisms occurring simultaneously, such as alterations or up-regulation of the target, reduced intracellular accumulation of the drugs, and overexpression of drug efflux pumps including Cdr1p, Cdr2p [ATP Binding Cassette (ABC) Family], and Mdr1p (Major Facilitator Family). To understand the role of phospholipids on Cdr1p (drug exporter)-mediated drug resistance in yeast, the phospholipids biosynthesis genes PSD1, PSD2, CHO2, and OPI3 were deleted by homologous recombination, in Saccharomyces cerevisiae strain already overexpressing Cdr1-GFP of Candida albicans as a heterologous system. The disruption was confirmed by both normal PCR as well as RT-PCR. The effect of phospholipids biosynthesis gene deletion was analysed on Cdr1p-GFP-mediated drug resistance as well as its localization. The change in drug sensitivity was confirmed by microdilution and agar-based spot-assay. The outcomes authenticate that phospholipids biosynthesis disruption makes the cell sensitive to several unrelated drugs including fluconazole, with Δpsd1/Cdr1-GFP being worst affected. Interestingly, unlike sterols and sphingolipids, the localization of Cdr1p was unaffected by phospholipid biosynthesis gene disruption. Concomitantly, phospholipids mutants showed an increase in reactive oxygen species (ROS) generation, leading to reduced cell growth. These mutants were also unable to grow on non-fermentable carbon sources, indicating mitochondrial dysfunction. Most importantly, the drug sensitivity mediated by phospholipid biosynthetic disruption was found to be synergistic with mitochondrial dysfunction, resulting in further reduction of growth.

Keywords: Candida, drug resistance, lipids, plasma membrane, mitochondrial dysfunction, Non-fermentable carbon etc.

ABSTRACT (PMP008)

MANAGEMENT OF CADMIUM ADAPTED SALMONELLA TYPHIMURIUM INDUCED INFECTION BY ENHANCING THE EFFICACY OF AMPICILLIN IN THE PRESENCE OF PLUMBAGIN

Sripratyusha Gandham, Professor Praveen Rishi***
Department of Microbiology. Panjab University, Chandigarh, 160014
Email sripratyushagandham2308@gmail.com, rishiparveen@pu.ac.in***

The emergence of multidrug-resistant strains arising as a result of co-selection of metal and antibiotic resistance has proven to be a big hurdle in the development of effective therapy. Therefore, there is an immediate need to look for alternative approaches to combat this escalating resistance. The role of efflux pumps inhibitors holds a special significance in this scenario. Therefore, the present study was designed to assess the efficacy of plumbagin in combination with a conventional antibiotic: ampicillin against cadmium adapted Salmonella enterica serovar Typhimurium infection in a mouse model. Preliminary studies including growth kinetics of the strain and estimation of intracellular concentration of cadmium using FAAS, were performed. In vitro inhibitory activity and synergy between two agents was confirmed by micro-broth dilution assay. This was followed by establishment of mouse peritonitis model using the cadmium adapted strain. Thereafter the in vivo efficacy of the adjunct was confirmed on the basis of decrease in the bacterial burden in the vital organs of the mice as well as reduction in the level of oxidants, coupled with restoration of histo-architecture. To the best of our knowledge, this is the first report on the in-vivo validation of combination therapy against infection caused by metal induced antibiotic resistant strain of Salmonella Typhimurium. The observations obtained from the present study can be used to formulate viable strategies to curb the increasing resistance not only against Salmonella but against other Gram-negative infections as well.

ABSTRACT (PMP009)

EMERGENCE OF COLISTIN-RESISTANT HYPERMUCOVISCOUS HYPERVIRULENT KLEBSIELLA PNEUMONIAE IN TAMIL NADU

Shanthini Thamaraiselvan1, Prasanth Manohar1, Archana Loganathan1, Ramesh N1***
1Antibiotic resistance and Phage therapy Laboratory, Department of Biomedical Sciences, School of Biosciences and Technology, Vellore Institute of Technology, Vellore, Tamil Nadu, India.
*Email *Shanthini.ibt@gamil.com, **drpnramesh@gamil.com*

