INSCR
Indian Network
for Soil Contamination
Research

MICROBES IN SUSTAINABLE DEVELOPMENT

November 15-18, 2021

Book of Abstracts

6th Annual International E-Conference

Indian Network for Soil Contamination Research (INSCR)

phiXgen

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ABOUT

INSCR

INDIAN NETWORK FOR SOIL CONTAMINATION RESEARCH

The Industrial Revolution has led to a global problem of soil contamination. Soil is a natural resource and its loss and degradation directly impacts the food we eat, the water we drink, the air we breathe, our health and the health of all other organisms on the planet. Healthy soils are the key to food security and our sustainable future. They help sustain food production, mitigate and adapt to climate change, filter water, and improve resilience to natural disasters like flood, drought affecting the world economy.

In 2002, the International Union of Soil Sciences (IUSS) made a resolution proposing the 5th of December be World Soil Day in order to celebrate the importance of soil as a critical component of the natural system and a vital contributor to human well-being, Indian Network for Soil Contamination Research (INSCR) was established in early 1999. INSCR is a registered society under the society's registeration act XXI of 1860 with registration no. 34693 dated 22nd April 1999.

Five International Conferences has been organized under various themes, highlighting the importance of maintaining healthy ecosystems by addressing the growing challenges in soil management, fighting soil biodiversity loss and encouraging government organization, communities and individuals around the world. This year 6th International Conference under the theme "Microbes in Sustainable Development" is being organized in November 2021. The various themes proposed are in direct relation of microbes playing a significant role in soil as a critical component of the global natural system and as a vital contributor to human-being.

Gaumukh: Pout of the Gangotri Glacier and the origin of Bhagirathi River, one of the primary headstream of the Holy Ganges. Gangotri glacier has receded nearly 1.5 km in the last 30 years.

The Vision & Mission of the Conference…

Microorganisms play an important role in the existence of human beings on earth. They have immense potential to be used in development of bioactive compounds, fermentation, bioremediation, waste management, biofuel generation, industrial & agricultural products, education, research and much more. The present Conference will emphasize on the role of microbes in achieving the 17 goals of sustainable development which were proposed in 2016 with the objective of providing the fundamental necessities including food, cloth, shelter and healthcare facilities to all strata of society. The major challenges being faced by the humans including drug resistance, emergence of new diseases, increasing food production and climate issues will be discussed in depth by the experts of their respective field. Along with this, the Conference will provide a common platform to the researchers and academicians from esteemed Institutes across the world to share their ideas and experiences. Participants will be benefitted with the knowledge of different branches of Microbiology including Agricultural Microbiology, Industrial Microbiology, Clinical Microbiology, Marine Microbiology to name a few. Participants would also be given an insight into the career perspectives of Microbiology and introduction of Microbiology at basic level of education.

PROFESSOR RUP LAL
FNA, FNASc, FNAAS, FAMI

It is an honor to welcome you to the 6th Annual International e-Conference of International Network of Soil Contamination Research - INSCR 2021 on “MICROBES IN SUSTAINABLE DEVELOPMENT” being organized in association with Department of Zoology, University of Delhi, Acharya Narendra Dev College, Deen Dayal Upadhyaya College, Gargi College, Kirori Mal College, Maitreyi College, Ramjas College, Sri Venkateswara College, University of Delhi (DU), PG Department of Zoology, Magadh University, C.M.P. College, Allahabad University & Phixgen Pvt. Ltd, from 15th to 18th November 2021.

The idea to host the INSCR is to build a research network highlighting the importance of Microbes in Sustainable development. The various sub themes proposed in the conference are in direct accordance of microbes having an indispensable position in the environment & vital to human well-being. We are happy to initiate the conference on an interesting note with two pre-conference workshops on ‘Art of Scientific Writing & Communication’ & ‘Hands-on to Computational Biology for (Meta) Genomics Analysis’. All our efforts are always directed towards promoting Microbiology literacy amongst the society especially at a child-centric level. The conference program includes a wide range of sessions, including agricultural, environmental, food, industrial, clinical, and space microbiology. We expect in-depth discussions centered around the sustainable development goals (SDG) and the role played by microbes in attaining them. One of the major highlights this year is the ‘Session on Women in Science’.

Experts from all walks of biological sciences have been invited to share their knowledge with participants and we hope that exchange of ideas proceeds with maximum benefit to all. Participants would be given an insight into career prospective of Microbiology & introduction of Microbiology at basic level of education.

With the unprecedented pandemic still looming above us, the conference is being conducted in an online mode only.

I look forward to welcoming you to the online 6th Annual International e-Conference of the International Network of Soil Contamination Research.

Thank you,
Rup Lal

PROFESSOR YOGENDRA SINGH
FNA, FNASc, FASc

Dear colleagues and guests,

It is my great pleasure to welcome you to the 6th Annual International e-Conference of International Network of Soil Contamination Research-INSCR 2021 on “MICROBES IN SUSTAINABLE DEVELOPMENT” being organized in association with Department of Zoology, University of Delhi , Acharya Narendra Dev College, Deen Dayal Upadhyaya College, Gargi College, Kirori Mal College, Ramjas College, Sri Venkateswara College, University of Delhi (DU), PG Department of Zoology, Magadh University, C.M.P. College, Allahabad University & Phixgen Pvt. Ltd, from 15th to 18th November 2021. The idea to host the INSCR is to build a research network highlighting the importance of Microbes in Sustainable development. 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 conducted remotely through the use of advanced digital technologies.

The scientific program of INSCR International Conference 2021 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 program includes a wide range of sessions, including agricultural, environmental, food, industrial, clinical, and space microbiology. Sessions on “*Women in Science*” and the special session on Microbial Literacy for children & society under the “*Microbiology for Science and Society*” umbrella are the highlights of the conference this year. The students may also be interested in the two pre-conference workshops being held before the conference.

We have experts from across the field who will be attending the conference, 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

Prof. Balram Pani
Dean of Colleges
Patron, INSCR

Warm Greetings to all.

It gives me immense pleasure in writing this foreword for the book of abstracts of the oral and poster presentation to be presented at the 6th International E-conference of Indian Network of Soil Contamination and Research (INSCR) on "Microbes in Sustainable Development" to be held from 15th -18th November, 2021 organised in association with the Department of Zoology, University of Delhi, Acharya Narendra Dev College, Deen Dayal Upadhyaya College, Gargi College, Kirori Mal College, Maitreyi College, Ramjas College, Sri Venkateswara College, Khalsa College University of Delhi (DU), PG Department of Zoology, Magadh University, C.M.P. College, Allahabad University & Phixgen Pvt. Ltd.

The e-conference is conceptualized to spread the knowledge about recent developments in host-microbe interactions, clinical, agricultural, environmental, industrial, space and food microbiology.
Two pre-conference workshops on Computational Biology for beginners and Art of Scientific Writing and Communication will be organized prior to conference giving students and teachers a platform for hands-on training and will be helpful for them eventually.
There is bountiful participation from the national and international scientific fraternity as the conference is bringing together ~70 speakers from many Universities around the globe. There is an active participation from almost all Indian states. The program includes inaugural lectures, planery lectures and keynote lectures along with faculty and student of undergraduate colleges.
I am assured that all the participants and speakers will benefit from the conference. It is going to be helpful in their future scientific endeavors for most of the young researchers.
My best wishes for the organization of a successful and fruitful conference.

Prof. Balram Pani

Prof. (Dr.) Rajendra Prasad
VICE-CHANCELLOR

MAGADH UNIVERSITY

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Ref. No. ....

Date .November 13, 2021

Message

In my capacity as the patron, I am delighted to welcome enthusiastic participants from all over the world to the 6th International E-conference of the Indian Network of Soil Contamination and Research (INSCR) on "**Microbes in Sustainable Development**" to be held from 15th -18th November, 2021 organised in association with the Department of Zoology, University of Delhi, PG Department of Zoology, Magadh University, Acharya Narendra Dev College, Deen Dayal Upadhyaya College, Gargi College, Kirori Mal College, Maitreyi College, Ramjas College, Sri Venkateswara College, Khalsa College University of Delhi (DU), C.M.P. College, Allahabad University & Phixgen Pvt. Ltd.

Through this message, I would like to congratulate the entire team of young and experienced researchers/organizers. This event will provide inspiring insight into the emerging trends of research associated with microbes and sustainable development. The agenda is organized around scientific progress of current relevance. It is wonderful to see more than 70 speakers representing different Institutes/Universities from different parts of the country and abroad sharing their research on current aspects of the microbiome.

The sharing of research findings by internationally renowned microbiologists will undoubtedly be a rewarding experience for the participants. INSCR conference organizers deserve my appreciation and congratulations once again on their tremendous efforts, and I wish them a great deal of success for this conference.

Dr. Rajendra Prasad

Prof. Umesh Rai
Head, Department of Zoology, UoD
Co-Patron,INSCR

Warm Greetings to all.

I feel honoured in writing this foreword for the abstract book of the 6th International E-conference of Indian Network of Soil Contamination and Research (INSCR) on "Microbes in Sustainable Development" to be held from 15th -18th November, 2021 organised in association with the Department of Zoology, University of Delhi, Acharya Narendra Dev College, Deen Dayal Upadhyaya College, Gargi College, Kirori Mal College, Maitreyi College, Ramjas College, Sri Venkateswara College, Khalsa College University of Delhi (DU), PG Department of Zoology, Magadh University, C.M.P. College, Allahabad University & Phixgen Pvt. Ltd.
This conference has been planned in order to spread the knowledge about recent developments in host-microbe interactions, clinical, agricultural, environmental, industrial, space and food microbiology. Special attraction in the conference is going to be the Women in Science session and the endeavor of the organizers to educate the society about role of microbes in daily life.
Two pre-conference workshops on Computational Biology for beginners and Art of Scientific Writing and Communication will be organized prior to conference giving students and teachers a platform for hands-on training and will be helpful for them eventually.
There is bountiful participation from the national and international scientific fraternity as the conference is bringing together ~70 speakers from many Universities around the globe. There is an active participation from almost all Indian states. The program includes inaugural lectures, planery lectures and keynote lectures along with faculty and student of undergraduate colleges.
I am assured that all the participants and speakers will benefit from the conference. It is going to be helpful in their future scientific endeavors for most of the young researchers.
I wish for the successful and fruitful organization of this e-conference.

Dr. Sanjay Kumar,
Director CSIR-IHBT, Palampur
Co-Patron,INSCR

I am pleased to extend a very cordial welcome to all of you on the 6th International E-conference of Indian Network of Soil Contamination and Research (INSCR) on "Microbes in Sustainable Development". 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. The purpose behind this conference is to propagate the importance and recent trends in microbiology. The various thematic sessions will platform significant scientific innovations and emphasize the impact of microbes.

The conference will be headed by two pre-conference workshops on to ignite students with tools for Computational Biology for beginners and interesting facts and information to improve and enhance their publication skills. The preconference workshop will be helpful to the college students, research scholars and college teachers in developing skills.

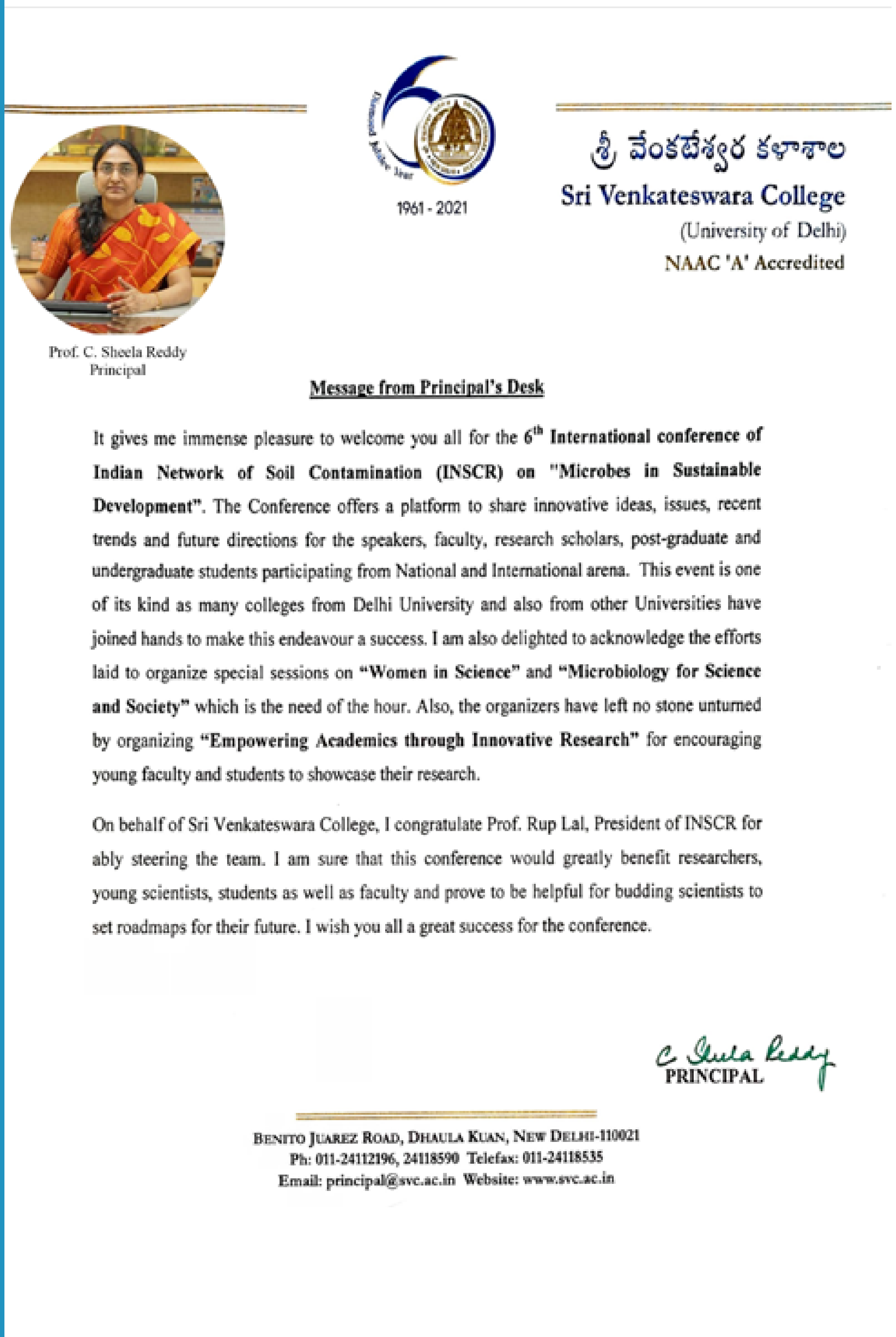
We have experts from across the field who will be attending the conference for all the three days—sharing their knowledge, and ideas. I look forward to hearing the presentations, achievements, opinions and views in the coming few days, which is not only going to inspire us but will also have an impact on our society.

On behalf of INSCR and the organizing committee, I welcome everyone!

Dr. Sanjay Kumar

Co-Patron

MESSAGES



1961 - 2021

శ్రీ వేంకటేశ్వర కళాశాల
Sri Venkateswara College
(University of Delhi)
NAAC 'A' Accredited

Prof. C. Sheela Reddy
Principal

Message from Principal's Desk

It gives me immense pleasure to welcome you all for the 6th **International conference of Indian Network of Soil Contamination (INSCR) on "Microbes in Sustainable Development"**. The Conference offers a platform to share innovative ideas, issues, recent trends and future directions for the speakers, faculty, research scholars, post-graduate and undergraduate students participating from National and International arena. This event is one of its kind as many colleges from Delhi University and also from other Universities have joined hands to make this endeavour a success. I am also delighted to acknowledge the efforts laid to organize special sessions on **"Women in Science"** and **"Microbiology for Science and Society"** which is the need of the hour. Also, the organizers have left no stone unturned by organizing **"Empowering Academics through Innovative Research"** for encouraging young faculty and students to showcase their research.

On behalf of Sri Venkateswara College, I congratulate Prof. Rup Lal, President of INSCR for ably steering the team. I am sure that this conference would greatly benefit researchers, young scientists, students as well as faculty and prove to be helpful for budding scientists to set roadmaps for their future. I wish you all a great success for the conference.

C. Sheela Reddy
PRINCIPAL

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Co-Patron

MESSAGES

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RC/PO/1106

09th November, 2021

PROF. MANOJ KUMAR KHANNA
PRINCIPAL, RAMJAS COLLEGE, DU

Dear colleagues and guests,

Ramjas College, University of Delhi is pleased to be associated with University of Delhi's Department of Zoology, Acharya Narendra Dev College, Deen Dayal Upadhyaya College, Gargi College, Kirori Mal College, Maitreyi College and Sri Venkateswara College, Magadh University's PG Department of Zoology, Allahabad University's C.M.P. College & Phixgen Pvt. Ltd in organizing the **6th Annual International e-Conference of International Network of Soil Contamination Research (INSCR)** titled **"MICROBES IN SUSTAINABLE DEVELOPMENT"** from **15th to 18th November 2021.**

The pandemic COVID-19 has brought to forefront the significance of microbial research, be it in microbial genomics, metagenomics, diagnostics or vaccine development. This is in addition to their already recognized importance in agricultural, industrial, clinical and environmental biology and biotechnology for the attainment of Sustainable Development Goals. **The central theme behind the INSCR 2021 conference is to facilitate understanding, discussions and inter-disciplinary collaborations for the advancement of microbial research and development.**

Various thematic sessions are carefully planned to host many renowned international and national speakers who will showcase important scientific advances in different aspects of microbiology and emphasize on the diverse impacts of microbes and their complex interactions. The sessions will not only be one-stop platform for knowing recent advancements but will also provide the requisite 'food for thought' for further advancements. Special sessions on **"Women in Science"** and **"Microbiology for Science and Society"** will touch upon the societal aspects including understanding the role, contribution and status of women in science and the rising need of Microbiology Literacy, respectively.

To equip early-stage researchers, scholars and graduate students with the necessary skills of basic computational biology and scientific writing three pre-conference workshops are also scheduled. Keeping in mind the exhaustive nature of online conferences, some cultural sessions, agar art competitions etc. are also planned.

All in all, the conference brings together experts from various fields of microbiology on one platform to facilitate bilateral exchange of knowledge, ideas and opinions that can shape the future discourse of microbial research required for the attainment of sustainable development.

I wholeheartedly welcome you all to be an active part of this enriching experience.

Looking forward to fruitful deliberations.

Best wishes,

Manoj K. Khanna

MESSAGES

Co-Patron

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Dated: 2nd November, 2021

FROM THE PRINCIPAL'S DESK

PROF. PROMILA KUMAR
PRINCIPAL, GARGI COLLGE, DU

As a Co-Patron of the 6th Annual International e-Conference of International Network of Soil Contamination Research-INSCR 2021, I take great pride in welcoming all the attendees of this Conference on "MICROBES IN SUSTAINABLE DEVELOPMENT".

The concept of sustainable development refers to the idea that humans should be able to meet their basic requirements while also ensuring that future generations can meet their basic needs. Achieving a balance between economic, environmental, and social needs is the focus of sustainable development. Climate change, energy consumption, waste production, threats to public health, natural resource management, and biodiversity loss are just a few of the challenges. In this setting, long-term development strategies are now required, where microorganisms play a critical role. Microbes not only stabilize the soil structure, allow plants to absorb nutrients, and control pests and diseases, but they also decompose organic matter and destroy toxic compounds, as well as serving as a soil health indicator. In the process of 'bioremediation,' bacteria are also used extensively to clean up pollution treatment. As a result, advances in microbiology, infectious diseases, microbial ecology, plant and animal pathology, and biotechnology promise to improve human life and environmental well-being. New opportunities have arisen as a result of social and scientific advances in these various domains.

Since this conference covers very global aspects on Microbiology from fundamental issues to practical applications, it is a must-attend for everyone interested in the future of microbiology and biotechnology.

We're looking forward to an excellent meeting with great scientists from different countries around the world and sharing new and exciting results, which is being held from November 15-18, 2021.

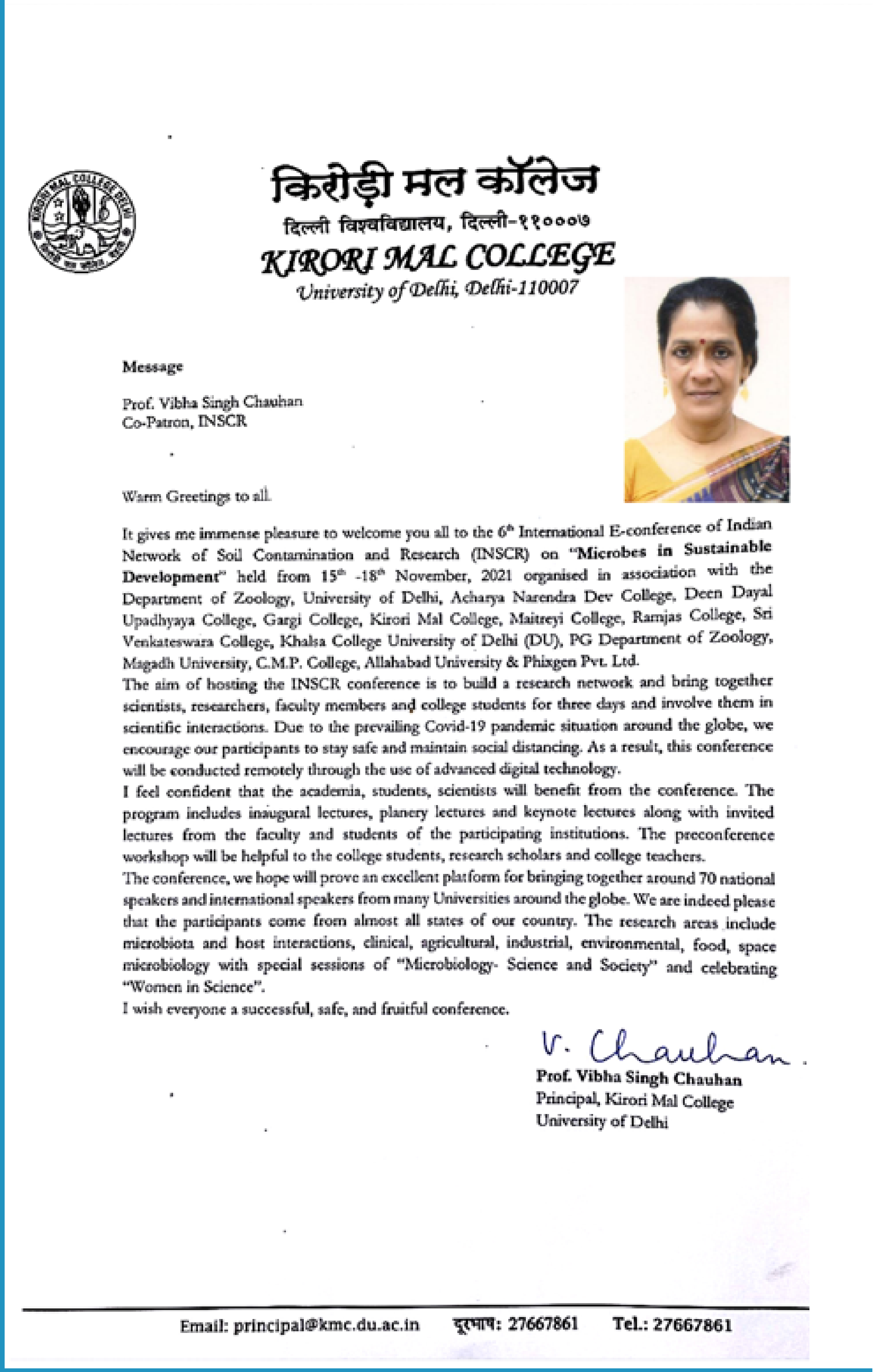
On behalf of the entire organizing committee, I welcome you and wish you a successful conference.