The recent emanation of colistin-resistant hypermucoviscous hypervirulent Klebsiella pneumoniae poses the major threat to public health and this emerging strain is unique from classic Klebsiella strains by producig increased capsule formation which makes them highly virulent by resisting phagocytosis. In this study, a total of 50 Klebsiella species obtained from various diagnostic centres and hospital were analysed for multidrug resistance and virulence nature by performing Disc diffusion and minimum inhibitory concentration (MIC), hypermucoviscous phenotype by string test, DNA isolation followed by identification of colistin-resistant genes and virulent genes using polymerase chain reaction (PCR). Based on colony morphology, Biochemical test and Vitek identification system it was found that (41/50,82%) were Klebsiella pneumoniae and (9/50, 18%) were Klebsiella oxytoca. All the isolates except two (48/50, 96%) were found to be multi drug resistance by disc diffusion. Among 50 Klebsiella spp. 26/50, 52% were resistant to colistin, last resort antibiotic. A total of 22/50 isolates were found to be hypermucoviscous among them 12 were resistant to colistin. Genotypic characterization reveals that 5/22 isolates were positive for rmpA gene and 8/22 were positive for capsular (K) serotypes and aerobactin gene which was resistant to colistin. Our study confirms the outbreak of colistin resistant hypermucoviscous and non hypermucoviscous hypervirulent Klebsiella pneumoniae in Tamil Nadu, therefore a diagnosis of hypervirulent Klebsiella pneumoniae must be screened carefully in patients with Klebsiella pneumoniae infection.
Keywords: colistin, Klebsiella pneumoniae, hypermucoviscous, serotypes.

ABSTRACT (PMP010)

BIOFILM CLEARANCE FROM BIOPOLYMER SURFACES BY COCKTAIL OF CARBOHYDRASES FROM ASPERGILLUS NIGER

Ritika Sahi, Arashdeep Kaur, Praveen Rishi, Sanjeev Kumar Soni
Department of Microbiology, Basic Medical Sciences-Block I, South Campus, Panjab University, Chandigarh
Email ritikasahi1997@gmail.com

Biofilm formation on both biotic and abiotic surfaces accounts for a major factor in spread of antimicrobial resistance. Due to their ubiquitous nature, biofilms are of great concern for environment as well as human health. In the present study, an integrated process for the economical co-production of a cocktail of carbohydrases from a natural variant of Aspergillus niger was designed. The enzyme cocktail was found to have a noteworthy potential to eradicate/disperse the biofilms of selected pathogens. For application of enzymes as an antibiofilm agent, the enzyme productivities were enhanced by statistical modelling using response surface methodology (RSM). The anti-biofilm potential of the enzyme cocktail was studied in terms of (i) in vitro cell dispersal assay (ii) release of reducing sugars from the biofilm polysaccharides (iii) the effect of enzyme treatment on biofilm cells and architecture by confocal laser scanning microscopy (CLSM). Potential of the enzyme cocktail to disrupt/ disperse the biofilm of selected pathogens from biopolymer surfaces was also assessed by field emission scanning electron microscopy (FESEM) analysis. Further, their usage in conjunction with antibiotics was assessed and it was inferred from the results that the use of enzyme cocktail augmented the efficacy of the antibiotics. The study thus provides promising insights into the prospect of using multiple carbohydrases for management of heterogeneous biofilms formed in natural and clinical settings.

ABSTRACT (PMP011)

ANTI-FUNGAL ACTIVITY OF HIGH-ALTITUDE MEDICINAL & AROMATIC PLANTS EXTRACT AND THEIR NANOPARTICLES AGAINST CANDIDA GLABRATA

Shivam Gupta, Khem Raj and Mohammad Riyaz*
*Email *shivamgupta11201120@gmail.com*

The intensive use of anti-fungal agents in recent years has dramatically increased anti-microbial resistance (AMR). This threatens the effective prevention and treatment of an ever-increasing range of infections caused by fungi, despite the introduction of the new antifungal agents. Recent advances in nanotechnology radically changed the way we diagnose, treat, and prevent various diseases in all aspects of human life. The study aim is to evaluate the anti-fungal activity of medicinal & aromatic plant extracts and its silver nanoparticles against selected isolates of C. glabrata. The present research used Silver nanoparticles, which were synthesized by the reduction of silver nitrate using plant extract. The antibiofilm activity of Silver nanoparticles was determined by total biomass quantification (Crystal Violet staining) and (XTT metabolic assay). Minimal inhibitory concentration (MIC) assays were performed using the micro-dilution methodology showed that all Silver Nanoparticles were fungicidal against the tested strains at very low concentrations (0.0097 to 0.0312 mg/ml). The plant extracts significantly inhibited biofilm formation at MIC/64 ($p < 0.05$). The biomass quantification of Silver nanoparticles is higher than plant extract against C. glabrata biofilms, by inhibiting around ⩽70% at a concentration range of (0.024 to 3.125 mg/ml). In general, all Silver nanoparticles promoted significant reduction of the mean number of cultivable biofilm cells after exposure to concentrations range of 1.25 to 5 mg/ml. The antibiofilm and antifungal results in this investigation depict the potential of high-altitude medicinal & aromatic plants extract and nanoparticles. Our studies promote the fact that the silver nanoparticles based antifungal agent's helps in the prevention of Candida-associated infection and diseases.

Keywords: antifungal drugs, anti-microbial resistance, biofilm, silver nanoparticles.

ABSTRACT (PMP012)

BOVINE MASTITIS AND ANTIMICROBIAL RESISTANCE

Sonia Tyagi, Pamela Singh ,Vipin Khasa* and Vipul Chaudhary*
Deenbandhu Choturam University of Science and Technology, Murthal, Sonipat-131039
*Email *tyagisonia12891@gmail.com*

Bovine mastitis also known as Intramammary infection (IMI) is an inflammatory disease of milk secretion tissues of the udder caused by microorganisms primarily bacteria. Bacteria penetrate and invade the secretory tissues of bovine mammary glands. The Streptococcus uberis, Streptococcus aglactiae, Staphylococcus aureus, Staphylococcus epidermis and Escherichia coli has been recognized in clinical and subclinical bovine mastitis. The most contagious bacteria which has been frequently detected is S.aureus. The persistence of S.aureus intracellularly in the macrophages and epithelium leads to greater difficulties in its therapy. Besides, this bacterium has the capacity to survive and remain in the special cell compartments (endosome and cytosol) contributing to substantial barriers to their wiping off from the body and creating a reservoir from which the recurrent infection can occur. Thus, once established, this fearsome pathogen does not respond to antibiotics treatment. Therefore, due to multidrug resistance of the pathogen leading to no cure but an antibiotic load in the animal body, the treatment become more challenging. Thus, the infection is an alarming concern for both animal and public health. The present study was designed to isolate and screen bacterial pathogens of bovine mastitis for their antibiotic susceptibility. A total of 22 samples out of 78 samples showed presence of Staphylococcus spp., E.coli and Pseudomonas. These isolates were further subjected to antibiotic susceptibility using 16 antimicrobial agents. Among the antibiotics selected for the antibiogram profiling; oxytetracycline, chloramphenicol, ampicillin, bacitracin, enrofloxacin were most effective drugs against Staphylococci. Staphylococcus spp. found to be resistant to colistin, cefoperozone, ceftizoxime. Limited resistance was seen against amoxiclav, azithromycin, ceftriazone. The most effective drugs against E.coli were enrofloxacin, colistin, chloramphenicol. However, Pseudomonas is sensitive to majority of antimicrobial agents.

Keywords: Antibiogram profiling, Bacterium, Bovine mastitis, Multidrug resistance, S. aureus

ABSTRACT (PMP013)

PIPERIDINE DERIVATIVE ELICITS THE BACTERICIDAL EFFECT AGAINST S. AUREUS

Siddhartha Kumar1, Antresh Kumar1, 2*
1Department of Biotechnology, Central University of South Bihar, Gaya, Bihar.
2Department of Biochemistry, Central University of Haryana, Mahendergarh, Haryana.
*Email *sidd2644@gmail.com*