Kumar

Prof. Promila Kumar
Principal (offg.)

MESSAGES

Co-Patron



किरोड़ी मल कॉलेज
दिल्ली विश्वविद्यालय, दिल्ली-११०००७
KIRORI MAL COLLEGE
University of Delhi, Delhi-110007

Message

Prof. Vibha Singh Chauhan
Co-Patron, INSCR

Warm Greetings to all.

It gives me immense pleasure to welcome you all to the 6th International E-conference of Indian Network of Soil Contamination and Research (INSCR) on "**Microbes in Sustainable Development**" held from 15th -18th November, 2021 organised in association with the Department of Zoology, University of Delhi, Acharya Narendra Dev College, Deen Dayal Upadhyaya College, Gargi College, Kirori Mal College, Maitreyi College, Ramjas College, Sri Venkateswara College, Khalsa College University of Delhi (DU), PG Department of Zoology, Magadh University, C.M.P. College, Allahabad University & Phixgen Pvt. Ltd.
The aim of hosting the INSCR conference is to build a research network and being together scientists, researchers, faculty members and college students for three days and involve them in scientific interactions. Due to the prevailing Covid-19 pandemic situation around the globe, we encourage our participants to stay safe and maintain social distancing. As a result, this conference will be conducted remotely through the use of advanced digital technology.
I feel confident that the academia, students, scientists will benefit from the conference. The program includes inaugural lectures, planery lectures and keynote lectures along with invited lectures from the faculty and students of the participating institutions. The preconference workshop will be helpful to the college students, research scholars and college teachers.
The conference, we hope will prove an excellent platform for bringing together around 70 national speakers and international speakers from many Universities around the globe. We are indeed please that the participants come from almost all states of our country. The research areas include microbiota and host interactions, clinical, agricultural, industrial, environmental, food, space microbiology with special sessions of "Microbiology- Science and Society" and celebrating "Women in Science".
I wish everyone a successful, safe, and fruitful conference.

V. Chauhan

Prof. Vibha Singh Chauhan
Principal, Kirori Mal College
University of Delhi

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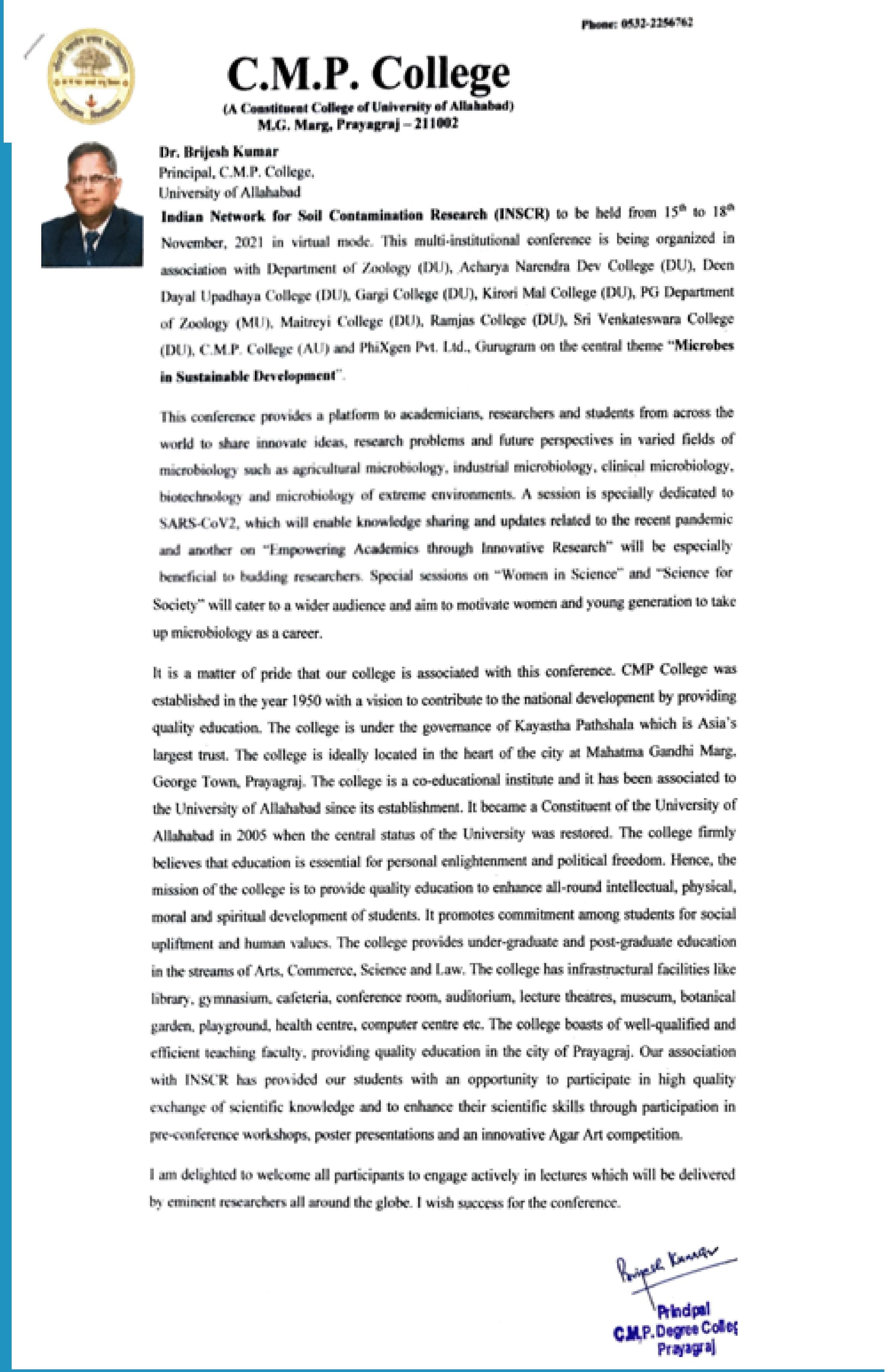
Co-Patron

MESSAGES



Phone: 0532-2256762

C.M.P. College

(A Constituent College of University of Allahabad)
M.G. Marg, Prayagraj – 211002

Dr. Brijesh Kumar
Principal, C.M.P. College,
University of Allahabad

Indian Network for Soil Contamination Research (INSCR) to be held from 15th to 18th November, 2021 in virtual mode. This multi-institutional conference is being organized in association with Department of Zoology (DU), Acharya Narendra Dev College (DU), Deen Dayal Upadhaya College (DU), Gargi College (DU), Kirori Mal College (DU), PG Department of Zoology (MU), Maitreyi College (DU), Ramjas College (DU), Sri Venkateswara College (DU), C.M.P. College (AU) and PhiXgen Pvt. Ltd., Gurugram on the central theme "**Microbes in Sustainable Development**".

This conference provides a platform to academicians, researchers and students from across the world to share innovate ideas, research problems and future perspectives in varied fields of microbiology such as agricultural microbiology, industrial microbiology, clinical microbiology, biotechnology and microbiology of extreme environments. A session is specially dedicated to SARS-CoV2, which will enable knowledge sharing and updates related to the recent pandemic and another on "Empowering Academics through Innovative Research" will be especially beneficial to budding researchers. Special sessions on "Women in Science" and "Science for Society" will cater to a wider audience and aim to motivate women and young generation to take up microbiology as a career.

It is a matter of pride that our college is associated with this conference. CMP College was established in the year 1950 with a vision to contribute to the national development by providing quality education. The college is under the governance of Kayastha Pathshala which is Asia's largest trust. The college is ideally located in the heart of the city at Mahatma Gandhi Marg, George Town, Prayagraj. The college is a co-educational institute and it has been associated to the University of Allahabad since its establishment. It became a Constituent of the University of Allahabad in 2005 when the central status of the University was restored. The college firmly believes that education is essential for personal enlightenment and political freedom. Hence, the mission of the college is to provide quality education to enhance all-round intellectual, physical, moral and spiritual development of students. It promotes commitment among students for social upliftment and human values. The college provides under-graduate and post-graduate education in the streams of Arts, Commerce, Science and Law. The college has infrastructural facilities like library, gymnasium, cafeteria, conference room, auditorium, lecture theatres, museum, botanical garden, playground, health centre, computer centre etc. The college boasts of well-qualified and efficient teaching faculty, providing quality education in the city of Prayagraj. Our association with INSCR has provided our students with an opportunity to participate in high quality exchange of scientific knowledge and to enhance their scientific skills through participation in pre-conference workshops, poster presentations and an innovative Agar Art competition.

I am delighted to welcome all participants to engage actively in lectures which will be delivered by eminent researchers all around the globe. I wish success for the conference.

Brijesh Kumar

Principal
C.M.P. Degree Colleg
Prayagraj

Co-Patron

MESSAGES

ACHARYA NARENDRA DEV COLLEGE
Preparing for the future...
आचार्य नरेंद्र देव कॉलेज
तैयारी भविष्य की...
University of Delhi दिल्ली विश्वविद्यालय | NAAC accredited: A Grade एन.ए.ए.सी मान्यता प्राप्त: 'ए' ग्रेड

Prof Ravi Toteja
Officiating Principal

Ref./ संदर्भ: ANDC /2021/1278
Dated/ दिनांक: 09/11/2021

Dear Delegates and Participants

It gives me immense pleasure to welcome you all to the 6th Annual International e-Conference of International Network of Soil Contamination Research-INSCR-2021 on "**Microbes in Sustainable Development**"

Theme of the conference is very appropriate in today's scenario. Anthropogenic activities have caused much damage to the environment. It becomes our responsibility to safeguard the environment. Exploiting microbes to protect environment is one of the strategies towards safeguarding the environment. The topics of the conference are very well chosen and are very relevant. I am sure that views shared by the eminent speakers in this conference will help all of us in gaining insight of how these tiny living organisms can help in sustainable development.

I am happy to learn that there are pre-conference workshops also. These types of workshops help in gaining in-depth knowledge of the subject.

This conference aims to bring various stakeholders together and I am sure that deliberations during the conference would be fruitful for the humankind.

I on behalf of Acharya Narendra Dev College wishes a grand success to the event and appreciate the efforts put in by all members of the organizing team for holding this conference very meticulously.

Professor Ravi Toteja

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MESSAGES

Co-Patron

दीन दयाल उपाध्याय कॉलेज
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दिल्ली रा. रा. क्षेत्र सरकार द्वारा 100% वित्त पोषित, 100% funded by Govt. of NCT of Delhi
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Dear Delegates,

I am delighted in acknowledging the INSCR International Conference 2021 collaboratively being organized by Department of Zoology and several colleges of University of Delhi, Magadh and Allahabad University on **"Microbes in Sustainable Development"**. Today the world around us has many social, environmental and health issues which need to be addressed carefully and this conference is a great step towards instilling awareness for making this planet a better place by seeking sustainable options. Properly nurtured, our young minds will grow up to initiate and implement the modifications our society so desperately requires. Amidst the prevailing pandemic where the entire humanity is a witness to what havoc a tiny virus is capable of, it has become imperative to bring into light the immense capabilities and potential of these microbes. While the general perception towards them is negative, it is the right time to unravel the beneficial influences of these tiny creatures to the younger generation. As an educational institution focused towards moulding young minds and producing good citizens, we at Deen Dayal Upadhyaya College have always promoted activities that provide students the awareness and the exposure to deal with and solve issues.

I appreciate the organizing committee for showing a keen interest in organizing a successful Conference and contributing new ideas and research findings. I wish them for their endeavours to spread knowledge and awareness which undoubtedly is the need of the hour. The entire organizing team from our college welcomes you to have three days of brain-storming and mind-changing experience for a better future where we visualize our students to be microbial literate in true sense. The college has always been enthusiastic about encouraging young minds to indulge in more than just their curriculums and try to expand their horizons. So, I eagerly await the conference and more importantly, of inspiring change.

Best wishes,

Prof. Hem Chand Jain
Officiating Principal,
Deen Dayal Upadhyaya College
(University of Delhi)

MESSAGES

Co-Patron

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MAITREYI COLLEGE
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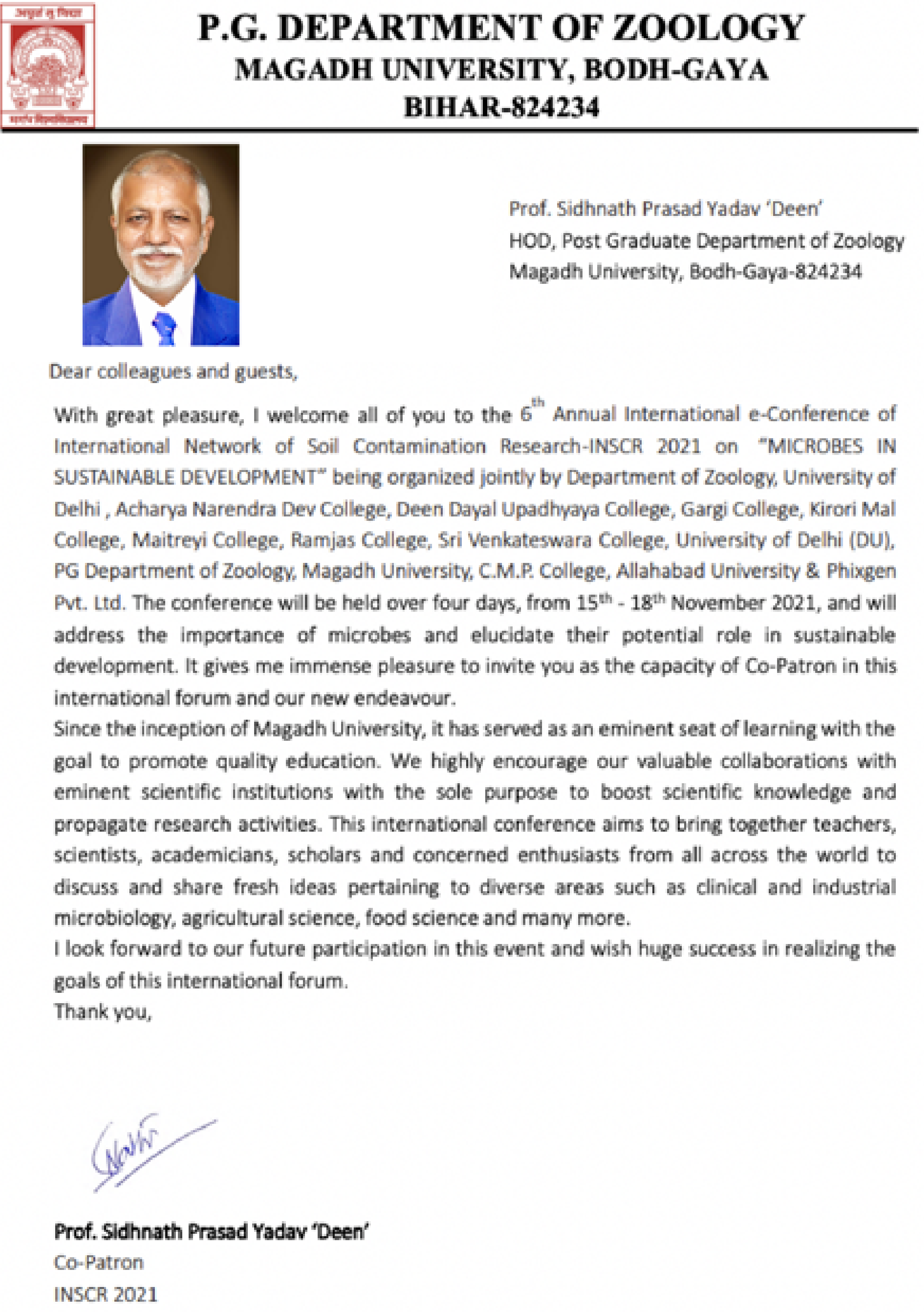
PROF HARITMA CHOPRA
PRINCIPAL, MAITREYI COLLEGE, DU

Dear colleagues and guests,

It gives me immense pleasure to welcome you all to the 6th Annual International e-Conference of International Network of Soil Contamination Research-INSCR 2021 on "MICROBES IN SUSTAINABLE DEVELOPMENT" being organized in association with Department of Zoology, University of Delhi, Acharya Narendra Dev College, Deen Dayal Upadhyaya College, Gargi College, Kirori Mal College, Maitreyi College, Ramjas College, Sri Venkateswara College, University of Delhi (DU), PG Department of Zoology, Magadh University, C.M.P. College, Allahabad University & Phixgen Pvt. Ltd, from 15th to 18th November 2021. This conference aims to bring together renowned researchers, professionals, educators and students to share innovative ideas, current research developments and future directions in the dynamic field of microbiology. The role of microbiologists in microbial sciences has been greatly highlighted due to the COVID-19 pandemic. So, I am pleased to note that more than 70 prominent researchers including eminent microbiologists from various Institutes/Universities from different parts of the country and abroad would be presenting their research at the virtual event.

Thanks to all members of the Organising Committee for this relevant and important conference. I am sure that this conference would provide an enriching platform for all the stakeholders. With great pleasure and pride, I welcome all the participants and convey my best wishes for INSCR 2021 e-conference.

Prof. Haritma Chopra
Officiating Principal



P.G. DEPARTMENT OF ZOOLOGY
MAGADH UNIVERSITY, BODH-GAYA
BIHAR-824234

Prof. Sidhnath Prasad Yadav 'Deen'
HOD, Post Graduate Department of Zoology
Magadh University, Bodh-Gaya-824234

Dear colleagues and guests,

With great pleasure, I welcome all of you to the 6th Annual International e-Conference of International Network of Soil Contamination Research-INSCR 2021 on "MICROBES IN SUSTAINABLE DEVELOPMENT" being organized jointly by Department of Zoology, University of Delhi , Acharya Narendra Dev College, Deen Dayal Upadhyaya College, Gargi College, Kirori Mal College, Maitreyi College, Ramjas College, Sri Venkateswara College, University of Delhi (DU), PG Department of Zoology, Magadh University, C.M.P. College, Allahabad University & Phixgen Pvt. Ltd. The conference will be held over four days, from 15th - 18th November 2021, and will address the importance of microbes and elucidate their potential role in sustainable development. It gives me immense pleasure to invite you as the capacity of Co-Patron in this international forum and our new endeavour.

Since the inception of Magadh University, it has served as an eminent seat of learning with the goal to promote quality education. We highly encourage our valuable collaborations with eminent scientific institutions with the sole purpose to boost scientific knowledge and propagate research activities. This international conference aims to bring together teachers, scientists, academicians, scholars and concerned enthusiasts from all across the world to discuss and share fresh ideas pertaining to diverse areas such as clinical and industrial microbiology, agricultural science, food science and many more.

I look forward to our future participation in this event and wish huge success in realizing the goals of this international forum.

Thank you,

Prof. Sidhnath Prasad Yadav 'Deen'
Co-Patron
INSCR 2021

COLLEGE OF COMMERECE, ARTS & SCIENCE
A constituent unit of Patliputra University, Patna
Patna, Bihar 800020

Prof. Tapan Kumar Shandilya
Principal – College of Commerce, Arts & Science
Patliputra University, Patna
https://cocaspatna.ac.in/

College of Commerce, Arts and Science, Patna is a NAAC Re-accredited Grade 'A' college, a constituent unit of Patliputra University, Patna, established in 1949 by Pt. Indu Shekhar Jha on the advice of Dr. Rajendra Prasad. It is one of the oldest colleges of Patna and is known for imparting quality undergraduate and postgraduate education. The college was established with a pious motive to make quality education accessible for aspiring youths without any discrimination based on socio-cultural-economic grounds. After the journey of more than seven decades this institution has achieved its mission and vision to a greater extent for which it was established, and it is a matter of satisfaction that today this institution is acclaimed throughout the state for its high academic standards. College of Commerce, Arts and Science is opportune to have a galaxy of faculties who command a rare distinction in academic excellence and whose accomplishments in academia are appreciated universally.

This college has excellent infrastructure with automated central library linked to world-wide free information flows and databases, well equipped laboratories and congenial and natural campus ambience and classrooms. However, the volume of publication in peer reviewed journals with high impact factor and citation index is moderate but the quality of research is of course worth citing. Teaching and research in all faculties Science, Arts, Humanities, Commerce and Law are available up to PG level. About 14 vocational and add-on courses are being run in College of Commerce, Arts and Science, Patna. The college hopes to commensurate to the national standard in teaching as well as in research. Our institution visions to develop an educational set up to bring out a transformative change in the society by nurturing high moral and spiritual values in students, giving quality education in multiple disciplines, empowering the society through knowledge and quality research and fostering creativity and entrepreneurship in students and in this way making students a capable global citizen.

Prof. Tapan Kumar Shandilya
Co-Patron, INSCR

Anju Srivastava
Department of Zoology

Sukanya Lal
Ramjas College

Seema Makhija
AND College

Renu Gupta
Maitreyi College

Gauri Garg Dhingra
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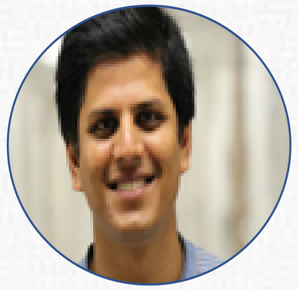

Roshan Kumar
Magadh University

Charu Tripathi
CMP College, AU

Utkarsh Sood
Phixgen Pvt. Ltd.