Staphylococcus aureus is an opportunistic pathogen responsible for superficial and invasive infections with higher morbidity and mortality. More than 40% of hospital and community mediated infections are attributed to the S. aureus which have been more problematic after emerging resistant against topical antibiotics. The readily Bioflim formation, enzymatic antibiotic inactivation (β-lactamse), alteration of target with decreased affinity for antibiotics (MRSA and VRSA) are majorly contribute to the resistant. The persistent chronic infections caused by these factors responsible for failure of S. aureus treatment. These challenges suggest the need for new antimicrobial agents against S. aureus infections. In the present study, we explored the bactericidal effect of diphenyl-butyl derivatives piperidine against both the non-clinical and clinical strains of S. aureus by targeting to explore their killing mechanism. Results of piperidine derivative show the distinct zone of bacterial inhibition with complete arrest the Staphylococcal growth at the minimum inhibitory concentration (MIC) 12.5µg/ml as observed by spot and micro-dilution assay, respectively. The cells were found to be completely eliminated with no viable cells within 120 min. The killing and anti-biofilm effects of the tested compound were also performed and attributed by ROS (reactive oxygen species) generation and suppression of toxin (α-haemolysin) production in treated cells as revealed by glutathione reduction assay and anti-virulent test. The piperidine derivative was found to be safe to use with no toxic effect on mammalian tissue (human and chicken blood). Taken together, this compound may be proven a leading molecule for the treatment of Staphylococcal infections.

ABSTRACT (PMP014)

DRUG SUSCEPTIBILITY PROFILE OF NONTUBERCULOUS MYCOBACTERIA ISOLATED FROM CLINICAL SAMPLES AT RAJASTHAN

Megha Sharma, Bharti Malhotra**, Shreya Khandelwal*
SMS Medical College, Jaipur, Rajasthan
Email meghabutolia@gmail.com, drbhartimalhotra@gmail.com***

Disease due to Nontuberculous Mycobacteria (NTM) has been increasing in developing country including India. NTM cause not only pulmonary infection but various other infections in immuno-compromised and immuno-competent host as well. NTM are resistant to many of the traditional antituberculous drugs, for proper treatment, Drug Susceptibility Testing (DST) is crucial. Its important to know the drug susceptibility profile of NTM in your region to initiate empirical therapy till results are available. In present study we carried out the DST of NTM for Rapidly Growing Mycobacteria (RGM) and Slow Growing Mycobacteria (SGM). To determine drug susceptibility profile of slow and rapidly growing NTM by standard broth microdilution method.DST of 20 (total 122 isolates) different species of NTM both RGM and SGM by standard broth micro-dilution method. The drugs tested against RGM were Amikacin, Ciprofloxacin, Cefoxitin, Clarithromycin, Doxycycline, Moxifloxacin, Minocycline and Trimethoprim and for SGM were Rifampicin, Clarithromycin, Ethambutol, Isoniazid and Moxifloxacin. Clarithromycin was tested only for M. avium complex (MAC) group. High resistant pattern were seen among RGM towards most of the drugs except Amikacin (76.1% sensitivity) followed by Moxifloxacin (46.5% sensitivity). Most of the slow growing NTM were also found extremely resistant to most of the drugs. Very high resistance was found in NTM. Hence it is imperative that DST is carried out in all NTM to know sensitivity profile so as to select appropriate drug for effective treatment. Since resistance was high a large panel of drugs with different concentration should be tested.

Keywords: Antibiogram profiling, Bacterium, Bovine mastitis, Multidrug resistance, S. aureus

ABSTRACT (PMP015)

ISOLATION AND CHARACTERIZATION OF MULTI-DRUG RESISTANT BACTERIA FROM A SEWAGE TREATMENT PLANT

*Deeksha Singh1, Raj Kumar Regar1, Vivek Kumar Gaur1 and Natesan Manickam1**
1Environmental Biotechnology Laboratory, CSIR-Indian Institute of Toxicology Research, Vishvigyan Bhavan, 31 Mahatma Gandhi Marg, Lucknow, Uttar Pradesh, 226001, India.
*Email * nmanickam@iitr.res.in*