Dear Participants,

It is indeed our pleasure to inform you that the Indian Network for Soil Contamination Research (INSCR) is organizing the 6th Annual International Conference on "Microbes in Sustainable Development" in association with Acharya Narendra Dev College, Deen Dayal Upadhyaya College, Gargi College, Kirori Mal College, Ramjas College and Sri Venkateswara College of University of Delhi along with PhiXgen Pvt. Ltd. from 15th to 18th November, 2021.

Established in early 1999, INSCR has formed a strong network that brought together several key researchers working on different aspects of contamination in soil environment spread across various academy, agricultural and industrial research institutions in association.

As we all know, the world is currently dealing with a pandemic caused by SARS-CoV-2 virus. 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 how sustainability can be achieved using microbes as the two cannot happen independently. Microbes affect our daily lives so much so closely that sustainability solutions cannot be seen without considering their significant impact on our lives. The target audience will be Post Graduate Students, Research Scholars, Faculties, and Scientific Community.

The conference has provided a unique opportunity for different colleges of DU and other prestigious institutes to co-organize the event along with PhiXgen Pvt. Ltd. & will also provide a platform to the leading scientists from India and abroad to forge ties with research partners from organizations involved in research in these areas. The delegates will also deliberate on exploring the possible avenues to foster technology transfer to the industry.
On behalf of INSCR, all the collaborating colleges & PhiXgen Pvt. Ltd., we invite you all to the conference and request you to make the event a grand success.
Organizing Secretaries, INSCR 2021

Sukanya Lal (Ramjas College, DU)
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Renu Gupta (Maitreyi College, DU)
Jaspreet Kaur (Maitreyi College, DU)
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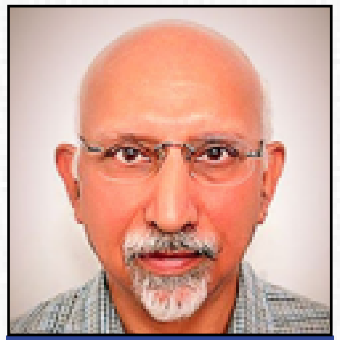

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PARTICIPATING INSTITUTIONS

The Department of Zoology is a constituent entity of the Faculty of Science, University of Delhi. Since its inception in 1947, it has been the foremost centre for learning in all aspects of Animal Sciences in India. In 1963, it was recognized as the Centre for Advanced Studies(CAS) and continues to enjoy this status by special assistance of the UGC-SAP program. UGC extended its CAS status in 2011 by providing special assistance for another five years. In the 60 years of its existence, the department is credited for producing several post-graduate students and awarding nearly 550 doctoral degrees. Its alumni are doing exceptionally well as teachers and scientists at various universities and research laboratories in India and abroad. At present, the department has 186 M.Sc., 14 M.Phil. &101 Ph.D. students. The current research and teaching in the Department include various aspects of Animal Physiology, Entomology, Fish Biology, Immunology, Developmental Biology, Cell Signalling, Cell Biology, Radiation Biology, Reproductive Biology and Endocrinology.

Sri Venkateswara College, a constituent College of University of Delhi offers undergraduate courses in Science, Commerce and Humanities. The college was the visionary realization of the spirited vision and dream of three stalwarts, Smt. Durga Bai Deshmukh, Dr. K.L.Rao and Dr. C. Anna Rao. Fired with the zeal of promoting the cause of education, the college was set up at New Delhi under the benign auspices of Tirumala Tirupati Devasthanams (T.T.D.) in 1961. Since then, the Upanishadic principle "Truth through self-education" has been the guiding principle in all our endeavors. From the outset, we have relentlessly pursued the ideals set by our founders and taken pride in creating a holistic learning atmosphere for students from diverse backgrounds at a minimum cost in our national capital for more than five decades.

The spirit of Gargi, the woman scholar from the Upanishads, guides the mission of Gargi college, which is to produce women of substance, whose feet will be rooted while their hands reach out to steer change and progress. It is desired that every student who passes through the portals of the college emerges as a wholly developed individual symbolizing the spirit of enterprise and inquiry that characterizes Gargi. There is a paradigm shift taking place in the educational focus in this college. The vision is to make this institute of higher education a centre of excellence by promoting & creating new knowledge and finding its applications by tapping the potentials of staff and students.

Founded in 1917, Ramjas College is one of the oldest colleges of Delhi. It has a proud history of being founded by Lala Rai Kedar Nath; the present campus was inaugurated by Dr. Rajendra Prasad, the first president of India. Dr. B. R. Ambedkar served as the Chairman of the Governing Body of the College. The college offers 8 Bachelor of Arts, 7 Bachelor of Science & 2 Bachelor of Commerce courses at UG level in addition to 18 PG courses in these streams. Ramjas dispenses modern language courses through its School of Foreign & Indian Languages (SFIL) and encourages its students and faculty to interact with scholars from all around the world through Centre for International Education (CIE).

Kirori Mal College first came into existence as Nirmala College in 1951, started by the American Jesuits in an evacuee building in Qutab Road, Old Delhi. It was established in 1954, as one of the leading institutions of higher learning as a constituent college of the University of Delhi. Kirori Mal College is one of the oldest institutions of the University of Delhi and is located in the University Enclave, the heart of the city. Set up along the Nehruvian model of 'a temple of higher learning for the spread of modernity', the college continues to cherish its ideal of providing an excellent yet affordable higher education to a large social cross-section of students as befitting a public-funded institution.

Established in 1990 in Karampura, the college shifted to its new campus in Dwarka in 2016 with a state of the art multistory building & all the features of a green structure. The college ranked 15th in the Overall College Category in NIRF, MHRD, GOI survey 2020 in which 1659 Colleges participated. The College is also a recipient of the prestigious Department of Biotechnology, GOI (DBT) Star College Program for the period 2018-2021. The college offers 9 UG Hons. along with 4 bachelor's program in addition to add-on courses. A plethora of activities like field visits, heritage walks, Conferences, Seminars, Workshops are frequently organized. College also works actively for the welfare of the Society & organizes various outreach programs for under-privileged children in remote rural areas.

Maitreyi College, a renowned women's college practices a pedagogical approach for holistic development of the students. The ever-increasing growth & progress of the institution can be comprehended by the way the college moved from the 86th position in NIRF ranking - 2018 to 35th position in 2020. Apart from offering courses in Arts, Commerce and Science to more than 3000 students at the UG level, the college also offers Certificate courses in Journalism & Web designing & Certificate/Diploma/Advanced Diploma in French, Spanish as non-credit add on courses. Maitreyi not only tries to create competent, aware & persevering students, it also makes them acutely conscious of their responsibility towards society.

The college is 30 years old and through all these years, it has helped to unfold the enormous potentialities of the students and empower them to meet the challenges of the future. ANDC is considered as one of the top colleges in India. This is evident from the NAAC score of 3.31 and 18th NIRF-2020 ranking. Our pedagogy is student centric. Several flagship schemes like Paramarsh, Unnat Bharat Abhiyan and DBT STAR COLLEGE SCHEME of Government of India have been sanctioned to the College. This year College has been granted DBT STAR STATUS by Department of Biotechnology. Collaborations like SPIE (USA) Chapter, Science Setu Programme and NPTEL-SWAYAM chapter continue to report robust progress at the national and international level.

Sri Guru Tegh Bahadur Khalsa College, a constituent college of University of Delhi, was established in 1951 and is maintained by Delhi Sikh Gurudwara Management Committee (DSGMC), a statutory body established under an act of the Parliament of India. Over the years, the College has carved a niche for itself and is known to be one of the leading colleges of University. At present there are 18 undergraduate programmes, 2 B.Tech. programmes, 12 postgraduate programmes, one postgraduate diploma, 2 undergraduate diplomas, and 9 certificate courses, making a total of 44 programmes. The focus of the College at the time of inception was to ensure a comprehensive social transformation through access to quality education.

The department was established in 1969, under the stewardship of late Prof. S. B. Singh, late. Dr T.R. Khan along with Dr. D. P. Sinha, Dr. S. P. Singh and Dr. T. K. Singh. In the 50 years of its existence, the department is credited for producing several PG students & awarding nearly 250 doctoral degrees. Apart from teaching, the faculty has been publishing its findings in peer-reviewed National & International journals and have authored several textbooks. Faculty members are presently collaborating with leading research institute of the country like CTR&TI, Ranchi with the objective of promoting the growth and development of Sericulture in the country. The department has made remarkable strides and is committed to continue working hard for excellence in Science.

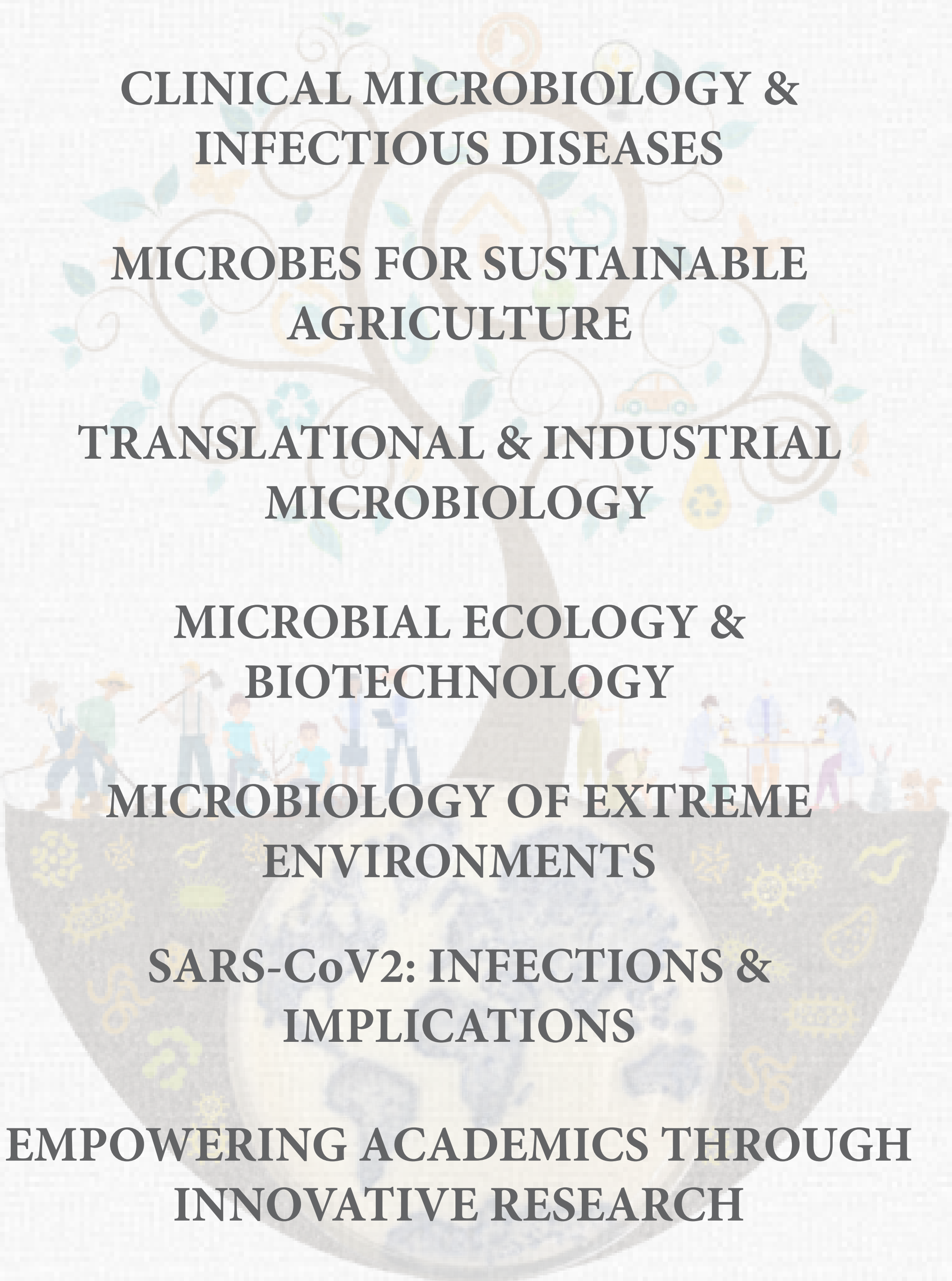
College of Commerce, Arts and Science, Patna (est. 1949) is a constituent unit of Patliputra University, Patna, established in 1949 is one of the oldest colleges of Patna and is known for imparting quality undergraduate and postgraduate education. It was established in 1949 by Pt. Indu Shekhar Jha on the advice of Dr. Rajendra Prasad. We are one of the oldest academic institutions in Patna. We strive to keep the legacy of our ancestors alive by imparting values, knowledge, and wisdom to our Students. \College was reaccredited with Grade – A in 2016 with CGPA of 3.10 / 4. Mission of college is to play a pivotal role to enable the country and state of Bihar, in particular, in developing high caliber trained accomplished academicians in the frontier areas of Academia.

CMP College was established in the year 1950 with a vision to contribute to the national development by providing quality education. The college is under the governance of Kayastha Pathshala which is Asia's biggest trust. The college is ideally located in the heart of the city at Mahatma Gandhi Marg, George Town. It became a Constituent of the University of Allahabad in 2005 when the central status of the University was restored. The college firmly believes that education is essential for personal enlightenment and political freedom. Hence, the mission of the college is to provide quality education to enhance all-round intellectual, physical, moral and spiritual development of students. It promotes commitment among student for social upliftment and human values.

phiXgen

PhiXGen is committed to delivering quality services with unmatched quality. The major focus of the firm is to work towards innovation, development, deployment, and commercialization of products and services. The work mandate includes providing technical services to beginners which primarily includes support for Next Gen Sequencing projects for Genomics, Transcriptomics and Proteomics studies. The wide scope of the firm also includes the onsite/ offsite/ online training courses for graduates/ post-graduates and corporates professionals. Our aim is to implement scientific knowledge for resolving issues related to meta(genomic) data analysis, bioproduct development, agricultural resource development, counseling, consultation, and training.

THEMES



HOST MICROBIOTA INTERACTIONS

CLINICAL MICROBIOLOGY & INFECTIOUS DISEASES

MICROBES FOR SUSTAINABLE AGRICULTURE

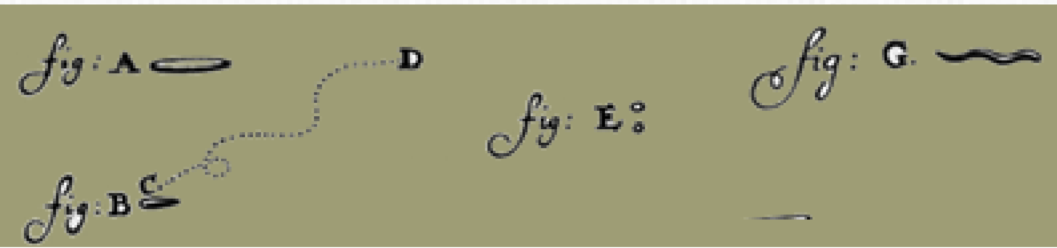
TRANSLATIONAL & INDUSTRIAL MICROBIOLOGY

MICROBIAL ECOLOGY & BIOTECHNOLOGY

MICROBIOLOGY OF EXTREME ENVIRONMENTS

SARS-CoV2: INFECTIONS & IMPLICATIONS

EMPOWERING ACADEMICS THROUGH INNOVATIVE RESEARCH



SPECIAL SESSION

WOMEN IN SCIENCE

SPEAKERS

Dr Hillary Lappin-Scott *(President, FEMS)*

Dr Atya Kapley *(CSIR-NEERI)*

Dr Kalai Mathee *(Florida Int. University, USA)*

Dr Agnieszka Dybala-Defratyka *(Lodz Univ. of Tech., Poland)*

Dr Rama Chaudhry *(Dept.of Microbiology, AIIMS)*

Prof. Anita Kamra Verma *(Dept of Zoology, Kirori Mal College, DU)*

Dr Bettina Sontag *(University of Innsbruck)*

SPECIAL SESSION

Science & Society

A child-centric effort to promote Microbial Literacy

Making a child microbiolgy literateshall create an informed future generation. This sesson envisages to communicate the basic concepts and methods of microbiologyto the younger generation because a time has become when it is imperative to understand the role of microbiology in creating a sustainable tomorrow

SPEAKERS

Prof. Eliora Ron *(President, International Union of Microbiological Societies)*

Prof. Kenneth Timmis *(Technical University of Braunschweig, Germany)*

Prof. Jack Glbert *(University of California)*

Prof. Terry McGenity *(University of Essex, United Kingdom)*

Prof. Paola Scavone *(Departamento de Microbiología, Montevideo, Uruguay.)*

Prof. Robert Metcalf *(Founder, Solar Cooker International)*

Prof. Rup Lal *(The Enery and Resources Institute, India)*

Dr. Shailly Anand *(Deen Dayal Uppadhyay College, University of Delhi)*

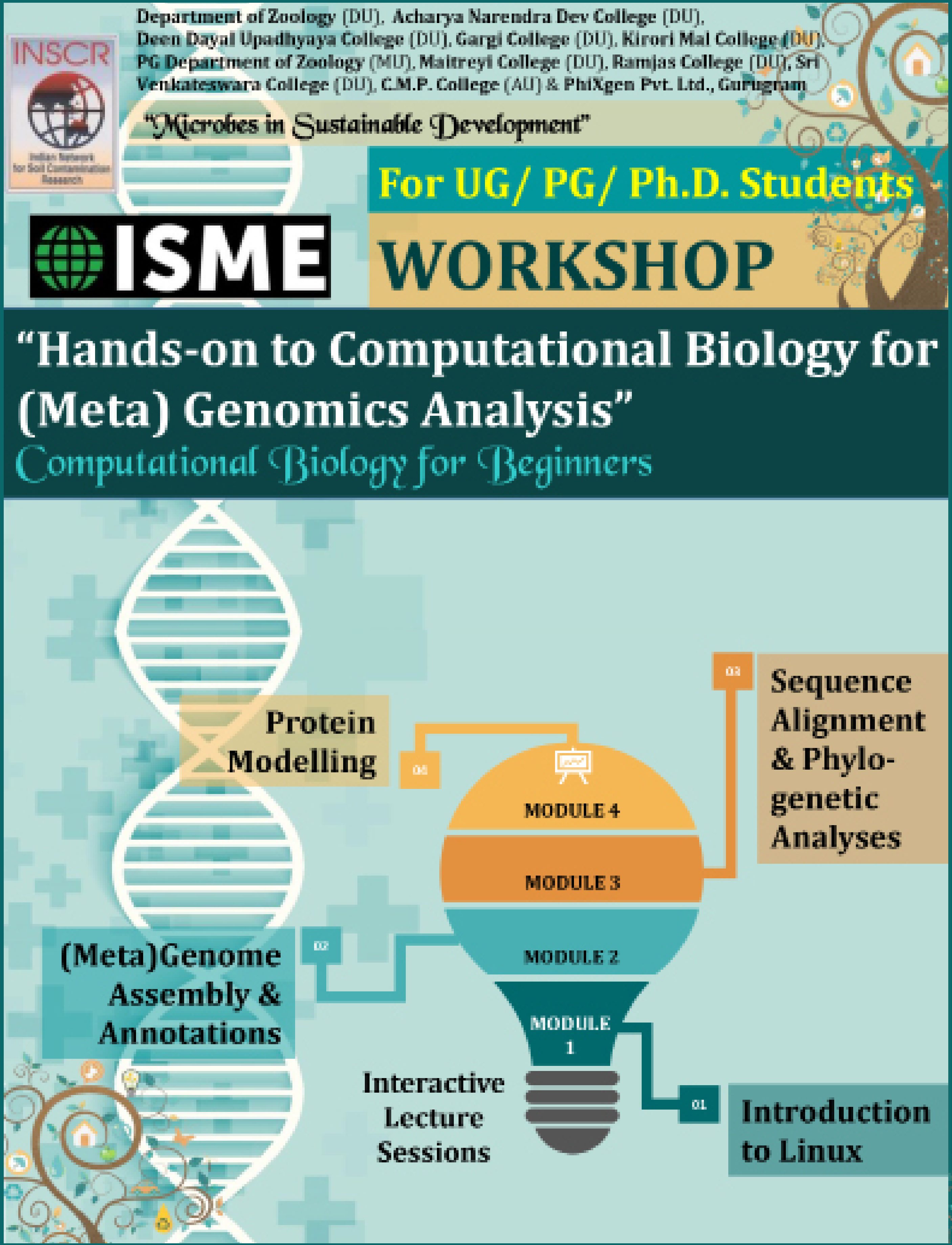
Dr. Charu Dogra Rawat *(Ramjas College, University of Delhi)*

INSCR
2021

PERFECT HUES

Agar Art Competition

Pre-Conference Workshop



Department of Zoology (DU), Acharya Narendra Dev College (DU),
Deen Dayal Upadhyaya College (DU), Gargi College (DU), Kirori Mal College (DU),
PG Department of Zoology (MU), Maitreyi College (DU), Ramjas College (DU), Sri
Venkateswara College (DU), C.M.P. College (AU) & PhiXgen Pvt. Ltd., Gurugram

"Microbes in Sustainable Development"

INSCR
Indian Network for Soil Contamination Research

ISME

For UG/ PG/ Ph.D. Students

WORKSHOP

"Hands-on to Computational Biology for (Meta) Genomics Analysis"

Computational Biology for Beginners

Interactive Lecture Sessions

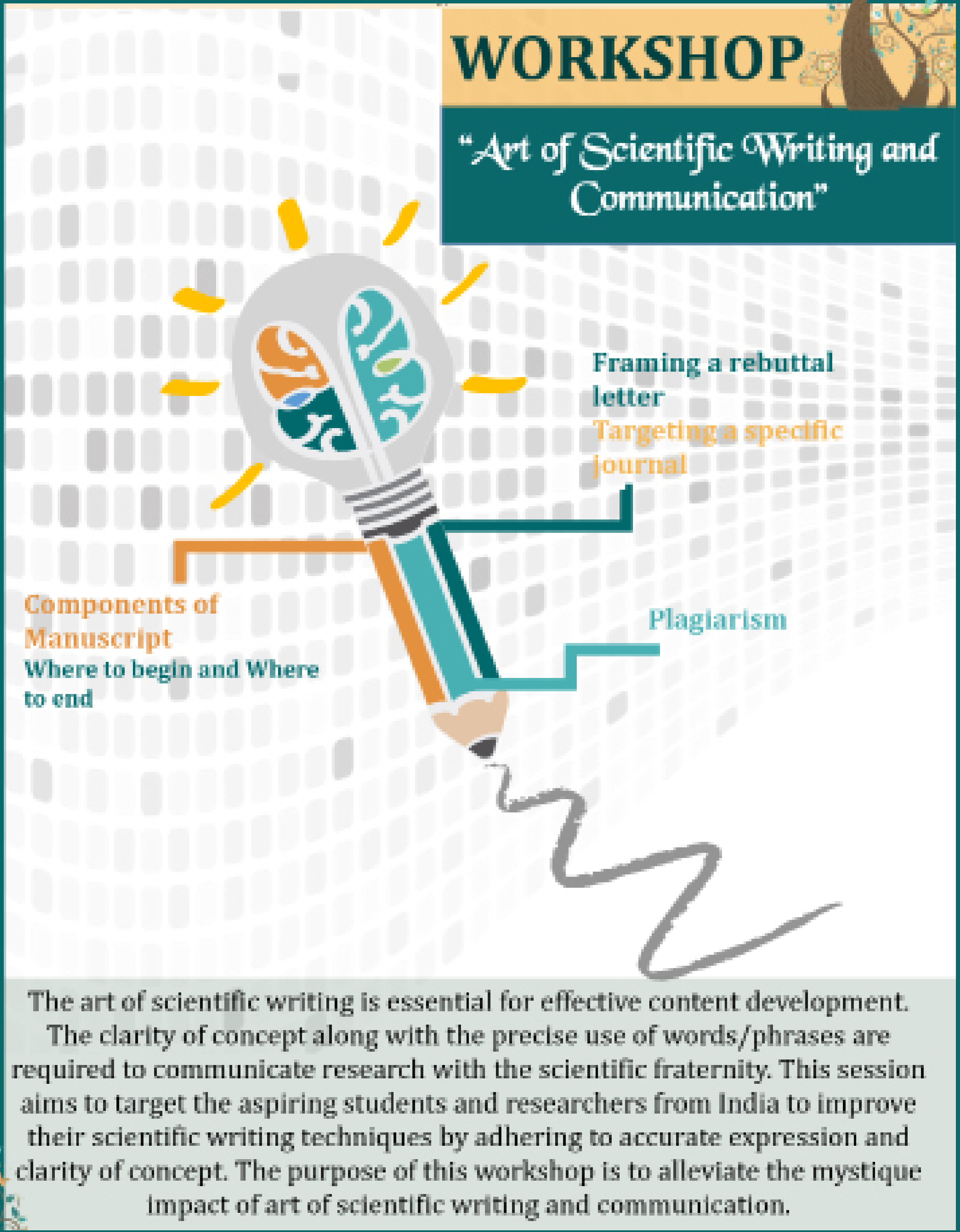
MODULE 1 — 01 Introduction to Linux

MODULE 2 — 02 (Meta)Genome Assembly & Annotations

MODULE 3 — 03 Sequence Alignment & Phylo-genetic Analyses

MODULE 4 — 04 Protein Modelling

Pre-Conference Workshop



WORKSHOP

"Art of Scientific Writing and Communication"

Framing a rebuttal letter

Targeting a specific journal

Components of Manuscript

Where to begin and Where to end

Plagiarism

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.