Antibiotic resistance is a critical health issue and currently it is a major crisis globally. Sewage treatment plants (STPs) usually act as reservoirs for antibiotic resistance development and further the effluents released from STPs into river bodies disseminate antibiotic resistance into the environment. In this study, samples from sewage treatment plant Bharwara, Lucknow was studied to assess the abundance of antimicrobial resistance present in it. Physico-chemical parameters and metal analysis of a total number of 8 samples were determined to assess key water quality parameters. These include chemical oxygen demand (COD), biological oxygen demand (BOD), total solids, chloride and phosphate contents which were found to be higher in downstream compared to upstream samples. In an effort to understand the occurrence of AMR, 7 multi-drug resistant bacteria were isolated using an enrichment protocol. These bacteria were identified based on 16S rRNA gene sequences and other biochemical methods as Proteus mirabilis, Providencia stuartii, Stenotrophomonas maltophilia, Escherichia coli and Klebsiella pneumoniae. Antibiotic susceptibility profiling using 20 antibiotics belonging to seven different families by disc diffusion method showed that these bacteria were highly resistant. Several studies have correlated heavy metal resistance with antibiotic resistance and it was verified by determining minimum inhibitory concentration of copper, cadmium, chromium, arsenic, nickel, cobalt, mercury and antibiotics such as erythromycin, penicillin, tetracycline, gentamycin, ciprofloxacin and nalidixic acid. Some of the genes associated with antibiotic resistant were also being identified to understand the role of environmental bacteria in transmitting ARGs that may lead to health hazards. This study will help us to understand selection pressure in environment leading to development and spread of antibiotic resistance.

Keywords: Sewage, Antimicrobials, Antibiotics and Pathogens

ABSTRACT (PMP016)

STIM1-ORAI1 SIGNALLING CATALYZE TLR-2-ER-STRESS AXIS INDUCED HKM APOPTOSIS IN M. FORTUITUM PATHOGENESIS

*Priyanka Dahiya1, Shibnath Mazumder1,2,**
1 Immunobiology Laboratory, Department of Zoology, University of Delhi, Delhi-110007, India
2 Faculty of Life Sciences and Biotechnology, South Asian University, New Delhi, 110021, India
*Email *priyu.22.pd@gmail.com*

Mycobacterium fortuitum, rapid growing, acid-fast positive, non-tuberculous mycobacterium, is one of the common etiologic agents of piscine mycobacteriosis and also reported to cause protracted illness in immuno-compromised and immuno-competent humans. However, the mechanisms underlying M. fortuitum-induced pathogenesis remains elusive. Fish possess an elaborate immune system, and shows remarkable similarities with the elements of mammalian immune system. It has been successfully used as a model to understand the molecular pathogenesis and immunology of several diseases including tuberculosis. Headkidney is an important lymphoid organ in fish, and headkidney macrophages (HKM) are critical for countering a wide variety of pathogens. Using HKM from Clarias gariepinus, we report that M. fortuitum infection triggers TLR-2/MyD88 upregulation and that TLR-2 mediated internalization of M. fortuitum is imperative to the induction of pathogenic effects. Inhibiting TLR-2 signalling alleviated HKM apoptosis, thereby favouring bacterial survival. Additionally, inhibitor and siRNA based studies revealed that TLR-2-mediated cytosolic calcium (Ca2+)c elevation is instrumental for eliciting ER-stress in infected HKM as evidenced by downregulation in mRNA expression profile of ER-stress marker, CHOP (CCAAT/enhancer-binding protein-homologous protein). Further, ER-stress triggered the activation of membrane-proximal calcium entry channels comprising stromal interaction molecule 1 (STIM1) and calcium-release activated calcium channel 1 (Orai1), critical for sustaining (Ca2+)c level. Silencing of STIM1/Orai1 signalling alleviated HKM apoptosis and enhanced bacterial survival. We conclude that TLR-2-induced ER-stress activates STIM1/Orai1 in response to M. fortuitum infection and that STIM1/Orai1 signalling dependent continuance of (Ca2+)c level maintains pro-apoptotic environment to induce HKM apoptosis and bacterial clearance.