Scientific Program

6th
Annual International Conference
INDIAN NETWORK FOR SOIL
CONTAMINATION RESEARCH (INSCR)
Microbes in Sustainable Development
15-18 November 2021
PROGRAMME

Day 1: 15th November, 2021

Inauguration

IST (hrs)	Event [ROOM A]
1700 – 1715	**Welcome Address by the President: Rup Lal**
1715 – 1725	**Introduction to INSCR: A. K. Dikshit**
1725 – 1735	**DU VC Address/Dean Colleges**
1735 – 1745	**Introduction to Participating Institutions**
1745 - 1750	**Abstract Book Release**
1750 - 1850	Inaugural Lecture 1 **Chair: Kenneth Timmis and Rup Lal** **Mitch Schulte** (Program Scientist, NASA Headquarters, Washington, DC) *"The Mars 2020 mission and NASA's search for ancient life"*
1850 - 1900	**Cultural Music Event**
1900 - 1910	**The Painting Video**
1910-1950	Inaugural Lecture 2 **Jack Gilbert** (University of California, San Diego, USA) *"The human microbiome in precision medicine"*
1950-2000	**Concluding Remarks of Day 1: Gauri Garg Dhingra** (Karori Mal College, DU)

Day 2: 16th November, 2021 (Tuesday)

IST (hrs)	Event	
0900-0940	Inaugural Lecture 3 **Chair: Sanjay Kumar and Rup Lal** **Edward F. deLong** (Professor, University of Hawaii, Honolulu, United States) *"Towards Four Dimensional Microbial Systems Biology in the Sea"*	
	Session 1 (0945-1545) [ROOM A] *Microbial Ecology* **Chair: Pratyoosh Shukla** **Co-Chair: Nirjara Singhvi, Mansi Verma, Roshan Kumar**	Session 2 (0945-1545) [ROOM B] *Microbes in Sustainable Agriculture* **Chair: Praveen Rishi** **Co-Chair: Jaspreet Kaur, Ankita Dua, Anjali Saxena**
0945-1015	Keynote Lecture **Louis-Marie Bobay** (Assistant Professor, University of North Carolina) *"Biological species concept in Bacteria"*	Keynote Lecture **Appa Rao Podile** (Vice Chancellor, University of Hyderabad) *"Microbiome-based approaches for sustainable development"*
1020-1040	**Vivekanand** (Assistant Professor, Malaviya National Institute of Technology, Jaipur) *"Biogas and microbial communities"*.	**Sunil Pabbi** (Head, Division of Microbiology, ICAR - IARI) *"Cyanobacterial Biofertilizer For Sustainability of Rice Based Cropping"*
1045-1105	**Gunjan Pandey** (Research Scientist, CSIRO, Australia) *"Biochemistry and genetics of pinoresinol mineralization in bacteria"*	**Venkata Ramana** (Professor, University of Hyderabad) *"Exploring the unexplored bacterial phyla members of India"*
1110-1130	**Natesan Manickam** (Chief Scientist, CSIR-Indian Institute of Toxicology Research) *"Occurrence of Microplastics/ plastics in the marine and terrestrial Environment: Assessing diverse plastisphere bacterial communities and microbiome"*	**Nataraja Karaba** (Professor, University of Agricultural Sciences, Bangalore) *"Manipulation of specific traits linked to abiotic stress tolerance in crop plants using endophytes"*
1130-1145	Tea Break	
1150-1220	Keynote Lecture **Anushree Malik** (Institute Chair Professor, CRDT, IIT Delhi) *"Microbial consortia mediated environmental remediation for textile sector"*	**Om Prakash** (Scientist, NCMR-NCCS) *"The Archaea lead in the Ecology of Landfill- Leachate of Pune Municipal Site"*
1225-1245	**S. Dayananda** (Professor, University of Hyderabad) ""	**Kapudeep Karmakar** (Assistant Professor, Uttar Banga Krishi Vishwavidyalaya, Koch Bihar) *"Contamination of food-chain by human pathogens dwelling in rhizosphere: Life cycle and remedies"*
1250-1310	**MKR Mudiam** (Senior Principal Scientist, CSIR-Indian Institute of Chemical Technology) *"Analytical strategies to understand occurrence, fate and transport of emerging"*	**Praveen Rishi** (Professor, Panjab University) *"Bi-directional Elucidation of Probiotic Intervention for Neurological Manifestations at Gut-Brain Axis"*
1315-1400	Lunch Break	

1400-1430	Keynote Lecture **Mrutyunjay Suar** (Professor & Director General R&D, Kalinga Institute of Industrial Technology) *"Building Technology Enabling Ecosystem: Ideation to Enterprise"*	Keynote Lecture **V. C. Kalia** (NRF Fellow, Konkuk University, South Korea) *"Emerging Signal Molecules for Soil Enrichment and Plant Growth Promotion"*
1435-1455	**Pratyoosh Shukla** (Professor, Banaras Hindu University) *"Exploring novel avenues in microbial bioremediation: role of computational tools"*	**Sivakumar Uthandi** (Professor, Tamil Nadu Agricultural University, Coimbatore) *"Microbial volatile organic compounds (mVOC) for plant health"*
1500-1520	**Datta Madamwar** (Professor, Charusat) *"Deciphering and understanding the microbial synergy towards poly-aromatic hydrocarbon pollution: A metagenomic approach"*	**Ajay Kumar** (Associate Professor, Jacob Institute of Biotechnology and Bioengineering, SHUATS) *"Plant growth promoting microbes: A tool for healthy agriculture"*
1525-1545	**Nageswar Amanchi** (Assistant Professor, Department of Zoology, Nizam College) *"Alternative tools and tags in Pesticide Toxicology Research - A case study of Ciliates"*	**Virginia Filipello** (PostDoc Fellow, Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna, Italy) *"Blue strikes again: Re-emergence of Chromogenic Pseudomonas fluorescens in Dairy Products. Rapid Identification and Strain Characterization in the Dairy Plant"*
1550-1630	**Plenary Lecture [ROOM A]** **Chair: Rup Lal** **Co-Chair: Roshan Kumar** **Andreas Bechthold** (Professor, University of Freiberg, Germany) *"Tailoring enzymes involved in natural product biosynthesis"*	
1630-1645	Tea Break ☕	
	Session 3 (1650-1920) [ROOM A] *Women in Science* **Chair: Anju Srivastava** (Professor, DU), **Sukanya Lal** **Co-Chair: Seema Makhija, Jasvinder Kaur**	**Session 4 (1650-1920) [ROOM B]** *Host Microbiota Interactions* **Chair: Sunil Pabbi** **Co-Chair: Utkarsh Sood, Charu Tripathi**
1650-1720	Keynote Lecture **Agnieszka Dybala-Defratyka** (Associate Professor, Lodz University of Technology, Poland) *"Computational redesign of LinA and LinB enzymes"*	Keynote Lecture **Sanjay Kumar** (Director, CSIR-IHBT, Palampur) *"Himalayan microbial technologies for society, industry, and the environment"*
1725-1755	Keynote Lecture **Bettina Sontag** (Senior Scientist, University of Innsbruck, Austria) *"The key role of ciliates in the microbial food web of lakes."*	Keynote Lecture **Yogesh Shouche** (Scientist, NCCS, Pune) *"Human Microbiome: Indian Perspective"*
1800-1820	**Atya Kapley** (Principal Scientist, CSIR-NEERI) *"Role of Microbes in Environmental Rejuvenation"*	**Roshan Kumar** (Assistant Professor, Magadh University, Bodhgaya, Bihar) *"Phylogenetic Relationships and Potential Functional Attributes of the Genus Parapedobacter: A Member of Family Sphingobacteriaceae"*
1825-1845	**Rama Chaudhry** (Professor, Department of Microbiology, AIIMS, New Delhi) *"Antimicrobial Resistance and its Impact on United Nation Sustainable Development Goals"*	**Gaurav Sharma** (DST-INSPIRE Faculty Fellow, Institute of Bioinformatics and Applied Biotechnology, Bengaluru) *"Diversity and evolution of chemosensory and flagellar systems amongst Family Vibrionaceae"*
1850-1920	Keynote Lecture **Kalai Mathee** (Professor, Florida International University, USA) *"Agricultural plants as a potential source for human and animal transmission of extremely drug resistant Pseudomonas aeruginosa"*	**K. Annapurna** (Principal Scientist, IARI) *"Soil Microbiome: Carriers of Soil Health and Sustainable Agricultural Systems"*
1930-2010	**Plenary Lecture [ROOM A]** **Chair: Atya Kapley and Rup Lal** **Co-Chair: Jasvinder Kaur** **Hilary Lappin-Scott** (Honorary Distinguished Professor at Cardiff University, Founder and Director, Lappin-Scott Consulting Ltd.) *"Supporting women in science careers, why it is everyone's job and biofilm research"*	

Day 3: 17th November, 2021

IST (hrs)	Event			
0900-0940	**Plenary Lecture [ROOM A]** **Chair: V. C. Kalia** **Co-Chair: Shailly Anand** **Craig Cary** (Professor, Department of Biological Sciences, The University of Waikato, New Zealand) *"In Extremis: Discovering the Unique Microbial Ecology of Antarctica's Terrestrial Refugia"*			
0940-1020	**Plenary Lecture [ROOM A]** **Hauke Smidt** (Professor, Wageningen University, Netherlands) *"Exploring microbial drivers of halogen cycling in pristine and polluted environments"*			
1020-1030	Tea Break ☕			
	Session 5 (1030-1300) [ROOM A] *SARS CoV-2* **Chair: Jyoti Prakash Tamang** **Co-Chair: Shailly Anand, Helianthous Verma, Renu Solanki** (Deen Dayal Upadhyay College)	**Session 6 (1030-1310) [Room B and Room C]** *Empowering Academics through Innovative Research*		
		Faculty Oral Talks **[ROOM B]** **Chair: Ravi Toteja** (Principal, ANDC) **Co-Chair: Charu Dogra Rawat, Jaspreet Kaur**		*Student Oral Talks* [ROOM C] **Chair: Om Prakash** **Co-Chair: Priya Singh, Pushplata** (Ramjas College)
1030-1100	Keynote Lecture **Debojyoti** (Senior Scientist, CSIR- IGIB, New Delhi) *"Reading and writing the genome with precision"*	1030-1040	OF1 **Ishan Saini** (Assistant Professor, Indira Gandhi University, Rewari)	OS1 **Sourik Das** (DAICENTER and Bioinformatics Centre, Sikkim University, Gangtok)
		1040-1050	OF2 **Reedhu Raj** (Assistant Professor, Govt. Victoria College, Palakkad, Kerala)	OS2 **Priyambada Pariyar** (DAICENTER and Bioinformatics Centre, Sikkim University, Gangtok)
		1050-1100	OF3 **Helianthous Verma** (Assistant Professor, Ramjas College, University of Delhi)	OS3 **H. Nakibapher Jones Shangpliang** (DAICENTER and Bioinformatics Centre, Sikkim University, Gangtok)
1100-1120	**Shazia Haider** (Assistant Professor, JIIT, Noida) *"Advances in the research of the SARS-CoV-2 molecular structure and pathogenesis from a systems biology approach"*	1100-1110	OF4 **Tikam Chand Dakal** (Assistant Professor, Mohanlal Sukhadia University)	OS4 **Piyush Goel** (Indian Institute of Technology, Indore)
		1110-1120	OF5 **Juliet Roshini and Mohan Raj** (Assistant Professor, Nitte University Centre for Science Education and Research)	OS5 **Jeeva Susan Abraham** (Acharya Narendra Dev College, University of Delhi)

1120-1140	**Mansi Verma** (Assistant professor, Sri Venkateswara College, University of Delhi) *"Combating SARS-CoV-2 using drugs and phytocompounds"*	1120-1130	OF6 **Harish Rajak** (Sr. Assistant Professor, Institute of Pharmaceutical Sciences, Guru Ghasidas University, Bilaspur (CG))	OS6 **Samarth Sharma** (Department of Biotechnology, Prayagraj)
		1130-1140	OF7 **Janmejay Pandey** (Sr. Assistant Professor, Department of Biotechnology, School of Life Sciences, Central University of Rajasthan)	OS7 **Srishti Singh** (CMP PG College, University of Allahabad, Prayagraj)
1145-1205	**Baljeet Kaur** (Assistant Professor, Hansraj college, University of Delhi) *"Relevant gene selection in cancer microarray datasets"*	1140-1150	OF8 **Rajni Gupta** (Professor, Kirori Mal College)	OS8 **Rashi Raj** (Sri Venkateswara College, University of Delhi)
		1150-1200	**Break**	
		1200-1210	OF9 **Jasleen Kaur Kalia** (Associate Professor, Dyal Singh College, University of Delhi)	OS9 **Vanya Garg** (Galgotias University)
1210-1230	**Milan Surjit** (Associate Professor, Thsti - Translational Health Science and Technology Institute, Faridabad) *"Host-pathogen interactions during SARS-CoV-2 infection: insights from virus-host RNA-protein interactome studies"*	1210-1220	OF10 **Suman Sharma** (Associate Professor, Ramjas College, University of Delhi)	OS10 **Shweta Mishra** (CMP Botany Department)
		1220-1230	OF11 **Rita Rath** (Associate Professor, Dyal Singh College, University of Delhi)	OS11 **Nirmala Akoijam** (North-Eastern Hill University)
		1230-1240	OF12 **Sadhna Gupta** (Associate Professor, Dyal Singh College, University of Delhi)	OS12 **Sukhjeet Kaur** (IIT Bombay)
1235-1255	**Manjula Kalia** (Associate Professor, Regional Centre for Biotechnology) *"Pharmacological modulation of autophagy as a potential therapeutic for Japanese encephalitis"*	1240-1250	OF25 **Neeraja Sood** (Associate professor, Dyal Singh College, University of Delhi)	OS13 **Shikha Gupta** (Amity Institute of Biotechnology, Amity University, Uttar Pradesh, Noida)
		1250-1300	-	OS14 **Sonam Antil** (Department of Microbiology, COBS&H, CCS HAU, Hisar, Haryana)
		1300-1310	-	OS37 **Saya Laishram** (Acharya Narendra Dev College)
1300-1320	**Ujjwal Neogi** (Karolinska Institute, Stockholm, Sweden) *"Multi-omics analysis to understand the host metabolic reprogramming during SARS-CoV-2 infection associated with disease severity"*	**INSCR GB Meeting**		
1330-1400	Lunch Break 🍽			

1400-1440	**Plenary Lecture [ROOM A]** **Chair: Natesan Manickam** **Co-chair: Princy Hira** (Maitreyi College, DU) **Hans H. Richnow** (Head, Department Isotope Biogeochemistry, Helmholtz Centre for Environmental Research - UFZ, Germany) *"Isotope Fractionation Concept For Characterization of Degradation Processes of Hexachlorocyclohexanes In The Environment And Along Food Webs"*	
1445-1525	**Plenary Lecture [ROOM A]** **Chair: Natesan Manickam** **David van de Vijver** (Associate Professor, Viroscience department, Erasmus Medical Centre, Rotterdam, the Netherlands) *"The impact of preexposure prophylaxis on HIV prevention. Meeting the United Nations goal of ending the AIDS pandemic in 2030"*	
	Session 7 (1530-1800) [ROOM A] *Microbiology of Extreme Environments* **Chair: Umesh Rai** (HoD, DU) **Co-Chair: Gauri Garg Dhingra, Princy Hira**	**Session 8 (1530-1855) [ROOM B]** *Translational and Industrial Microbiology* **Chair: Mrutyunjay Suar** **Co-Chair: Nitish mahato, Vineet K. Singh, Sumit Sahni**
1530-1600	Keynote Lecture **Anil Saxena** (Director, NBAIM) *"Archaea as an option for plant growth promotion and abiotic stress management"*	Keynote Lecture **Anirban Roy Choudhury** (Senior Principal Scientist, CSIR - Institute of Microbial Technology, Chandigarh) *"Process development and scale up for production of microbial exopolysaccharides: Petri plate to pilot plant"*
1605-1625	**Rakshak Kumar** (Scientist, CSIR - Institute of Himalayan Bioresource Technology, Palampur) *"Exploration of Himalayan microbes for the Improvement of hill agriculture"*	**Jyoti Prakash Tamang** (Professor, Sikkim University) *"Integrative Metagenomics and Metabolomics of Some Himalayan Fermented Foods: Microbial Communities and Health Benefits"*
1630-1650	**Tanu Jindal** (Group Additional Pro Vice Chancellor (R&D); Director, Amity Institute of Environmental Toxicology, Safety and Management) *"Exploration Of Extremophiles For Potential Bioremediation & Biotechnological Applications"*	**Vikas Sood** (Assistant Professor, Jamia Hamdard University) *"Host-pathogen interactions during SARS-CoV/2 infection: insights from virus-host RNA-protein interactome studies"*
1655-1715	**Anita Kamra Verma** (Professor, Kirori Mal College, University of Delhi) *"Exploiting Microbial Factories for Nanoparticle Synthesis: Novel Nano-biotechnological based Sustainable Bioremediation of Environmental Contaminants"*	**Sanjukta Subudhi** (Area Convener, Microbial Biofuels and Biochemicals, TERI, New Delhi) *"Fermentative production of 2,3 Butane Diol: A sustainable pathway for renewable chemical production"*
1715-1730	Tea Break ☕	
1730-1800	**S. Venkatachalam** (DST-SERB Post Doctoral Researcher, Ministry of Earth Sciences, Government of India) *"Microbial ecology of Arctic fjords and associated glacier foreland ecosystems in the changing climatic era"*	Keynote Lecture **Ganesh D. Saratale** (Associate Professor in the Department of Food Science and Biotechnology, Dongguk University, South Korea) *"Microbial biopolymers production by utilizing lignocellulosic biomass resources: A sustainable green approach"*
1805-1825	**Charu Tripathi** (CMP College, University of Allahabad, Prayagraj) *"Insights Into The Lifestyle Of A Thermophilic Genus Thermus"*	**Kashyap Dubey** (Associate Professor, JNU, New Delhi) *"Biofoundry of lipstatin from Petriplate to Bioreactor"*
1830-1850	-	**Utkarsh Sood** (The Energy and Resources Institute (TERI), Delhi) *"Scale-up and commercialization of 24-desmethyl rifampicin effective against resistant strains of*