ABSTRACT (PMP017)

IDENTIFICATION OF SECRETORY AND CELL SURFACE-ASSOCIATED PROTEINS OF LEISHMANIA DONOVANI FOR EPITOPE PREDICTION AND VACCINE DESIGN

Munawwar Karim 1 and Yusuf Akhter 2*
1 Centre for Computational Biology and Bioinformatics, School of Life Sciences, Central University of Himachal Pradesh, Shahpur, District-Kangra, Himachal Pradesh 176206, India.
2 Department of Biotechnology, Babasaheb Bhimrao Ambedkar University, Vidya Vihar, Raebareli Road, Lucknow, Uttar Pradesh 226025, India
*Email *karim.cuhp@gmail.com*

Leishmaniasis, a vector-borne disease threatens approximately 350 million people living in endemic areas, with 1.3 million new cases estimated annually and counts among the top neglected tropical diseases. The most severe and life-threatening form of leishmaniasis is Visceral Leishmaniasis (VL), caused by the Leishmania donovani. VL affects the poorest people living across the globe and has a high fatality rate in the absence of treatment. Chemotherapy despite being effective factors like high costs, toxicity, and long-term and complicated regimens compromise most chemotherapeutic regimens. There is a need for new therapies which are safer and more effective and eventually lead to elimination of the disease. As most infected individuals who recover from the infection become resistant to subsequent infection, there is strong possibility of developing safe and effective vaccine as no licenced vaccine exists at present. Complete proteome of L. donovani provides useful starting point to identify potential parasite peptides which may evoke immune response in the human host and may likely be used as vaccine candidates. Proteins associated with the cell surface or secretory in nature are likely to possess potentially antigenic peptides. In this study we have utilized in silico approaches for identification of cell surface-associated and secretory proteins viz. GPI-anchored proteins, Trans Membrane Helix (TMH) containing proteins and secretory proteins of L. donovani using bioinformatics tools. We have also predicted T-cell epitopes in these identified proteins using IEDB-AR. Our work suggests that the identification of unique immunogenic epitopes provides considerable scope for design of new vaccines which may provide protective immunity against leishmaniasis and potentially help eliminate the disease.

Keywords: VL; Leishmania donovani; GPI-anchored protein; TM helix proteins; epitope; vaccine

ABSTRACT (PMP018)

ANTIBIOTIC RESISTANCE PATTERNS IN ESCHERICHIA COLI STRAIN ISOLATED FROM SHIPRA RIVER, UJJAIN

Sakshi Sardana, Paromita Sarbadhikary*
Department of Life Science, Shri Vaishnav Institute of Science, Shri Vaishnav Vidyapeeth Vishwavidyalaya, Indore, Madhya Pradesh
*Email *sardanasakshi22@gmail.com*

Increased, inappropriate and overuse of antibiotics has resulted in increased incidence of antibiotic resistant bacteria in aquatic environments. This has become the major source of dissemination of antibiotic resistant bacteria to humans. Among all the enterobacteriaceae, emergence of multidrug resistance (MDR) Escherichia coli (E. coli) has become a major concern due to the failure of antibiotic therapy even to advanced ***β***- lactam antibiotics and fourth generation cephalosporins. Hence this study was conducted to determine the prevalence and antibiotic sensitivity pattern of E. coli isolated from the Shipra river as a measurement of water quality parameters of the river. Prevalence and isolation of E. coli in water samples collected from Ramghat, Shipra river, Ujjain was done on MacConkey and EMB agar. Identification of E. coli was conducted using standard biochemical assays. Further, study of their antibiotic susceptibility pattern was carried out by the Kirby-Bauer method in comparison of E. coli Lab strain. Colonies grown on MacConkey and EMB agar were preliminarily screened by their colony morphology, color and Gram-staining techniques. Further identifications of E. coli isolates involved relevant biochemical tests with indole positive, methyl-red positive, citrate negative and urea negative results, along with gas, acid producer and motility. The E. coli isolate showed less sensitivity to all the tested antibiotics amoxicillin (30 µg), gentamicin (10 µg), ciprofloxacin (5 µg), and nalidixic acid (30 µg) as compared to E. coli Lab strain. Further, the E. coli isolate was also found to be less sensitive to third generation cephalosporin ceftriaxone (30 µg), while found to be significantly sensitive to fourth generation cephalosporin cefepime (30µg). This study indicates increased prevalence of resistant strain of E. coli in Shipra river, which showed significant multidrug resistance to antibiotics, which are commonly prescribed against E. coli infections.