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	Target for Combating MDR Bacteria"	1010-1020	**OF19** **Nar Singh Chauhan** (Professor, Maharshi Dayanand University Rohtak , Haryana)	**OS23** **Swati Maurya** (Acharya Narendra Dev College, Delhi University)
1020-1035	**Tea Break** ☕			
1040-1110	Keynote Lecture **Eddie Cytryn** (Environmental Microbiologist, Institute for Soil, Water and Environmental Sciences, ARO, Volcani Agriculture Research Center, Israel) *"Understanding environmental dimensions of antibiotic resistance"*	1035-1045	**OF20** **Debashis Banerjee** (Assistant Professor, Amity University)	**OS24** **Anup K. Singh** (ICGEB, New Delhi)
		1045-1055	**OF21** **Poonam Dwivedi** (Associate Professor, Ramjas College,University of Delhi)	**OS25** **Mrunali Patel** (Ganpat University)
		1055-1105	**OF22** **Renu Baweja** (Assistant Professor, Shivaji College, University of Delhi)	**OS26** **Achamma Thomas** (Mahatma Gandhi University,Kottayam,Kerala)
		1105-1115	**OF23** **Anina James** (Assistant Professor, Deen Dayal Upadhyaya College, University of Delhi)	**OS27** **Kruti Dave** (Ganpat University)
1115-1135	**Vineet Ahuja** (Professor, MD, Department of Gastroenterology and Human Nutrition, AIIMS, New Delhi) *"Human Gut Microbiome and Microbiome Manipulation Therapies"*	1115-1125	**OF24** **Smriti Bajpai** (Faculty Bhavan's Vivekananda College, Hyderabad)	**OS28** **Siddhi Bangale** (Hislop School of Biotechnology, Hislop College, Nagpur)
		1125-1135	**OF13** **Vidhi Chaudhary** (Assistant Professor, Daulat Ram College, University of Delhi)	**OS29** **Xiao Liu** (Helmholtz-Centre for Environmental Research – UFZ)
1140-1200	**Biswajit Kundu** (Professor, IIT-Delhi) *"Enzyme engineering through iterative learning: the case of L-asparaginase"*	1135-1145	**OF26** **Rekha Kumari** (Associate Professor, Miranda House)	**OS30** **S Sripoorna** (Acharya Narendra Dev College, University of Delhi)
		1145-1155	**OF27** **Priya Singh** (Assistant Professor, Maitreyi College, University of Delhi)	**OS31** **Shruti Sinha** (Department of Technology, Savitribai Phule Pune University)
1200-1230	Keynote Lecture **Praveen Gupta** (Director & HOD, Neurology Department, Fortis Hospital, Gurugram) *"Gut microbiology in multiple sclerosis"*	1155-1205	**OF28** **Samadhan Yuvraj Bagul** (Scientist, ICAR-Directorate of Medicinal & Aromatic Plants Research, Gujarat)	**OS32** **Swati Sharma** (Department of Biotechnology)
		1205-1215	**OF14** **Manisha Arora Pandit** (Assistant Professor, University of Delhi, Kalindi College)	**OS33** **Ishita Pahwa** (Amity University Uttar Pradesh, Noida)
		1215-1225	**OF30** **Sumit Sahni** (Assistant Professor, Acharya Narendra Dev College, University of Delhi)	**OS34** **Sumedha** (Department of environmental sciences, Sri Venkateswara College)
1235-1255	**Bhabatosh Das** (Associate Professor, Translational Health Science and Technology Institute) *"Decontamination of Bacteria from Antibiotic Resistance"*	1225-1235	**OF31** **Anupama Shukla** (Associate Professor, Acharya Narendra Dev College, University of Delhi)	**OS35** **Jyoti Bakshi** (Guru Jambheshwari University of Science & Technology)
		1235-1245	**OF32** **Parminder Kaur** (Assistant Professor, Khalsa College)	**OS36** **Drashya** (Acharya Narendra Dev College)

		1245-1255	-	**OS15** **Dilbag Singh** (ICAR- Indian Agricultural Research Institute, New Delhi-110012)
		1255-1305	-	**OS37** **Pritam Kumar Sinha** (MA Gandhi Studies and Peace, IGNOU)
1300-1320	**Sachin Khurana** (Scholar, Walter and Eliza Hall Institute For Medical Research, Australia) *"Parasites are Beautiful: Microscopy bases approaches to study parasitic diseases"*	1305-1315	-	**OS39** **Aryan Arora** (Department of Environmental Sciences, Sri Venkateswara College)
		1315-1320	-	**OS40** **Pynbanlang Kharnaior** (Department of Microbiology, Sikkim)
1320-1400	Lunch Break 🍴			

1400-1730	**Session 10 [ROOM A]** ***Microbiology for Science and Society*** **Chair: N.K. Ganguly, Kenneth Timmis and Rup Lal** **Co-chair: Shailly Anand, Charu Dogra Rawat**
1400-1430	Keynote Lecture **Kenneth Timmis** (Professor, Technical University of Braunschweig, Germany) *"The International Microbiology Literacy Initiative"*
1430-1500	Keynote Lecture **Terry McGenity** (Professor, University of Essex, United Kingdom) *"Visualizing the invisible: class excursions to ignite children's enthusiasm for microbes"*
1500-1530	Keynote Lecture **Rup Lal** (NASI-Senior Scientist Platinum Jubilee Fellow, TERI) *"Microbiome and Human Health: Societal Perspective"*
1530-1600	Keynote Lecture **Daniel McDonald** (Professor, University of California, San Diego, United States) *"Diet from a perspective: The Microsetta Initiative"*
1600-1630	Keynote Lecture **Paola Scavone** (Principal Investigator, Departamento de Microbiologia, Montevideo, Uruguay) *"The use of comics for microbial literacy in children"*
1630-1650	**Shailly Anand** (Assistant Professor, Deen Dayal Upadhyaya College, University of Delhi) *"Microbes in Sustainable Development"*
1650-1710	**Charu Dogra Rawat** (Associate Professor, Ramjas College, University of Delhi) *"Inquiry, Inclusivity and InRoads: the 3 Is in the M(I)crob(I)ology Educat(I)on"*
1710-1740	Keynote Lecture **Robert Metcalf** (Emeritus Professor, California State University, USA) *"Bringing Evidence-Based Microbiology to the Community Level in Lower Nyakach, Kenya, to Eliminate Waterborne Disease"*
1800-1840	***Valedictory Ceremony*** [ROOM A]
	Chief Guest: Paola Scavone **Guest of Honour: Balaram Pani** (Professor and Dean of Colleges, University of Delhi)
1800-1810	Welcome: **Ravi Toteja** (Principal, ANDC)
1810-1815	INSCR Journal Release: **Rup Lal**
1815-1825	Agar Art Competition Winners Announcement
1825-1830	Prize Distribution
1830-1840	Concluding Remarks and Vote of Thanks: **Sukanya Lal** (Professor, Ramjas College, DU)

BIOSKETCH

bio.

Dr. Mitch Shulte, Ph.D

Program Scientist,
NASA Headquarters, Washington, DC

Prof. Edward Francis DeLong received his Bachelor of Science in Bacteriology at UC Davis, and Ph.D. in Marine Biology at Scripps Institute of Oceanography at the UC San Diego. He was a Professor at UC Santa Barbara in the Department of Ecology for seven years, Science Chair at the Monterey Bay Aquarium Research Institute for seven years, and a Professor at MIT in the Department of Civil and Environmental Engineering, and the Department Biological Engineering for 10 years. For the past 8 years DeLong has served as a Professor of Oceanography at the University of Hawaii, Manoa. There, DeLong serves as co-Director for the Center for Microbial Oceanography: Research and Education (C-MORE). DeLong is a recipient of: The Vladimir Ivanovich Vernadsky Medal of the European Geosciences Union (2008), the Proctor and Gamble Award in Applied and Environmental Microbiology (2008), the ASM D.C. White Research and Mentoring Award (2009), the UC Davis College of Biological Sciences Outstanding Alumni Award (2012), and the A. G. Huntsman Medal for Excellence in Marine Science (2014). DeLong is an elected member of the U. S. National Academy of Sciences, and an elected Fellow in the American Academy of Microbiology, the American Academy of Arts and Sciences, the American Association for the Advancement of Science, and the European Molecular Biology Organization. DeLong served as the President of the International Society of Microbial Ecology from 2018-2020, and now serves as its acting Past President, until August 2022.

Jack Gilbert, Ph.D

Professor, University of California
San Diego, United States

Professor Jack A Gilbert earned his Ph.D. from Unilever and Nottingham University, UK in 2002, and received his postdoctoral training at Queens University, Canada. From 2005-2010 he was a senior scientist at Plymouth Marine Laboratory, UK; and from 2010-2018 he was Group Leader for Microbial Ecology at Argonne National Laboratory, a Professor of Surgery, and Director of The Microbiome Center at University of Chicago. In 2019 he moved to University of California San Diego, where he is a Professor in Pediatrics and the Scripps Institution of Oceanography. Dr. Gilbert uses molecular analysis to test fundamental hypotheses in microbial ecology. He has also set up core molecular laboratories at Argonne National Laboratory, University of Chicago and UCSD, as well as running his own molecular genomics laboratory at all 3 locations.

He co-founded the Earth Microbiome Project and American Gut Project. He has authored more than 350 peer reviewed publications and book chapters on microbial ecology. He is the founding Editor in Chief of mSystems journal. In 2014 he was recognized on Crain's Business Chicago's 40 Under 40 List, and in 2015 he was listed as one of the 50 most influential scientists by Business Insider, and in the Brilliant Ten by Popular Scientist. In 2016 he won the Altemeier Prize from the Surgical Infection Society, and the WH Pierce Prize from the Society for Applied Microbiology for research excellence. In 2019 he was elected to the Philosophical Society of Washington. He also co-authored "Dirt is Good" published in 2017, a popular science guide to the microbiome and children's health. He founded BiomeSense Inc in 2018 to produce automated microbiome sensors.

Edward F. DeLong, Ph.D

Professor, Daniel K. Inouye Center for Microbial Oceanography: Research and Education University of Hawaii, Manoa, SOEST

Prof. Edward Francis DeLong received his Bachelor of Science in Bacteriology at UC Davis, and Ph.D. in Marine Biology at Scripps Institute of Oceanography at the UC San Diego. He was a Professor at UC Santa Barbara in the Department of Ecology for seven years, Science Chair at the Monterey Bay Aquarium Research Institute for seven years, and a Professor at MIT in the Department of Civil and Environmental Engineering, and the Department Biological Engineering for 10 years. For the past 8 years DeLong has served as a Professor of Oceanography at the University of Hawaii, Manoa. There, DeLong serves as co-Director for the Center for Microbial Oceanography: Research and Education (C-MORE). DeLong is a recipient of: The Vladimir Ivanovich Vernadsky Medal of the European Geosciences Union (2008), the Proctor and Gamble Award in Applied and Environmental Microbiology (2008), the ASM D.C. White Research and Mentoring Award (2009), the UC Davis College of Biological Sciences Outstanding Alumni Award (2012), and the A. G. Huntsman Medal for Excellence in Marine Science (2014). DeLong is an elected member of the U. S. National Academy of Sciences, and an elected Fellow in the American Academy of Microbiology, the American Academy of Arts and Sciences, the American Association for the Advancement of Science, and the European Molecular Biology Organization. DeLong served as the President of the International Society of Microbial Ecology from 2018-2020, and now serves as its acting Past President, until August 2022.

Andreas Bechthold, Ph,D

Professor
University of Freiberg, Germany

Prof. Dr. Andreas Bechthold is currently serving as Director of the Institute for Pharmaceutical Sciences and Head of the Department of Pharmaceutical Biology and Biotechnology at Freiburg University since 2001. He has also served as Dean of various Board Committees since then. He is also member of many academic societies in University of Freiberg. He has been awarded with various scholarships and awards including Phoenix-Pharmaceutical Science Prize for the year 2006 and 2021. His research interest focusses on Microbiology and Pharmaceutical Sciences. He has published more than 190 research articles, reviews and book chapters with around 8000 citations with a h-index of 52.

Professor Hilary Lappin-Scott, OBE

Professor, Cardiff University
Founder and Director, Lappin-scott Consulting Ltd.

Hilary Lappin-Scott is an Honorary Distinguished Professor at Cardiff University in the UK. She was the Senior Pro-Vice Chancellor at Swansea University, after a 20 year research career at Exeter University. During her career Professor Lappin-Scott has been the elected President of three learned societies, the Microbiology Society UK (formerly the Society of General Microbiology), the International Society for Microbial Ecology (ISME) and currently is the President of the Federation of European Microbiological Societies. She was a Plenary speaker at the AMI a few years ago.

Professor Lappin-Scott's research group has worked on unravelling the complexity of interactions within biofilms and the molecular mechanisms of survival within biofilms, as well as the survival of microbes and biodegradation of pollutants in natural environments. She has supervised over 50 early career researchers to higher degrees. More recently Professor Lappin-Scott has focused on supporting women in STEM and speaks globally on such issues. Professor Lappin-Scott was awarded an OBE in 2018 for her contributions to microbiology and supporting women in STEM.

Dr. Craig Cary

Professor, School of Science
University of Waikato

Dr Craig Cary is a microbial ecologist and a Professor in the School of Science at the University of Waikato. He completed his Bachelor of Science degree at the Florida Institute of Technology in 1976, a Master of Science (MSc) at San Diego State University in 1982, and a PhD at the University of California, San Diego's Scripps Institution of Oceanography in 1989. Craig then went on to do his postdoctoral work as a Research Assistant Professor at Oregon State University for the next four years. He took his first academic position at The University of Delaware, the USA, in 1994 until moving to New Zealand and the University of Waikato in 2004. His research for more than 30 years has focused on studying microbial life in extreme environments. He has participated in over 29 deep-sea expeditions to hydrothermal vents, including over 45 dives in deep ocean research submersibles. His work includes 18 seasons in Antarctica with over 24 deployments to study microbial life in polar deserts, thought to be the coldest, driest place on earth. Craig is currently researching microbial communities that inhabit the high-temperature soils on the summit of Mt. Erebus in Antarctica, the most southern active volcano on the planet. He leads a team at the University of Waikato's International Centre for Terrestrial Antarctic Research (ICTAR) and is currently an Assistant Vice-Chancellor at the University of Waikato. Craig‘s research includes the use of advanced molecular genomic, metagenomic, and metatranscriptomic tools to survey the composition, structure and function of extreme microbial systems. He is the Director of the Thermophile Research Unit at the University of Waikato and currently has 8 PhD students and four postdocs researching various government-supported projects focused on New Zealand and Antarctica.

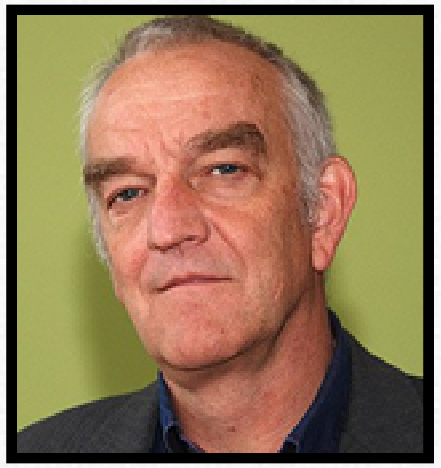
Hauke Smidt, Ph.D

Head, Laboratory of Microbiology,
Wageningen Univ. & Research
Stippeneng 4, 6708 WE Wageningen, The Netherlands

Prof. Dr. Hauke Smidt (1967, MSc 1995 in Biotechnology, TU Braunschweig, Germany; PhD 2001 in Microbiology, WUR) is an expert in microbiome research. Since 2003, Hauke Smidt heads the Microbial Ecology Group at the Laboratory of Microbiology, Wageningen University & Research. His research focuses on the integrated application of innovative cultivation and functional genomics-based methods to study composition and activity of microbial communities. Key areas of interest are addressed within national and international multi-investigator consortia, and include i) Microbiota associated with the intestinal tract in humans, production animals and wildlife ii) Microbial communities in environmental biotechnology, and iii) Microbes and their

cellular biomarkers as proxies for ecosystem life history & environmental change. In this context, research in the Smidt group increasingly follows a OneHealth philosophy that links environmental, human and animal health, including but not limited to the spread of antibiotic resistant bacteria and their genes.

Hauke Smidt currently supervises approximately 20 PhD students in national and EU projects. In 2008, Hauke Smidt has been appointed Visiting Professor at Nanjing Agricultural University, and since 2010, he holds a Personal Chair in "Complex Microbial Ecosystems" at Wageningen University. He is editor in chief of ISME Communications and senior editor of Microbiome and Animal Microbiome. Since 2020, Hauke Smidt is Scientific Director of the UNLOCK research infrastructure for microbiome research, which has received 15M€ funding from the Dutch Research Council (NWO) in 2020 for the coming 10 years.



Hans H Richnow, Ph.D

Head, Department Isotope Biogeochemistry, Helmholtz Centre for Environmental Research - UFZ, Germany.

Professor Hans Richnow studied Geology at the University of Hamburg (Diploma in Geology 1986) and received his PhD (Dr. rer. nat.) in Geoscience at the Faculty of Geosciences University of Hamburg in 1991. He completed his Habilitation in Geochemistry in 1998 (University of Hamburg, Faculty of Geosciences). Since 2004 his is Head of the Department Isotope Biogeochemistry – Helmholtz Centre for Environmental Research – UFZ. He established the Centre for Chemical Microscopy – ProVIS at the Helmholtz Centre for Environmental Research in 2015 a unique facility with high-end analytical equipment for analysis of biogeochemical processes. Dr. Richnow has published more than 310 articles and book chapters and belongs to the frequently cited scientist in Germany. (In Oct 2021 his h-factor was 59 and his work received more than 11.550 citations, source Web of Science, Thomson Reuters). He is a member of the editorial board of the Journal of Contaminant Hydrology, Frontiers in Microbiology and a frequent reviewer of national and international journals. He serves as the evaluator for scientific projects from various funding agencies (European Community, German Research Foundation, Swiss National Science Foundation, FNR – Luxembourg National Research Fund, NOW Netherlands, ANR France, NSC Poland, Chinese Academy of Sciences (CAS), and others).

His research interest and expertise is related to development of stable isotope fractionation concepts for tracing chemicals in the environment, analysis of structure, function and activity of microbial communities governing biogeochemical processes and analysis of the spatial dimension of biogeochemical reaction (e.g. biofilms, metal corrosion, mineral microbe interaction, rhizosphere processes.

David Van De Vijver, Ph.D

Associate Professor, Viroscience department
Erasmus Medical Centre, Rotterdam, the Netherlands

David van de Vijver is an associate professor at the viroscience department of the Erasmus Medical Centre in Rotterdam, the Netherlands. His research focuses on the impact of antiretroviral and antiviral drugs on prevention of viral diseases and on the emergence and transmission of drug resistance. He is an advisor to WHO on HIV drug resistance. Dr van de Vijver is the coordinator of the Querido honors program for medical students at Erasmus University. Dr van de Vijver has been the author of over 100 publications which have been published in journals such as Lancet Infectious diseases, Lancet regional health, Science, Clinical infectious diseases, AIDS and the journal of infectious diseases. Dr van de Vijver is the principal investigator of the NIH funded project "Novel mechanisms contributing to failure of dolutegravir-containing cART in clinical practice"

Jizhong Zhou, Ph.D

Professor,
University of Oklahoma, United States.

Dr. Jizhong Zhou is a George Lynn Cross Research Professor and Presidential Professor in the Department of Microbiology and Plant Biology, School of Civil Engineering and Environmental Sciences, and Director for the Institute for Environmental Genomics, University of Oklahoma, Norman, OK. He is also an Adjunct Senior Scientist at Earth and Environmental Sciences, Lawrence Berkeley National Laboratory, and an Adjunct Professor at School of Environment, Tsinghua University. He has authored numerous publications, with total citations of > 55,000 and H-index of 123 (Google Scholar), on microbial genomics, genomic technologies, microbial ecology, molecular evolution, bioinformatics, systems microbiology, network ecology, and ecosystem modeling, in the fields of climate change, groundwater bioremediation, wastewater treatments, bioenergy, and theoretical ecology. He was recognized as a global influential researcher by all three major complementary metrics: (i) 2018-2020, Global Highly Cited Researcher (top 0.1%) in microbiology, (ii) 2020 World's most cited researcher (99.9% percentile) across all science & engineering fields, and (iii) most highly cited researcher (H-index > 100) according to Google Scholar Citations. He received the 2019 ASM Award for Environmental Research for recognizing an outstanding scientist with distinguished research achievements in microbial ecology and environmental microbiology, Ernest Orlando Lawrence Award in 2014 – DOE's scientific award established by President Dwight Eisenhower in 1959, R&D 100 Award in 2009 as one of 100 most innovative scientific and technological breakthroughs, Federal Laboratory Consortium (Southeast) Award for Excellence in Technology Transfer, 2005, and Presidential Early Career Award for Scientists and Engineers in 2001. He is an Editor-in-Chief for mLife, a senior Editor for ISME J, an Associate Editor for Microbiome, and a former Senior Editor for mBio and Applied and Environmental Microbiology. He is a Fellow of International Water Association, American Academy of Microbiology, Ecological Society of America, and American Association for Advancement of Science.

Louis-Marie Bobay , Ph.D.

Assistant Professor, Biology department
University of North Carolina Greensboro

Dr. Louis-Marie Bobay is an Assistant Professor in the Biology department at the University of North Carolina Greensboro since 2018. His background integrates molecular biology, microbiology, evolutionary biology, genomics, and bioinformatics. During his PhD at Pasteur institute (Paris, France), he worked on the evolution of prophages in bacteria and developed expertise in microbial evolution, population genetics and bioinformatics. As a postdoctoral fellow at UT Austin, he started working on recombination in bacteria and developed approaches that use the patterns of recombination to infer species borders in bacteria. Dr. Bobay is now leading diverse projects at UNCG. He is developing new approaches to infer recombination rates in bacteria using Approximate Bayesian Computation (ABC) and Machine learning. He is also working on adaptive evolution and the dynamic of gene diversity in bacteria.

Anushree Malik, Ph.D.

Institute Chair Professor
Centre for Rural Development and Technology
Indian Institute of Technology (IIT) Delhi

Professor Anushree Malik is currently Institute Chair Professor, Centre for Rural Development and Technology at the Indian Institute of Technology (IIT) Delhi. Her lab is credited with highly cited innovations in Environmental Biotechnology such as robust strains/microbial consortia, easily storage and transportable formulations and low cost bioreactor designs. Advance research on algal mediated wastewater treatment, CO2 sequestration, biogas/biocrude development and a novel fungal bioharvesting process have been delivered. Developed bioreactors are being tested on-site to treat Barapullah drain water and agricultural fields at IARI fields. She received DST-Lockheed Martin India Innovation Growth Program (IIGP) Award for developing unique mycotablets for decolorization of dye wastewater. The pilot scale on-site validation of the technology for the treatment of extremely harsh textile effluents has been accomplished in collaboration with a leading Textile Industry. Prof. Malik has filed 5 patents, has more than 200 scientific papers with around 8975 citations, h-INDEX: 44; i-10 INDEX: 116. She is a recipient of prestigious Japan Society for Promotion of Science (JSPS) fellowship (2002) and Fellow Award of BRSI (2019). In 2020, she is recognized as top 2% scientist from India all over the world under the subject area, "Biotechnology" with 154th rank.

Mrutyunjay Suar, PhD

Director General-R&D, KIIT University &
CEO, KIIT Technology Business Incubator
Bhubaneswar, Odisha

Dr Mrutyunjay Suar is the Director General of R&D at KIIT University and the CEO of KIIT Technology Business Incubator (KIIT-TBI). An entrepreneurial professor with PhD in Molecular Microbiology from University of Delhi in the year 2003 and trained as postdoc at ETH Zurich, Switzerland (Feb 2004-June 2007). He returned to India and established the School of Biotechnology in 2007 under KIIT University which became a Centre of excellence awarded by DBT, GoI. He also established KIIT-TBI, promoting deep tech start-up companies.

Under his leadership, KIIT-TBI nurtured more than 230 start-up companies in last 10 years and created 4000+ jobs and established Centre of Excellence in incubation in the area of Digital Health, Diagnostics & Precision agriculture, supported by Department of Sc & Tech, Govt of India. He is a passionate mentor and has been deeply involved mentoring deep-tech startup companies and helped them to take them through their journey from ideation to enterprise creation.

He has received several recognitions including Samanta Chandrasekhar Award-2019 from Odisha Bigyan Academy, American Society of Microbiology (ASM) Professorship award in 2012 and visited UCLA, USA, GP Chatterjee memorial award during 102nd Indian Science Congress, Future young technical leaders by STARS Switzerland in 2010. He also attended Global Entrepreneurship leadership Symposium at HAAS Business School, USA and visited UC Berkley.

Appa Rao Podile, PhD

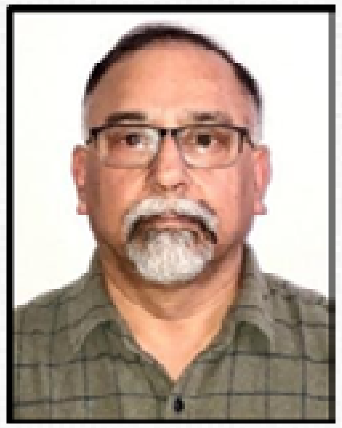
Vice Chancellor
University of Hyderabad

Professor Appa Rao Podile has over 32 years of teaching and research experience. He served as the Vice Chancellor of the University of Hyderabad and is currently a Senior Professor. He works in the area of molecular plant-microbe interactions, with a more recent focus on the soil and crop microbiome of legumes. His research group critically examines the chemical signals in plant-microbe interactions with special emphasis on chitooligosaccharides and root exudates.

Professor Podile is an elected Fellow of all major science academies of India including Indian National Science Academy, Indian Academy of Sciences, Bangalore, National Academy of Agricultural Sciences, New Delhi, National Academy of Sciences, Allahabad, Association of Microbiologists of India, New Delhi, and founding Fellow of Telangana Academy of Sciences, Hyderabad. Professor Podile served as President of the Association of Microbiologists of India.

He is a recipient of the prestigious J.C. Bose Fellowship from DST, Tata Innovation Fellowship from DBT, K.C. Mehta Memorial Award in Crop Protection from National Academy of Agricultural Sciences, Rangaswami Award in Agricultural Microbiology from the Association of Microbiologists of India, Outstanding Young Scientist Award from the Indian Society of Mycology and Plant Pathology, and Goyal Science Foundation's Rajib Goyal Young Scientist Award in Agriculture. Indian Science Congress Association has conferred the Millennium Plaque of Honour, and Dr. Ram Manohar Lohia Avadh University, Faizabad, U.P. conferred an Honorary Doctor of Science on Prof Podile.

A committed teacher, Prof Podile has guided 24 students towards their PhDs, besides 4 M.Phils. At present, 5 Ph.D. students and 2 Post-Doctoral Fellows work in his group. Currently, Prof Podile's lab is supported through a SERB grant and the J.C. Bose Fellowship from DST, with a major research grant in nanotechnology from DBT. Prof Podile has a formidable publication and citation record, with about 110 papers in high-impact journals and about 25 book chapters with over 4400 citations with an H-index of 38.



V.C. Kalia, Ph.D

NRF Fellow, Konkuk University, South Korea

Dr. Kalia is currently working as Professor at Konkuk University, Seoul, Korea. His research interests include Microbial Diversity, Bioenergy, Genomics and Quorum Sensing. He is the Fellow of the National Academy of Sciences (FNASc), with 9964 citations and an h-index of 54. Dr. Kalia has 170 publications in prestigious journals to his credit and has been instrumental in publishing 14 edited books in Springer Nature. He is the editor-in-chief of Indian Journal of Microbiology. He is currently serving as the editor of PLoS ONE and Journal of Microbiology and Biotechnology. Dr. Kalia has been conferred with prestigious fellowships from the Danish Government, French Govt., Korean Govt., and American Society

Agnieszka Dybala-Defratyka, Ph.D.

Associate Professor,
Lodz University of Technology, Poland

Dr. Agnieszka Dybala-Defratyka received her Ph.D. Degree in Chemistry in 2003 from the Lodz University of Technology, Poland. She spent different periods of her scientific career in laboratories at University of Nebraska-Lincoln (1998-1999), University of Minnesota, Minneapolis (2002, 2011-2012 as a Fulbright Scholar).

From 2016 she is an Associate Professor at the Faculty of Chemistry, Lodz University of Technology where she works as a researcher and academic teacher. In her professional career she was also involved in establishing and running a scientific journal devoted to broad chemistry problems. Her research interests include modeling enzymatic reactions and their chemical models. In order to elucidate their mechanisms she utilizes isotope effects determined theoretically and compares them to available experimental data.

Kalai Mathee, BSc, MSc, PhD, MPH

Professor of Molecular Biology and Infectious Diseases, Herbert Wertheim College of Medicine, Florida International University, Miami, USA

Dr. Kalai Mathee is the first Florida International University (FIU) faculty member inducted as a Fellow of the American Academy of Microbiology. Mathee is a professor and researcher at the FIU Herbert Wertheim College of Medicine (HWCOM). Of the two Malaysians ever inducted, she is the second and the first woman who was also educated in her vernacular language of Tamil.

Mathee received her PhD in Microbiology and Immunology (focus on molecular microbiology) at the University of Tennessee, Memphis in 1992, and Masters in Public Health, majoring in health policy and management in 2018 from Florida International University. A native of Malaysia, she obtained a Bachelor of Science in Genetics (1984) and a Master of Science (1986) in Microbial Genetics from the University of Malaya.

Mathee joined FIU in 1999 as an assistant professor in the Department of Biological Sciences. When the FIU medical school was created, she became the first founding faculty and the founding chair of the HWCOM Department of Molecular Microbiology and Infectious Diseases. She rose up to the rank of Professor in 2010. She founded the FIU Global Health Conference in 2011 and the Global Health Consortium in 2014. In 2011, she received the Faculty Award for Excellence in Mentorship. That was topped by the 2011 President's Council Worlds Ahead Faculty Award, the highest honor at FIU. In 2014, she was one of the inaugural recipients of the international New England Biolabs Passion in Science Award for exemplary scientific mentorship and advocacy.

She has mentored 160+ individuals from professors to middle-school students. Along with her mentees, she has published more than 130 articles and several book chapters in the fields of alginate gene regulation, antimicrobial resistance, microbiome (soil, lung, gut and vaginal), alternate therapeutics, forensic science, comparative genomics, and bioinformatics. She has five patents to her credit. She has given 120+ lectures across the globe. She also serves as the editor-in-chief along with Norman Fry of Public Health England of the Journal of Medical Microbiology, the first international editor in its 50-year history.

Bettina Sonntag

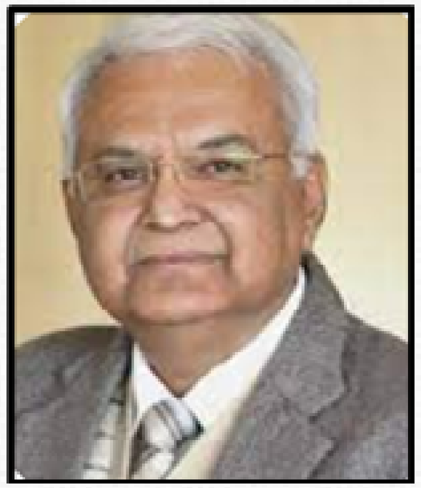
Senior Scientist,
University of Innsbruck, Austria

Dr. Sonntag is Head of the Research group 'Ciliate ecology and taxonomy' Research Department for Limnology. The research group focuses on the ecology, biodiversity and taxonomy of ciliates mainly in lakes, to understand the autecology of ciliates in planktonic food webs. She did her Ph.D. on "Seasonal dynamics of ciliates and flagellates in a deep oligotrophic lake (Traunsee, Upper Austria) influenced by saline and alkaline industrial sludge" from Institute of Zoology & Limnology at the Leopold-Franzens-University of Innsbruck (LFUI). Her most recent and ongoing research projects focuses on protist ecology, biodiversity and taxonomy in lakes. To understand the autecology of especially ciliates in planktonic food webs, she studied these protists on an alpha-taxonomic level including morphological, molecular and ecological approaches.

She has more than 40 publications in various International Journals with high impact factor. Dr. Sonntag has been awarded with various research grants and is the editorial Board member of Frontiers in Microbiology and Biology.

Sanjay Kumar, PhD

Director
CSIR-IHBT, Palampur



Dr. Sanjay Kumar Joined CSIR-Institute of Himalayan Bioresource Technology as a Scientist in 1990; master's degree from G.B. Pant Univ. of Agric. and Technology, and PhD from IARI, New Delhi; received post-doctoral training at Texas Tech University (USA), Rothamsted Research (UK), and Kansas State University (USA).

His major research contributions include discovery of a novel carbon fixation pathway and its transplantation in a heterologous system to reduce photorespiratory losses leading to photosynthetic gain and yield enhancement (work lauded by international fraternity), discovery of autoclavable superoxide dismutase, its characterisation and modification, plant adaption mechanism at high altitude, cloning of genes for secondary metabolite synthesis and imparting stress tolerance, deciphering the mechanisms of winter dormancy and drought stress in tea, enumerating molecular aspects of secondary metabolism in medicinal plants for catechins, picrosides, steviosides, shikonins and podophyllotoxin biosynthesis. Significant contributions on transcriptome and genome sequencing of Himalayan plants and development of nutraceuticals using traditional/Ayurvedic knowledge. He vitalised several initiatives for empowering the farmers, which include successful procurement and introduction of asafoetida and Monk fruit in the country, introduction of saffron and apple in non-traditional areas and promoted aromatic and floriculture crops in mountain farming.

He holds several international patents and has >170 research/review articles, book chapters, edited book etc. Some of his key contributions have percolated to major reviews and book also.

Debajyoti Chakrobarty

Senior Scientist
CSIR-IGIB

Dr. Debojyoti Chakraborty holds a PhD in molecular biology from the Medical Faculty, Technical University of Dresden having completed his PhD at the Max Planck Institute of Molecular Cell Biology and Genetics. His research areas include therapeutic genome editing and stem cell biology. He focuses on developing precise tools for gene correction and next generation diagnosis and applies them in understanding brain function through cerebral organoids.

A. K. Saxena, Ph.D

Director
NBAIM

Dr. A.K. Saxena is working as Director, ICAR- National Bureau of Agriculturally Important Microorganisms, Mau. He joined Agricultural Research Services in 1989 and since then worked in various capacities at ICAR-IARI and ICAR-NBAIM. His major research interests are in the area of plant–microbe interactions and molecular diversity analysis of bacteria. He successfully transferred the microbe based technologies to entrepreneurs, leading to increased coverage of land under microbial inoculants. He has to his credit 190 Research publications and 38 book chapters. He is the recipient of Best Teacher award of IARI; XIV Shri Hari Krishan Shastri Memorial Award (2013), Distinguished Scientist Award from Asian PGPR Society (2014), Prof G. Rangasamy award of AMI (2015), Prof. Abrar Mustufa Khan Memorial award at IPS- AMU National Conference (2018), Prof. B.N. Johri award of AMI (2018), Prof K.S. Bilgrami award (2019) of SPR and Prof. S.R. Vyas Memorial award of AMI. Till date he has guided 9 Ph.D and 11 M.Sc students and at present guiding three Ph.D students. He was elected as fellow of National Academy of Agricultural Sciences, Academy of Microbiologists of India and Indian Mycological Society.

Dr.Anirban Roy Choudhury

Senior Principal Scientist,
CSIR-Institute of Microbial Technology, Sector 39 A,
Chandigarh

Dr. Anirban Roy Choudhury, a fermentation technologist obtained PhD from Jadavpur University, Kolkata. He has been working for past 15 years at the interface of academia and industry trying to gain knowledge and scientific insights through research with the objective of developing pilot scale fermentation processes. His group has contributed enormously in establishing and developing a state-of-the-art bioprocess and fermentation facility at the CSIR-Institute of Microbial Technology. Notably, he is one of the very few scientists who did realize the untapped potential of polysaccharides before they gained prominence and therefore, is now considered one of the pioneers in the field. Along the Government's 'Make in India' theme, his group has designed, and validated bioprocess of production including scale-up to 500 L fermenter of pullulan. This was a significant success of Dr. Anirban's group as the cost-effective and optimized large-scale production process utilizes agri-industrial residues as media component and commercialization of such a process would result in creating wealth from waste. Expectedly, the process is now ready for transfer and has drawn attention from numerous industries across the country.

Additionally, Dr. Anirban and his group have been actively pursuing research on isolation, characterization and development of various novel microbial polysaccharides. His group has reported marine bacteria-derived several new polysaccharides with remarkable industrial implications. More recently, his group has been venturing into developing materials from polysaccharides using a green chemistry approach. These materials have shown promising potential for replacing conventionally used synthetic and non-biodegradable polymers. His group has been able to develop intelligent hydrogels and nanogels from these biodegradable biopolymers, which can be of use in wastewater amelioration by removing industrial contaminants. With the prior experience of designing and developing polysaccharide-based nanoemulsions for delivery of curcumin, one of the most widely explored bioactive compounds, his group is presently involved in developing suitable delivery modes for the labile and lipophilic bioactive molecules. It is noteworthy that, Dr. Anirban's group has been able to consistently publish their scientific findings, which hold the basis of production, process optimization and application development of microbial polysaccharides, in journals of international repute.

Ganesh D. Saratale, Ph.D

Scientist,
Department of Food Science and Biotechnology
Dongguk University, Korea

Dr. Ganesh Dattatraya Saratale currently works as Associate Professor in the Department of Food Science and Biotechnology, Dongguk University, South Korea. He obtained Ph.D. degree in Biochemistry in 2006 and conducted postdoctoral research in Taiwan, South Korea and India. He has received numerous prestigious domestic and international academic awards including; meritorious Departmental research fellowship (during Ph.D., India), Young Scientist award (Govt. of India), Brain Korea-21 (BK-21) (South Korea) and also completed two major research projects related to Lignocellulosic biorefineries. He has more than 185 publications in peer-reviewed scientific journals with total citations more than 8300 and his H-index is 50 (Google Scholar) to his credit. He edited two books and also contributed 16 book chapters. His name was featured in Stanford University's global list of top 2% scientists for the year 2019 and 2020 in the Environmental Engineering field. He served as Editorial board member of many journals including Polymers, Applied Nano, Bioengineering International, Frontiers in Bioscience-Landmark, Nanomanufacturing and also worked as Guest Editor for International Journal of Hydrogen Energy and Bioresource Technology Reports (Elsevier). His major research focuses on the development of lignocellulosic biorefineries for biopolymers, hydrogen, ethanol and value added biochemicals production. His research interest as well devoted towards algal biofuels production, environmental biotechnology, bioelectrochemistry, nanotechnology and their application towards energy, environment, agriculture and medical fields. He also delivered keynote speeches and invited talks in various conferences, seminars and workshops.

Taifo Mahmud, Ph.D

Professor,
Oregon State University, United States

Dr. Taifo Mahmud is a Professor in the College of Pharmacy at Oregon State University (OSU). He is also Co-Founder and Chief Scientific Advisor of Gadusol Laboratories, Inc., and Managing Director of the International Indonesian Scholars Association for the United States and Canada. Prior to coming to OSU in 2003, he was a Research Assistant Professor (2000-2003) and Postdoctoral Research Associate (1997-2000) at the University of Washington. He received his Ph.D. (in 1997) and M.Sc. (in 1994) from Osaka University, and his Apothecary (in 1991) and B.S. (in 1989) from the University of North Sumatra. His group employs a multidisciplinary approach that utilizes cutting-edge technologies in molecular genetics, enzymology, and chemistry to produce novel pharmaceuticals. He has published over 100 peer-reviewed research articles, three book chapters, more than 250 conference abstracts and lectures and ten patent applications. His research program has been funded by various federal agencies in the U.S., such as NIH, NSF, and USDA, as well as foundations and pharmaceutical companies. Currently, he is Co-Director of an NIH T32 Training Program at the OSU College of Pharmacy. He has been a member of several Scientific Advisory Boards, Journal Editorial Boards, and Grant Proposal Review Panels. Dr. Mahmud has received a number of awards, including the Young Investigator Achievement Award from the American Society of Pharmacognosy (2006), the Phi Kappa Phi Emerging Scholar Award (2007), the OSU OnPoint Faculty of the Game (2014), and the OHSU Distinguished Faculty Research Award (2020). One of his inventions has led to the birth of Gadusol Laboratories, Inc., a biotech company that develops and produces natural sunscreens.

Eddie Cytryn, Ph.D

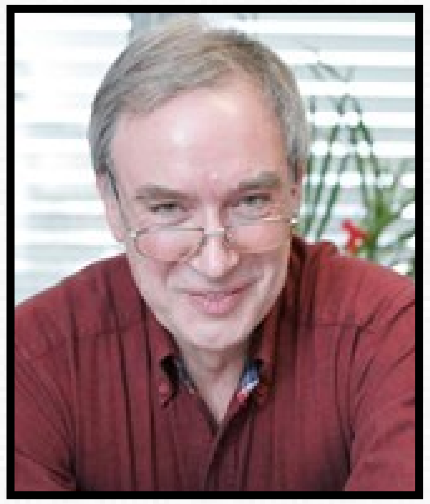
Head of the Deptt. of Soil Chem., Plant Nutrition & Microbiology
Institute of Soil, Water and Environmental Sciences
Volcani Center, Agricultural Research Organization

Dr. Cytryn is a Senior Researcher at the Institute of Soil, Water and Environmental Sciences at the Agricultural Research Organization (Volcanic Center), and a lecturer at the Hebrew University Faculty of Agriculture. He completed an MSc in Environmental Sciences and a PhD in Animal Sciences at the Hebrew University of Jerusalem, after which he spent two years as a postdoctoral fellow at the University of Minnesota. Dr. Cytryn's research centers on various aspects of environmental microbiology and microbial ecology. He is especially interested in plant-microbe interactions and environmental and agricultural dimensions of antimicrobial resistance (AMR). For the past ten years, his lab has investigated impacts of treated wastewater irrigation, animal husbandry and aquaculture on AMR, using isolation and culture independent methods to delineate microbial communities and antibiotic resistance genes. This includes application of next-generation sequencing based metagenomic approaches coupled to advanced bioinformatics pipelines. He has been active in several European research networks including COST Action ES1403- "New and emerging challenges and opportunities in wastewater reuse" and is currently the coordinator of the EU-PRIMA consortium "Decision support-based approach for sustainable water reuse application in agricultural production (DSWAP)". Dr. Cytryn has received numerous national and international grants and prizes. He has close to 50 publications in high impact peer-reviewed journals, and published six book chapters.

Karen Lloyd, Ph.D

Associate Professor,
University of Tennesse, Knoxville

Dr. Karen G. Lloyd received her undergraduate degree from Swarthmore College in Biochemistry, and switched to Marine Sciences for her MS and PhD both obtained with Dr. Andreas Teske at the University of North Carolina. She was a post-doctoral researcher for two and a half years with Dr. Bo Barker Jorgensen at the Center for Geomicrobiology at Aarhus University before starting her faculty position in the Microbiology Department of the University of Tennessee in Knoxville. Her research combines multi-omic and geochemical approaches to study deep subsurface microbes in a variety of environments, including marine sediments, terrestrial hot springs, and Arctic permafrost. She has given two TED talks and lives in Knoxville with her scientist husband and two children



Kenneth Timmis, Ph.D

Professor,
Technical University of Braunschweig, Germany

Prof. Kenneth Timmis has devoted his career to analysing and rebuilding the genetic machinery of bacteria, pioneering many of the essential tools of biotechnology. He has gone on to design and engineer bacterial strategies to remove environmental pollutants from contaminated soil and water.

His early studies of microbial molecular genetics clarified how bacteria reproduce their genetic material in the form of plasmids. He then demonstrated the 'minimal replicon', the minimum set of genes needed for a plasmid to reproduce — a concept central to cloning genetically altered bacteria for sequencing or biotechnology — and to clone entire metabolic pathways.

In parallel with his molecular approach, he has made detailed studies of microbial ecology, especially in relation to soils and hydrocarbons, enabling him to design novel biochemical pathways for bioremediation. In 2014, he proposed a strategy to stimulate economic revival in Southern European countries by harnessing the skills of young scientists to create new chemicals.

His Research focus is mainly on microbial genetics, microbial ecology, microbial pathogenesis, microbial biotechnology. Prof. Timmis has more than 400 publications with more than

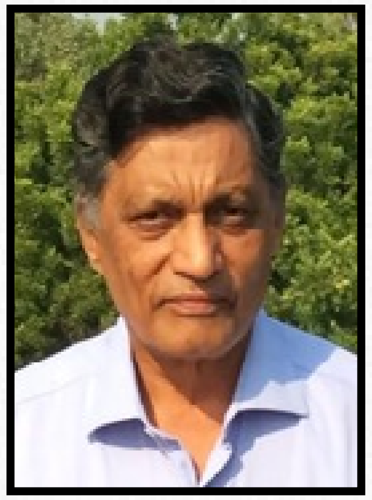
350 papers in international journals practicing peer review. h-index 119. He has been and continues to be the Editor of different scientific journals like he is the Founding Editor-in-Chief: Environmental Microbiology (1998-present), and Microbial Biotechnology (2007-present).
His current activities include the International Microbiology Literacy Initiative; digital DIY primary healthcare; microbial biotechnology for sustainable development goals.

Terry J McGenity, Ph.D

Professor, School of Life Sciences
University of Essex, UK

Terry McGenity is a Professor of Environmental Microbiology at the University of Essex, UK. His PhD, investigating the microbial ecology of ancient salt deposits (University of Leicester), was followed by postdoctoral positions at the Japan Marine Science and Technology Centre (JAMSTEC, Yokosuka) and the Postgraduate Research Institute for Sedimentology (University of Reading). He has broad interests in microbial ecology and diversity, particularly with respect to carbon cycling (especially the second most abundantly produced hydrocarbon in the atmosphere, isoprene), and is driven to better understand how microbes cope with, or flourish in hypersaline, desiccated and poly-extreme environments, and how they may remain alive over geological time. He is passionate about teaching microbiology, and has played a small part in the International Microbiology Literacy Initiative, led by Professor Ken Timmis.