ABSTRACT (PMP019)

A NOVEL MULTI-ENZYME PREPARATION PRODUCED FROM ASPERGILLUS NIGER USING BIODEGRADABLE WASTE: A POSSIBLE OPTION TO COMBAT BIOFILMS FORMED ON ABIOTIC SURFACES

Harmanpreet Kaur, Arashdeep Kaur, Valbha Rishi, Sanjeev Kumar Soni, Praveen Rishi*
Department of Microbiology, Panjab University, Chandigarh-160014, India
Email harmanvirk36330@gmail.com

Biofilm formation is a remarkable strategy adopted by microorganisms, and exopolymeric substances (EPS) encasing the microbes provide exceptional benefits, including resistance to antimicrobial agents and mechanical stability. Since exopolysaccharides constitute a predominant part of the EPS matrix, targeting and disrupting polysaccharides might disperse biofilms from abiotic surfaces such as medical implants, industrial equipments and pipelines. In this study, we isolated and identified a fungus, Aspergillus niger APS, a single organism capable of producing multiple carbohydrases using biodegradable waste. The cultural and environmental conditions were optimized for higher yields of all the enzymes using a one-variable at a time(OVAT) approach. The biofilm removal efficiency of the enzyme cocktail was tested against the in-vitro biofilms of Salmonella enterica serovar Typhi, Staphylococcus aureus and Escherichia coli and the cocktail of carbohydrases was found to reduce the biofilm biomass. The disruption of biofilm architecture was also evidenced by Field emission scanning electron microscopy (FE-SEM). Furthermore, the cocktail of carbohydrases was also found to be effective against the viscous slime or 'Black gunk' formed inside the kitchen drainage pipes(KDP) under natural conditions. The study envisions the use of multiple carbohydrases as an anti-biofouling agent, and to our knowledge, this is the first report on the biotreatment of abiotic surfaces for the removal of biofilms/slime formed under natural conditions.

ABSTRACT (PMP020)

IDENTIFICATION OF RV1985C FROM MYCOBACTERIUM TUBERCULOSIS AS A NOVEL NUCLEOID ASSOCIATED PROTEIN

*Ekta Tyagi a, Chetkar Chandra Keshavam a, Manisha Kochhar b, Ranjana Seth c, Rakesh Kumar Seth a, Meetu Gupta d, Yogendra Singh a**
aDepartment of Zoology, University of Delhi,Delhi-110007,
bNational Institute of Immunology, Delhi-110067
cDeshbandhu College, University of Delhi, Delhi-110019
dCSIR-Institute of Genomics and Integrative Biology, Delhi-110007
*Email *ysinghdu@gmail.com*

Tuberculosis, a serious global threat on human health leads to about a million deaths per year, caused by single infectious agent Mycobacterium tuberculosis. It is one of the most successful human pathogen because of its ability to adapt within host environmental conditions. Bacterial genomic DNA must be efficiently compacted to fit inside the cell. This efficient compaction is facilitated by several factors such as macromolecular crowding, DNA supercoiling, and Nucleoid-Associated Proteins (NAPs). NAPs are one of the most abundant proteins associated with nucleoid and are highly basic in nature. These proteins are promiscuous DNA binding proteins and help in compaction through bending, bridging and wrapping the DNA molecule. Besides being a major determinant of genome organization, these proteins are also involved in regulation of multiple cellular processes such as replication, transcription, repair and recombination, bacterial physiology and virulence by regulating gene expression globally. In this report, we have identified Rv1985c, a homolog of E. coli NAP IciA as a novel nucleoid associated protein encoded in the genome of Mycobacterium tuberculosis. Results from our study showed that Rv1985c is a sequence and structure independent DNA-binding protein and it also protects DNA from DNaseI mediated enzymatic activity, which are signature characteristics of NAP family of proteins. An enhanced survival during late stationary phase of Mycobacterium smegmatis mc2155 overexpressing Rv1985c gene as compare to vector control is probably due to genomic DNA protection by Rv1985c under several DNA damaging stress condition. These results suggest that Rv1985c may have a role in latency and chronic stage of M. tuberculosis infection.