Rup Lal, PhD



ISME Ambassador & NASI Senior Scientist Platinum Jubilee Fellow,
The Energy and Resources Institute, New Delhi

Prof. Rup Lal is the NASI Senior Scientist Platinum Jubilee fellow at The Energy and Resources Insititute, IHC Complex, New Delhi. He is the Fellow of Indian National Science Academy (INSA), New Delhi (FNA), Fellow of National Academy of Sciences, Allahabad, India (FNASc), Fellow of National Academy of Agricultural Sciences (FNAAS) and the Fellow, Academy of Microbiological Sciences (FAMSc), India. He has over 40 years longstanding experience in teaching, administration and research. He has supervised nearly 70 Ph.D. thesis and mentored more than 120 M.Sc/M. Tech and under-graduate students. Prof. Rup Lal specialized himself in the area of microbial diversity, genomics and metagenomics. Prof. Lal was Editor-in-Chief of Indian Journal of Microbiology (2006-2013) and also serving as a member of the editorial board in various leading scientific journals like mSystems, Environmental Microbiology, Environmental Microbiology Reports, BMC Biotechnology, BMC Biochemistry, Microbial Biotechnology and many more. He has over 200 publications in peer-reviewed journals with 6915 ISI citations & h-index 42.Prof. Rup Lal was Chairman of Board of Research Studies (2008-2010), Head, Department of Zoology (2007-2010), Dean, Faculty of Science (2007-2010), Dean, Examination (2012-2016), Member of Executive Council and Academic Council and member of several national and international bodies. He is a member of various committees of DBT, DST, MOEFCC. Professor Lal is the recipient of several prestigious fellowships including the Alexander Von Humboldt Fellowship(Germany), DBT Overseas Fellowship and Indo-USASM Professorship in Microbiology. Presently, he is the Ambassador of ISME (International Society for Microbial Ecology), The Netherlands to the Indian Ocean Region.

Daniel McDonald, Ph.D.

Scientific Director, Microsetta Initiative and the American Gut Project
School of Medicine, UC, San Diego

Dr. Daniel McDonald is the Scientific Director for The Microsetta Initiative and the American Gut Project, run by the School of Medicine at UC San Diego. His research focuses on the complex microbial communities associated with humans, with the environment, and how to scale microbiome analysis to large sample sizes. He has been heavily involved in the development of popular computational tools, such as QIIME, Qiita, and PICRUSt, and redeveloped the commonly used phylogenetic algorithm, UniFrac, to support hundreds of thousands of microbiome samples. His publication record in human associated studies includes examining treatment naive inflammatory bowel disease patients, forensic uses of the microbiome, the identification of novel dietary parameters associated with microbial composition, and integration of multi-omic data. Dr. McDonald received a BS and PhD in Computer Science from the University of Colorado at Boulder.

Paola Scavone, PhD.

Associate Professor
Instituto de Investigaciones Biológicas Clemente Estable

Dr. Scavone is presently Associate Professor in Microbiology, Department of Microbiology, Instituto de Investigaciones Biológicas Clemente Estable, Montevideo, Uruguay. She was a Postdoctoral Fellow in the University of Brighton, UK. She is the President of Uruguayan Society of Microbiology, and also Member of Comicbacterias group and Microbial Literacy Initiative. She is also nominated as the Young Ambassador for Uruguay by the prestigious American Society of Microbiology.
Since 2000 Dr. Scavone has been working with uropathogenic P. mirabilis strains and have evaluated different strategies to prevent urinary tract infections. She has been working to evaluate the usage of fimbrial proteins as protective antigens against UTI using different bacterial delivery systems. Her areas of research and publication include biofilms, host-pathogen interaction and development of nanoparticles for biofilm prevention and eradication. Dr. Scavone has more than 36 publications in various journals of high impact factor and repute. She is also the Guest Associate Editor with Frontiers in Cellular and Infection Microbiology and has edited and reviewed numerous publications.

Robert Metcalf, Ph.D.

Associate Professor
Instituto de Investigaciones Biológicas Clemente Estable

Robert Metcalf is a Professor Emeritus at California State University, Sacramento, where he taught microbiology courses from 1970-2012. His expertise in solar cooking enabled him to travel to low-income countries to demonstrate that with sunshine and a simple solar cooker, there is an alternative to fire for cooking. He also demonstrated that contaminated water could be pasteurized when heated to 65°C using solar or fire to heat the water.

To overcome the difficulty of performing microbiology tests on water sources in low-income countries, he developed a compact Portable Microbiology Laboratory (PML) that includes the 10 ml Colilert P/A test and the 1.0 ml E. coli count Petrifilm used in the food industry. Overnight results correlate with WHO disease risk categories: low, moderate, high, and very high.

Metcalf works with the CBO Friends of the Old (FOTO) in Lower Nyakach, Kenya, teaching FOTO staff to bring evidence-based microbiology to the community level and replace myths about waterborne disease with science. Metcalf and FOTO received the IDEXX Water Humanitarian Award in 2018 and 2020. The FOTO strategy could be replicated worldwide. With a PML, anyone can be a water microbiologist.

Vivekanand Vivekanand, Ph.D

Assistant Professor
Malaviya National Institute of Technology, Jaipur

Dr Vivekanand is working as Head and Assistant Professor at Centre for Energy and Environment, Malaviya National Institute of Technology (MNIT) Jaipur, India. He has completed PhD from Indian Institute of Technology (IIT) Roorkee, India. He has been awarded with 'Ramalingaswami Re-Entry Fellow' (Highly prestigious fellowship from DBT – Govt. of India) and another highly prestigious 'National Doctoral Fellowship' from All India Council for Technical Education (AICTE), New Delhi and Institute Assistantship at IIT Roorkee, India. He was working as postdoctoral research scientist for 7 years in Sweden and Norway. At University of Gothenburg, Sweden he was awarded seed grant from 'The Royal Society of Arts and Sciences' Sweden to work on low-lignin oats. Subsequently he worked on 'Biomass to Bioenergy' projects with premier Norwegian Biomass Research Group at Norwegian University of Life Science at Norway's National Facility of Biogas. He has keen research interest and expertise in marine and terrestrial biomass, organic wastes, pretreatment, bioprocessing as well as its conversion for bioenergy applications. He is currently working on Indo-EU, Indo-Egypt, Indo- Austrian bioenergy projects as PI funded by DST and EU. Also, he has successfully completed ECR, RLS projects sponsored by DST, DBT. He is closely associated with Norwegian Centre for Bioenergy Research, Norwegian Institute for Agricultural & Environmental Research (NIBIO), SLU, Cambi and TINE AS for conducting biomass-based research targeting the development and advancement of upcoming generation of biofuels.

Presently, he has 69 international research articles (citations >2068, h-index 24) published in SCI international journals of high repute and impact, conferences (>29) and authored book chapters (>8). He was interviewed by University of Gothenburg, Sweden for extraordinary performance and DD Rajasthan.

Dr Vivekanand has recently been invited by The Research Council of Norway and DST-Govt. of India at Norwegian Institute of Bioeconomy Research, Oslo for expert talk. He has also been invited by Clean Water Norway, Nordic Centre in India, IIT Delhi, IFAT, IIT Indore, BHU Varanasi, Govt. College of Technology-Coimbatore (as Resource Person for Faculty Development Program), and many more prestigious institutes and universities for expert lectures and knowledge sharing.

Gunjan Pandey, Ph.D

Research Scientist
CSIRO, Australia

Gunjan did his PhD from the Institute of Microbial Technology (CSIR), Chandigarh in 2004 and immediately joined the Commonwealth Scientific and Industrial Research Organisation (CSIRO) in Canberra, Australia as a postdoctoral fellow. Gunjan was promoted to a research scientist in 2008 and to a senior research scientist in 2011. Most of Gunjan's research is focused on exploring and exploiting microbial gene-enzyme systems involved in degradation of natural and xenobiotic recalcitrant compounds. He has over 60 ISI listed publications.

Mohana Krishna Reddy Mudiam

Research Scientist
CSIRO, Australia

Dr. Mohana Krishna Reddy Mudiam completed his Masters in Chemistry from NIT, Warangal in 1999. He did his Ph.D. in Plant Metabolomics from Central Forensic Science Laboratory (Osmania University), Hyderabad in 2005 and joined as Scientist at CSIR-Indian Institute of Toxicology Research, Lucknow. He received a BOYSCAST fellowship to pursue his postdoctoral work at Johns Hopkins Medical Institutions, Baltimore/USA in 2007. He has 20 years of research experience in Analytical and Bioanalytical Chemistry with applications in Environmental, Health, Food, Pharmaceutical and Forensic Sciences. His group research interests are mainly focused in understanding the occurrence/fate, transport and accumulation of chemicals in Food, Environment and Biological samples using latest analytical and metabolomics approaches. Our efforts yielded several miniaturized analytical methods for the analysis of toxicants/contaminants in various food, biological and environmental matrices. He successfully established metabolomics in India as a comprehensive screening tool to understand/evaluating the (i) toxicity of xenobiotics in various model organisms,

(ii) effect of ripening agents on the fruit metabolome and (iii) metabolic profiles in plants through Phytometabolomics. Currently, he is focusing on establishing a GLP compliant analytical facility for Biosimilars characterization at CSIR-IICT, Hyderabad. Dr. Mudiam also looking after various activities in the capacity of Deputy Quality Manager of NABL accredited analytical facility, Faculty of AcSIR, NABL Technical Assessor and Member of Two Scientific Panels at FSSAI. He guided 8 Ph.Ds. so far and currently 11 Ph.D. students and 11 Project Staff including 2 RAs are working in his laboratory. He authored 96 publications in peer-reviewed international journals with more than 3050 citations (h index of 35). He is instrumental in conducting several analytical skill development programs and seminars at National and International level. He is looking after Business Development activities of the Analytical Department at CSIR-IICT. He is recipient of CSIR Technology Award for Innovation for his work on COVAXIN, Fellow of Andhra Pradesh Academy of Sciences (FAPAS), Fellow of Telangana Academy of Sciences (FTAS), Dr AK Singh Memorial Young Scientist Award, ABAP Young and Senior Scientist Awards and several other appreciations. He visited countries like USA, Germany, France, Australia, China and Taiwan as part of his scientific collaborations and/or assignments.

Natesan Manickam, Ph.D

Chief Scientist,
CSIR-Indian Institute of Toxicology Research

Prof. Natesan Manickam is a Chief Scientist at Indian Institute of Toxicology Research which is a national institute under the Council of Scientific & Industrial Research, Government of India. He is currently heading the 'environmental biotechnology division' and is also coordinator of 'environmental toxicology' group. Current research focus of Manickam includes bioremediation of persistent toxicants, eco-toxicology risk assessments, microbial genomics, and profiling of antimicrobial resistance from waste and river water streams. Recent research undertaken on national mission is Namami Gange (Clean Ganges-River) assessment of physico-chemical water quality parameters, microbial pathogens/diversity including the bacteriophage profiling. In an effort to restore the contaminated hazardous sites, a challenging filed remediation is chlorinated pesticide namely lindane (gammexane, hexachlorocyclohexane) is being implemented at a location near Lucknow, India to safeguard the communities living in near vicinity of the polluted site. Ecotoxicology based risk assessment using OECD approved test organisms is an integral part of the project to evaluate of safety of the soil. He has also developed two microbial technologies which are under field feasibility tests for developing eco-friendly process for remediation the pesticides. Very recently taken he has taken up studies on bioprospecting plastic degradation as plastic pollution has become a globally threat affecting the biodiversity and human health.

Pratyoosh Shukla, Ph.D,

Professor, School of Biotechnology, Institute of Science
Banaras Hindu University, Varanasi-221005, India

Prof. Pratyoosh Shukla is presently working as Professor at School of Biotechnology, Banaras Hindu University, Varanasi. Prior to joining BHU, he was working as Professor and Head, Department of Microbiology, Maharshi Dayanand University, Rohtak, India. He was awarded with Indo-USA Research Professor at University of Cincinnati, USA. He has been recently appointed as Visiting Guest Professor in South China University of Technology, Guangzhou China. Prof. Shukla recently received D.Sc. in Microbiology from Barkatullah University, Bhopal, India in 2020 and he did his Ph.D. in Microbiology from the Medicine faculty, A.P.S. University, Rewa, India in 2002. He was awarded with NRF- DUT Post-Doctoral Fellowship during 2008-2009 in Enzyme Technology at Durban University of Technology, Durban. His research areas include enzyme technology and protein bioinformatics. He has 19 years research and 21 years of teaching experience in reputed universities of India and abroad. He has written more than 28 book chapters, one patent, published more than 200 peer reviewed publications in reputed SCI journals like Trends in Biotechnology, Bioresource Technology, Advanced Functional Materials, Trends in Genetics, Trends in Microbiology, Current Opinion in Environmental Science & Health, Biotechnology Advances, Journal of Biological Engineering, Frontiers in Microbiology, Biotechnology for Biofuels, Critical Reviews in Biotechnology, Critical Reviews in Food Science and Nutrition, Critical Reviews in Microbiology, Frontiers in Plant Sciences, PLOS One, RSC Advances, Applied Microbiology and Biotechnology etc. He has written 8 books which are published by Springer, CRC Press and Elsevier including Editor for Springer Briefs in systems biology series. He has carried out more than 13 R&D projects funded by national and international agencies as PI/Co-PI including prestigious Erasmus grant by European Union (EU). He has more than 4800 citations with H-index of 40 and i10 index of 115. He was recently also featured among a list of Indian Researchers who were Top 2% in 2019 –Stanford Study). He is Fellow of National Academy of Agricultural Sciences (FNAAS), Fellow of Academy of Microbiological Sciences (FAMSc), Fellow of Biotech Research Society of India (FBRS). He has received several awards, including Received 'Prof. S.B. Saksena, Award, Top 10 Best Researcher of India, NRF-DUT Post-Doctoral Fellowship Award, Danisco India Award in Probiotics & Enzyme Technology, Selected as scientist in Southern Ocean Antarctica Expedition, AMI Platinum Jubilee Award, Alembic Award etc. He is also serving as Editor in Indian Journal of Microbiology (Springer), Scientific Reports, Academic Editor (PLOS One), Editor (BMC Microbiology), Editor (Protein and Peptide Letters) and as Editorial Board Member & Reviewer in many journals. He also served as General Secretary of the Association of Microbiologists of India (AMI), for two terms from 2014-2020.

Datta Madamwar, Ph.D

Scientific Advisor
Charotar University of Science & Technology
Changa 388 421, Anand, Gujarat, India

Professor Datta Madamwar is currently working as Scientific Advisor at Charotar University of Science & Technology, Changa, Anand, Gujarat. He obtained his Ph.D from BITS, Pilani. He is a former Professor and Head, Department of Biosciences and former Dean, Faculty of Science at Sardar Patel University, Vallabh Vidyanagar. He worked as a Post-Doctoral Fellow at TIFR, Mumbai, University of Frankfurt and University of Konstanz and also served at BITS, Pilani. Professor Madamwar is a Microbial Biotechnologist with diverse research interest. His main research focus is on Microbial Bioremediation, Environmental Biotechnology, Non-aqueous Enzymology, and Cyanobacterial Biotechnology. His major work involves in development of eco-sustainable biotechnological solutions for the treatment of hazardous industrial wastewaters. He is investigating the taxonomic profile and functional diversity of microbial community inhabiting industrially contaminated sites using –omics approach. He has provided a concept for the enzyme catalysis in apolar organic solvents without the loss of enzyme activity. He has reported various novel, efficient and rapid methods of purification of phycobiliproteins. This has laid to crystallization and structure determination of phycobiliproteins and deposited various structures in protein data bank.

He is a recipient of coveted honor of "Life Time Achievement Award" of Biotech Research Society of India (BRSI) for the year 2019 and a recipient of European Commission Visiting Scientist Fellowship, Fellow of International Bioprocessing Association, Fellow of Biotech Research Society of India, Fellow of Association of Microbiologists of India, Fellow of Association of Biotechnology and Pharmacy and Gujarat Science Academy, BHU-Centennial Award of BRSI and member of several academic bodies. Dr. Madamwar is a member of several task force and advisory committees of the National funding agencies like DBT, DST, GSBTM. He is also a member of editorial board of several national and international journals. Professor Madamwar has published more than 270 research papers, several book chapters and one provisional American Patent to his credit. He is having an h-index of 62 and i-10 index of 193 with more than 12350 citations. He is a well traveled researcher with his research visits and gave invited talks in several countries including Germany, UK, Austria, Switzerland, France, USA, Greece, Malaysia, Singapore, Brazil, China, Finland and many others.

Nageswara Rao Amanchi, PhD

Assistant Professor of Zoology
Osmania University

Dr. Nageswara Rao Amanchi is an Assistant Professor of Zoology at Osmania University, Nizam College (Autonomous), Hyderabad, Telangana State, India. He has Masters in Zoology and obtained his Ph.D. in Zoology from Osmania University in the year 2007. His research interests lie in the area of Ecotoxicology of pesticides, heavy metals, metagenomics & bioremediation. Two of his students have been awarded PhD and three are pursuing for PhD. He completed two research projects funded by UGC and DBT successfully and published his research findings in national and International repute journals. He has collaborated with researchers in other disciplines of Life sciences, particularly environmental Sciences, biotechnology for bioremediation of pollutants, and Applied Toxicology. He is the instructor for both Undergraduate and Post-graduate programmes for the past 16 years besides research experience. He has associated actively in organizing several of national and international conferences, seminars and workshops for upcoming researchers and students in the University. He is life member in several academic bodies and reviewer to Ecotoxicology and environmental safety.

Sunil Pabbi, Ph.D.

Head and Principal Scientist, Division of Microbiology
ICAR, New Delhi

Prof. Sunil Pabbi, M.Sc. Honours and Ph.D. (Microbiology) from Panjab University, Chandigarh, India and presently Head, Division of Microbiology at ICAR-Indian Agricultural Research Institute, New Delhi- 10012, INDIA has over 35 years experience in research and teaching with major contributions in applied microbiology/phycology especially on use of microalgae/cyanobacteria as biofertilizer and other value added products. Dr. Pabbi has developed a commercially viable protocol for BGA biofertilizer production and the technology licensed to a number of entrepreneurs leading to its large scale production and use. A process for obtaining high purity phycocyanin pigment from cyanobacteria having application in food, cosmetic, pharmaceutical and analytics has also been developed and a patent filed for the same. Dr. Pabbi has so far carried out 15 different research projects and has over 85 publications (both national and international), authored one and edited 6 books. He is recipient of Prof. Y S R K Sarma Memorial Award (2013) and Distinguished Scientist Award (2019) by Society for Plant Research and Prof. S R Vyas Memorial Award (2018) of Association of Microbiologists of India (AMI). He has guided several M.Sc. and Ph.D. students and was awarded Best Teacher Award of ICAR-IARI for excellence in teaching and Best Professor in Microbiology Award by Agriculture Innovation Congress and CMO Global. Prof. Pabbi is a member of several National/International societies in the field of biology and on the Executive Board of Association of Microbiologists of India, Phycological Society, India and on the editorial board of Scientific Journals of repute. He is also nominated as Distinguished Honorary Advisor and Expert member, Board of studies of several universities in India.

His current research interests include application of microalgae in bioindustry and bioenergy, nutraceutical and functional food preparation using Spirulina, molecular structure and stability analysis of cyanobacterial phycobiliproteins.

Ch. Venkata Ramana, Ph.D.

Professor, Department of Plant Sciences
University of Hyderabad

Dr. Ch. Venkat Ramana is a Professor at the Department of Plant Sciences, University of Hyderabad. He is a TATA Innovation Fellow, awardee of E.K. Janaki Ammal national award for Microbial Taxonomy and Elected Fellow of The National Academy of Science (FNASc). His bacterial discovery group focuses on the discovery of new taxa with novel functions.

Prof. Nataraja Karaba N, Ph.D.

Professor, Department of Crop Physiology
University of Agricultural Sciences Bangalore

Prof. Nataraja Karaba N, (MSc(Agri), PhD) is a Professor at the Department of Crop University of Agricultural Sciences Bangalore (UASB). He has worked as a Scientist in the Rubber Research Institute of India, Kerala and the Institute of Wood Science and Technology, (ICFRE-Dehradun) Bangalore. He was a DST-BOYSCAST postdoctoral fellow at the Department of Molecular, Cellular, and Developmental Biology, Yale University, USA. He was a Visiting Scientist at Plant Research International, Wageningen University (Netherlands), University of Groningen (Netherlands), and Visiting Professor at, University of Saskatchewan, Canada. He is the recipient of the Sir CV Raman Young Scientists Award from the Government of Karnataka and the prestigious INSA Teachers Award 2020, from the Indian National Science Academy, New Delhi. He serves as an expert member on the advisory panels of the Department of Science and Technology, Government of India, and Govt. of Karnataka. He is an Associate Chief-Editor of Plant Physiology Reports (Springer).

Prof. Nataraja's major research interest is to understand the molecular basis of plant responses to drought and other abiotic stresses. He has published more than 89 peer reviewed papers in high-impact journals (PNAS, USA; Trends in Ecology & Evolution; Phytomedicine; Molecular Breeding; Plant Biotechnology Journal, etc.) and 10 articles in books. As a continuation of his major focus on abiotic stress, his team has initiated research to explore endophytes as a potential tool in modulating crop responses to abiotic stresses.

Kapudeep Karmakar, Ph.D

Assistant Professor, Soil Microbiology
Uttar Banga Krishi Viswavidyalaya (UBKV), Coochbehar

Kapurdeep Karmakar is currently posted as Assistant Professor in Soil Microbiology at Uttar Banga Krishi Viswavidyalaya (UBKV), Coochbehar. He did his BSc and MSc in Agricultural Sciences (BCKV, West Bengal and GB Pant University, Uttarakhand respectively) and his PhD in Microbiology and Cell Biology from Indian Institute of Science, Bangalore. His research interest is understanding of the free-living life cycle of human pathogens in agricultural fields. While making progress in the research, he received the Young Scientist award from Dr K V Rao Scientific Society, Hyderabad and from UAS-B under World Bank Sponsored CAAST Program under NAHEP from ICAR. His current research work at UBKV deals with the identification of pathogenic metagenomes in various ecosystems for preventing food-borne disease outbreaks. His lab is also interested in understanding the CRISPR-Cas system in various PGPR strains, in order to use their potential in generating effective bio-control agents against soil dwelling human pathogens. The lab also focusses on developing multi-stress adapted PGPRs via directed evolution.