ABSTRACT (PMP021)

PHYSIOLOGICAL RELEVANCE OF PRPC, A SERINE/THREONINE PHOSPHATASE IN THE LIFE CYCLE OF BACILLUS ANTHRACIS

Nitika Sangwan a,b, Neha Dhasman ab,Aakriti Gangwal b, Nishant Kumar c, Uma Dhawan a, Yogendra Singh b,
aDepartment of Biomedical science, Bhaskaracharya college of applied sciences, University of Delhi, Delhi-110075, India
bDepartment of Zoology, University of Delhi, Delhi-110007, India cInstitute of Genomics and Integrative Biology, Delhi-110007
*Email **ysinghdu@gmail.com*

Post-translational modification like phosphorylation, glycosylation, methylation, ubiquitination, etc are known to affect the biological properties and functions of proteins. Amongst these, phosphorylation is the most important modification as it regulates a variety of biological processes such as metabolism, cellular architecture, stress responses, and virulence of pathogenic bacteria. Bacillus anthracis is one such pathogenic bacterium that causes a fatal infectious zoonotic disease, anthrax. Sporulation and germination are the two major events in the life cycle of B.anthracis. Till date, three eukaryotic-like Serine/Threonine kinases (PrkC, PrkD, and PrkG) and only one Serine/Threonine phosphatase (PrpC) has been characterized in B. anthracis. The functional relevance of the lone phosphatase, PrpC has been shown in Bacillus subtilis, a non-pathogenic bacillus species but remains to be explored in B.anthracis. Here, we report the role of PrpC in the life cycle of B. anthracis. We generated prpC knockout strain (BAS ΔprpC) and observed attenuated growth as compared to the wild type strain (BAS WT). Additionally, we observed drastic reduction in sporulation and germination efficiency in the absence of PrpC, However, ultrastructure details of spore layers in ΔprpC strain were similar to the BAS WT. The ΔprpC strain showed significant bending and twisting across the bacterial chains along the longitudinal axis. We also observed defective toxins secretion in ΔprpC strain compared to BAS WT which is indicative of its role in anthrax pathogenesis.

ABSTRACT (PMP021)

COMPARATIVE ANALYSIS OF THE GENETIC DIVERSITY IN MULTI-DRUG RESISTANT E. COLI ISOLATED FROM ANIMAL FECES AND YAMUNA RIVER WATER, INDIA

Pooja Gulati, Megha Kaushik, Neha Khare*
Department of Microbiology, Maharshi Dayanand University, Rohtak, Haryana
*Email *pooja.micro@mdurohtak.ac.in*

In the present study E. coli were isolated from several sites of Yamuna River basin located in the Delhi and animal fecal samples. The antibiotic resistance patterns of the isolates were examined. Out of the 149 E. coli isolated, 81 from water samples and 16 from fecal samples were found to be multidrug resistant and used in further study. O-Serotyping was performed and depicted the presence of twenty-three different serotypes. Pathogenic serotypes were also identified suggesting a plausible release of these pathogenic strains from hospital wastes. Further these isolates were assessed for their genetic diversity using whole genome approach of rep-genomic fingerprinting. Combination of ERIC types and (GTG)5 types generated 77 genotypes (H1- H77). The genotype composition of E. coli isolates was highly diverse at all the sampling sites across Yamuna River. Specific locus based typing using PCR-Ribotyping and gyrB-RFLP was also performed to understand the presence of genomic groups and clonal relationship among the isolates. PCR-ribotyping and gyrB-RFLP although had low discriminatory power for differentiating E. coli isolates but provided insights into the source of isolation and within the E. coli. Overall, high genetic diversity was observed among E. coli isolates of the Yamuna River.

Several unique genotypes were observed in the aquatic isolates which were not shared with the animal isolates. Animal commensal isolates were clustered separately from the river isolates suggesting they these non-point sources do not contribute substantially. The spread of such diverse isolates in Yamuna River underscores the need of efficient management strategies in aquatic water bodies.

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