Praveen Rishi, Ph.D

Professor, Department of Microbiology,
Panjab University, Chandigarh

Prof. Rishi is currently working as Professor at Department of Microbiology, Panjab University, Chandigarh. She has over 30 years of teaching and research experience and has guided 28 PhD students. Her research interests include Medical Microbiology with special reference to biotherapeutics and diagnostics. She is the Fellow of Academy of Microbiological Sciences (FAMSc) and Indian Association of Biomedical Sciences (FABMS). Dr. Rishi has 145 publications in prestigious journals to her credit and has been instrumental in filing 6 patents. She is currently serving as the academic editor of PLoS ONE and Indian Journal of Microbiology. Prof. Rishi has been conferred with prestigious awards and fellowships, such as, Prof SR Vyas Memorial Award conferred by Association of Microbiologists of India at University of Hyderabad in Dec 2018; ICMR Dr. Y.S Narayana Oration Award for 2010, conferred in 2013, INSA Visiting Fellowship for year 2006-2007 and DBT Overseas Associateship by Ministry of Science and Technology (Govt. of India) for the year 2002-2003. She has held prestigious positions such as Dean, Faculty of Science, Panjab University, Chandigarh from 2015 to 2017, Chairperson, Department of Microbiology, Panjab University, Chandigarh (2014-2017) and is the President Elect of Association of Microbiologists of India for the year 2022-23.

U. Sivakumar, PhD

Department of Agricultural Microbiology
Tamil Nadu Agricultural University
Coimbatore, Tamil Nadu-641 003,India

Prof. Sivakumar Uthandi is a Professor of Agricultural Microbiology at Tamil Nadu Agricultural University (TNAU), Coimbatore, India; he received his basic, master's, and doctorate degrees from TNAU and gained Post-Doctoral experience at the University of Florida, USA. He was Dean of School of Post Graduate Studies, TNAU, Coimbatore. He has been a Visiting Associate Professor at the University of Florida, USA; and also visited Wageningen University, The Netherlands; BIC, Russian Academy of Sciences, Novosibirsk, Russia, and the University of Warwick, UK; AVRDC, Taiwan; and University of Jafna, Srilanka. He is now serving as Visiting Adjunct Professor at the University of Tokyo, Japan. With 25 years of teaching and research experience, he has about 127 research articles and obtained several recognitions in his academic and professional career, including 9 awards, 3 fellowships, and 4 patents (One –US and 2-Indian). He has authored more than 20 books, including edited and written and 15 book chapters. He is currently serving as a Chief Editor of 107 years old Madras Agricultural Journal. He is also known for several first reports such as archaeal laccase, root nodule associated endophytic yeast, microbiome of apoplast and guard cells, metabolites for plant signalling, etc. Recently he has been recognized as FRSB (Fellow of Royal Society of Biology) . He has established international collaboration with the Universities of Warwick, University of Wageningen, University of Florida, University of Tokyo, and Boreskow Institute of Catalysis, Russia. To his laurel, he has mobilized funds to a tune of INR 862 lakhs through various funding agencies ICAR, DBT, DST, and MHRD-FAST and offered 22 fellowships to students, which include 17 Masters and 5 Doctoral candidates.

Ajay Kumar, Ph.D

Assistant Professor,
Lovely Professional University, Punjab

Dr Ajay Kumar is currently working as Associate Professor in the Dept. of Industrial Microbiology at Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj (Uttar Pradesh). He pursued his Masters and PhD from CSK Himachal Pradesh Agriculture University, India where he worked on the development of liquid biofertilizers. During his PhD work he isolated and screened nitrogen fixers and phosphate solubilizers. Further, liquid biofertilizer formulations were prepared with efficient isolates and a survival study was conducted. He did his postdoctorate from North-West University, South Africa where his research was focused on food safety. In the postdoctorate his research was focused on molecular characterization of antibiotic resistant pathogenic bacteria isolated from food, water and cattle faecal samples. The characterization included the molecular profiling of antibiotic resistant genes, virulence genes and genetic fingerprinting. Dr Ajay has a vast teaching and research experience of ten years and supervised many UG and PG students for their research work. He has published many research papers and book chapters with National and International publisher of repute. Beside this, he also got patent for the development of liquid formulation which maintains longer shelf life of plant growth promoting bacteria. He also received prestigious Indian Summer Research Fellowship awarded by combined academy of sciences INSA, IAS and NAS.

Virginia Filipello, DVM, PhDScholar

Istituto Zooprofilattico Sperimentale della
Lombardia e dell'Emilia Romagna, Italy
Coimbatore, Tamil Nadu-641 003,India

Dr. Virginia Filipello, DVM, PhD, is a veterinarian in charge of the Food Control Laboratory of the Novara Chapter of the Istituto Zooprofilattico Sperimentale of Piedmont, Liguria, and Aosta Valley, and former researcher of the Istituto Zooprofilattico Sperimentale of Lombardy and Emilia-Romagna. She received her doctorate in Veterinary Sciences from the University of Turin, with a project on integrated listeriosis surveillance. She is working on foodborne pathogens and molecular epidemiology and is currently involved in research projects on L. monocytogenes, MRSA, and HEV. She is a specialist of the School in Technology and Pathology of Avian Species, Rabbits, and Wild Fauna of the University of Milan, during which she investigated HEV epidemiology in wild game. As part of the laboratory mandate she is involved in projects aimed at assisting Food Business Operators in dealing with problems linked to contamination by pathogenic and spoilage microbes.

Om Prakash, PhD

Scientist, NCMR-NCCS

Dr. Om Prakash is a Research Scientist and Curator of the anaerobic facility of the National Centre for Microbial Resource (NCMR) of the National Centre for Cell Science (NCCS) Pune, India. He received his M.Sc. degree in microbiology from Dr. RML Avadh University, Ayodhya and PhD in microbiology (2007) from University of Delhi under supervision of Prof. Rup Lal. Dr. Prakash conducted his 4.5 years of postdoctoral training in anaerobic microbiology from Florida State University, Tallahassee, FL, and Georgia Institute of Technology, Atlanta, USA, from the laboratory of Prof. Joel E. Kostka. After postdoctoral training, he joined the National Centre for Microbial Resource (NCMR), previously Microbial Culture Collection (MCC), in 2011. He has also worked as Research Faculty in Translational Science Laboratory (TSL) School of Biomedical Science, College of Medicine, Florida State University, under Department of Health Research (DHR) - Indian Council of Medical Research's (ICMR) supported long-term fellowship and senior Visiting Fellow in the Institute of Soil, Water and Environmental Sciences, Volcani Center, ARO-Israel under Indian National Science Academy (INSA) supported a bilateral program. Currently, he is serving as Chairman of the Subcommittee on Methanogenic Archaea of the International Committee on Systematics of Prokaryotes (ICSP). His area of interest is anaerobic microbiology. He is working on different aspects of anaerobes, including cultivation and characterization of tough to cultivate obligate anaerobic Bacteria and Archaea from diverse habitats, including landfill human-gut, clinical specimens. Fecal bio-banking, microbiome-preservation, anaerobic pathogenesis, and microbial response against antibiotics in anaerobic conditions are the main focus of his laboratory.

Dr. Atya Kapley

Principal Scientist
CSIR-NEERI

Dr. Atya Kapley has a strong biological research experience of 27 years, post PhD, she heads Environmental Biotechnology and Genomics Division at CSIR-NEERI. Her work focusses on two specific domains (i) Developing solutions based on basic research for environmental remediation, with specific reference to soil and water niche and (ii) Taking science to society. She has taken genomics research out of the lab and into the field by using genomic tools to understand target niches like soil, sludge or wastewater and develop bioremediation option for polluted niches. Using this approach, she has led a number of field scale projects at NEERI. She is now leading a team from different institutes that will develop the first ever microbial map of the holy Ganges, from Gangotri to Diamond Harbour. This will be the first ever baseline map of a river in our country.

Besides working in core subject areas, Atya is committed to creating awareness amongst citizens on responsibility sharing of environmental management. She has organized various awareness and outreach programs for the common man to showcase the threats to human health if the environment is not clean.

She works extensively to empower women in science. Atya is the Vice President of the Organization for Women in Science for the Developing World (OWSD), Asia Pacific region. OWSD is unit of UNESCO with Headquaters at TWAS, Trieste, Italy, that works to empower women in science. She has organized an international conference and various national events to connect and empower women in science and address the lack of women leadership in the country.

Prof. Rama Chaudhary, MD

Professor and Head, Department of Microbiology,
All India Institute of Medical Sciences, New Delhi
International Ambassador of American Society for Microbiology to India

Prof. Rama Chaudhry has done her MBBS from Lady Hardinge Medical College and MD in Microbiology from AIIMS, New Delhi. She has experience of over 35 years in the field of academics and medical-research, to her credit, she has over 200 research papers published in journals of both national and international repute. She has been associated with the research advisory and project review committees of national funding sectors such as the DBT and ICMR. She has guided MD, DM, DMID, PhD and M.Sc. Students. Dr. Chaudhry is actively involved in the research on Mycoplasma infections, Vector borne diseases, Antimicrobial resistance, gut microbiota and anaerobic bacteriology as well as bacteriophages. Her research work is published in reputed journals such as Nature, Lancet, Emerging Infectious diseases, British Medical journal, American J tropical medicine and hygiene etc. Dr Chaudhry is currently serving as International Ambassador of American Society for Microbiology to India and member of ASM Ambassadors leadership circle. She was past secretary and President of Indian Association of Mycoplasmologists, currently editor of IAM newsletter. Dr. Chaudhry is member of scientific advisory groups of various organizations and reviewer of journals such as JCM, EID etc.

She has been awarded SS Kelkar Gold medal in 2003, Indo-US-Professorship Award by American Society for Microbiology, USA 2006. She received the IAM fellow award for her significant contribution in the field of Mycoplasma and Indian Association of Medical Microbiologists (IAMM) Endowment Award in 2015.

Dr. K. Annapurna

Former Head
Division of Microbiology
ICAR-Indian Agricultural Research Institute

Dr. K. Annapurna was Head, Division of Microbiology, ICAR-Indian Agricultural Research Institute, India. She obtained her M.Sc. (1982) and Ph.D. (1986) degrees in Microbiology from Indian Agricultural Research Institute (IARI), New Delhi, India. She has been a pioneer researcher in the field of molecular ecology of legume - Rhizobium symbiosis, Azospirillum, Plant growth-promoting rhizobacteria (PGPR) and initiated work on soybean rhizobial genetic diversity. She has successfully developed a PCR based diagnostic marker for rapid detection of soybean Bradyrhizobium. Her research initiatives on WGS for symbiotic (Bradyrhizobium yuanmingense KAS-1) and free-living diazotrophs; Pseudomonas stutzeri KMS 55, Bacillus paralicheniformis KMS 80 and Azotobacter chroococcum W5 have opened possibilities for enhancing the N2-fixation potential through biotechnological interventions. Another diazotroph Azotobacter chroococcum HKD 15 strain with an ability to fix N2 constitutively has been developed, which has a great environmental, agronomical and economic significance. Her research into endophytes and soil metagenomics have identified potent biocontrol agents and genes coding for different antibiotics. She has also initiated research in the new area of "Plant and Soil Microbiome". Under her guidance, application of biofertilizers in unconventional crops has increased especially VAM. She is instrumental in commercializing the Biofertilizer Technology and Pusa Decomposer Technology in the Division of Microbiology and to date, the various technologies have been licensed to over 50 companies from IARI, India.

She has guided 27 M.Sc. and Ph.D. students, conducted many International and National workshops, and has been PI for many DBT, DST and ICAR funded research programs. She had collaborative projects : Indo-Australian, Indo-Austrian, Indo-UK, Indo-US and Indo-German. She is recipient of IARI Best Teacher Award (for excellence in Teaching), DBT Recognition for Women Leaders in Biosciences, Women Leadership Award by Indian Chapter of Asian

PGPR Society, Endeavour Executive Award (Australia), INSA Award (INSA, India), Award for Excellence in PGPR Research (Asian PGPR Society for Sustainable Agriculture) and Eminent Scientist Award (DRASS). She is Fellow of Microbiologist Society of India (FAMSc) and recipient of "Life Time Achievement Award from VIWA (2021). She has edited books on Microbial and Eco-friendly Solutions.

Gaurav Sharma, Ph.D

DST-INSPIRE Faculty Fellow
Institute of Bioinformatics and Applied Biotechnology, Bengaluru

Dr. Sharma is a DST-INSPIRE Faculty Scientist at the Institute of Bioinformatics and Applied Biotechnology, Bengaluru, since August 2019. Earlier in 2011, he completed his M.Sc. in Biotechnology from the School of Biotechnology, Jawaharlal Nehru University, New Delhi, India. Later he was awarded the Ph.D. degree in Microbial Genomics from Jawaharlal Nehru University, New Delhi, while working with Dr. Srikrishna Subramanian at the Institute of Microbial Technology (IMTECH), a renowned CSIR institute in Chandigarh, India. To gain research experience, he also worked with Prof. Mitchell Singer as a Postdoctoral Researcher at the University of California, Davis, in the Department of Microbiology & Molecular Genetics at the College of Biological Sciences. The broad focus of his lab is on microbial genomics, transcriptomics, and evolution to understand the physiology of a few model organisms such as Myxobacteria and Vibrio. His lab is also interested in understanding the plant-microbe interactions within Indian traditional medicinal plants using high throughput microbiome approaches. During the last two years, his lab is also involved in SARS-CoV-2 genomics and evolution.

Dr. Sharma is also an Editor for Microbiology Spectrum (a prestigious American Society for Microbiology journal) and an Associate Editor for Genomics journal. He has also been awarded several prestigious awards such as the DST-INSPIRE Faculty award, AMI Best 'Faculty Oral Presentation' Award, European Molecular Biology Organization Travel Award, UC Davis Postdoctoral Scholar Association Travel Award, ASM Postdoctoral Travel Award, DBT International Travel Fellowship, etc., to name a few.

Roshan Kumar, Ph.D.

Department of Zoology, University of Delhi, New Delhi
Assistant Professor, Post-Graduate Department of Zoology, Magadh University, Bodhgaya, Bihar

Dr. Roshan Kumar is a native of Bihar. He obtained his B.Sc. (H) (2007-10) and M.Sc. (2010-12) degree in Zoology from the University of Delhi. He did his Ph.D. under the supervision of Prof. Rup Lal, Department of Zoology, DU in the year 2016. During his Ph.D., he was a visiting researcher at Helmholtz Centre for Environmental Research, Leipzig, Germany. After his Ph.D., he worked as a research associate (2017-18) at Centre for Environment Management of Degraded Ecosystem, University of Delhi. Thereafter, he worked as a Land O'lakes Post-Doctoral Fellow (2018-19) at the Department of Veterinary and Biomedical Sciences, South Dakota State University, SD, USA. Currently, he is working as Assistant Professor (September, 2019 onwards) at the Post Graduate Department of Zoology, Magadh University, Bodh Gaya, Bihar. His work mainly focuses on genomic and metagenomics uncovering the environmental and gut ecological aspects of microbiology. So far, he has more than 30 research /review publications and one book to his credit.

Shazia Haider , PhD

Assistant Professor
Jaypee Institute of Information Technology (JIIT)

Dr. Shazia Haider is an Assistant Professor in the Department of Biotechnology, Jaypee Institute of Information Technology (JIIT), Noida, Uttar Pradesh in 2019. She worked as a Senior research officer (SRO) in the Department of Neurology, AIIMS for two years. She also worked as an Assistant professor in the Department of Biotechnology, Sharda University and Research Associate in Delhi University for a year. She did her Ph.D. and Post-doc in the field of Bioinformatics from Jawaharlal Nehru University, New Delhi.

She had been awarded with project fellowships from different government funding agencies like DBT, DST, ICMR to pursue her research work. She was awarded prizes for most aesthetically pleasing network visualization in Cytoscape.

She has published her papers in reputed international journals like Briefing in Bioinformatics, Oxford, Scientific report, mSystems, Plos One, Frontier in Microbiology etc. Recently she published an E-letter in Science Journal.

Mansi Verma, Ph.D.

Assistant Professor,
Department of Zoology, Sri Venkateswara College
University of Delhi (South Campus)

Dr. Mansi Verma, Assistant Professor at Sri Venkateswara College, Delhi University, was born and brought up in India. She has completed Ph.D. in Molecular Biology in 2011 from University of Delhi. Dr. Mansi Verma is the recipient of AMI Young Scientist Award and has extensively worked on a soil dwelling microorganisms belonging to Phylum Actinobacteria. She was involved in sequencing genomes of two microorganisms of economic importance i.e., *Amycolatopsis mediterranei* S699 and Sphigobium indicum B90A. Presently, she is involved in comparative genome analysis of important human viruses like Dengue Virus and SARS-CoV-2. She has contributed around 30 research articles in journals of International reputation. Dr. Verma has also contributed 4 chapters of international repute, 1 of national reputation and 8 e-chapters to her credit. She has participated in more than 20 Conferences/ workshops and has been the invited speaker for many comnferences. She has successfully completed several projects as Principal Investigator. Recently, she has been awarded with Bill and Melinda Gates Abstract Award for ASM FEMS Conference.

Ujjwal Neogi Ph.D.

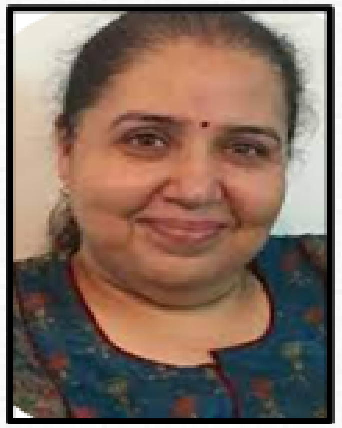
Associate Professor of Virology,
University of Missouri

Ujjwal Neogi, Ph. D., is Associate Professor of Virology, Karolinska Institute and Adjunct Associate Professor, University of Missouri, US. Dr. Neogi obtained his doctoral degree from Department of Medicine Huddinge, Karolinska Institutet (KI) in 2013. He joined the Department of Laboratory Medicine as Assistant Professor in 2015 continued as Group Leader since 2018, where his research focuses on multi-omics system biology studies in infectious diseases to understand the mechanism of disease progression, immune-control and immune-aging. Dr. Neogi has a longstanding research interest to understand the mechanisms of natural immune control in viral infection, focusing in particular on HIV-1 infected individuals called Elite Controllers (EC), who control HIV-infection spontaneously and more recently to other emerging and re-emerging viruses like SARS-CoV-2 and Crimean–Congo hemorrhagic fever (CCHF). He will speak on multi-omics analysis to understand SARS-CoV-2 pathogenesis.

Milan Surjit, Ph.D.

Associate Professor
Translational Health Science and Technology Institute

Dr. Milan Surjit is currently working as associate professor in Translational Health Science and Technology Institute, Faridabad. He completed his PhD from International Center for Genetic Engineering and Biotechnology, Delhi. His post doc was from Institute of Genetics and Molecular and Cellular Biology, Strasbourg, France. His research interest revolves around investigating the role of host-pathogen interactions in HEV pathogenesis and exploring the mechanism of viral translation and replication. He is also interested in development of a recombinant vaccine against HEV. He will enlighten us on host-pathogen interactions during SARS-CoV-2 infections.



Dr. Manjula Kalia

Associate Professor
Regional Centre for Biotechnology

Dr Manjula Kalia currently working as Associate Professor in regional Centre for Biotechnology is a leading virologist. She completed her Ph.D. from National Institute of Immunology followed by post doc from University of Calgary. Before joining RCB, she worked as fast tract scientist in NCBS Bangalore and scientist E at Translational Health Science and Technology Institute, Faridabad. Her research interest revolves around dissecting the interaction of Flaviviruses with host factors with special reference to cellular autophagic pathways. She will speak on pharmaceutical modulation of cellular autophagy to regulate Japanese encephalitis.

Rakshak Kumar, Ph.D

Scientist,
CSIR - Inst. of Himalayan Bioresource Technology, Palampur

Dr Rakshak Kumar is a Scientist in the field of Environmental Microbiology at CSIR-Institute of Himalayan Bioresource Technology (CSIR-IHBT). Before joining CSIR-IHBT, Palampur as DST INSPIRE Faculty and later as Scientist, he has completed his PhD from North Eastern Hill University, Shillong and Postdoc research in CSIR-Institute of Microbial Technology (CSIR-IMTECH), Chandigarh and Sikkim Central University, Gangtok. His research group aptly termed as "High Altitude Microbiology Laboratory (HAM-Lab)" focuses on exploring the microbial community from extreme environments of the Himalaya for its application in society and industry. His major research achievement targeted exploration of bacteria from Eastern and Western Himalaya for plant growth promotion and bioprospection for industrial applications. His group has also developed a reduced crop cycle production of a typical Himalayan mushroom called- Shiitake and have commercialized the technology to nine industrial partner that include mushroom's enrichment with Vitamin D. His recent research publications have provided solid scientific basis on the genomic evidence of plant beneficial bacteria and enzymes for industrial applications from the Himalayan unique niches. He has developed technologies and delivered products for accelerated compost degradation in cold hilly region for production of quality compost for crop improvements. His research efforts on Shiitake mushroom processing and enriched composting have led to establishment of five SFURTI, MoMSME clusters providing livelihood opportunities to 1150 people. He has more than 35 research articles in internationally peer reviewed journals and currently supervising eight PhD students.

Charu Tripathi, Ph.D.

Assistant Professor
CMP College,
University of Allahabad, Prayagraj

Dr. Charu Tripathi is working as an Assistant Professor at CMP College, a constituent college of University of Allahabad, Prayagraj. She has done masters in Zoology with specialization in Genomics from University of Delhi and Ph.D. from University of Delhi. Her doctoral work was based on characterization and genomics of microorganisms isolated from thermophilic niches in order to gain insights into the functional mechanisms evolved and genome-wide dynamics. Dr. Tripathi has published 11 research papers in reputed journals and 2 book chapters. She has supervised 14 masters dissertations and is currently supervising 1 PhD student. She has been awarded a research grant from UGC for establishing her lab. Her research interests include molecular microbiology, genomics and metagenomics.

Siddarthan Venkatachalam, PhD

NCPOR, Goa

Dr. Siddarthan Venkatachalam completed his Ph.D. from Bharathiar University, Coimbatore, India. He is a microbial ecologist and has been involved in research activities on three poles (the Himalayas, Antarctic and Arctic) during the course of his short career. He has published twenty-six research articles and is specialized in analysing large-scale high-throughput genome sequence data analysis (Amplicon sequencing, shotgun metagenomics-based genome assembly and annotations) and pan-metagenomics approaches for characterising microbial community structure and its functions from various ecosystems across space and time. He has initiated research activities in Plant-Microbe interactions for various agriculturally important crops at IARI.

As a part of Prof. R. Dorrington's research group at Rhodes University (RU) as a Post-Doctoral fellow he was first introduced to ocean sciences, and his passion for ocean sciences continues until now. At Rhodes University (RU), he was a lead researcher in various long-term monitoring projects in the Southern Ocean and Sub-Antarctic regions. He was also appointed as an honorary research associate at The South African Institute for Aquatic Biodiversity, where he was involved in establishing a genomics platform and training biologists with bioinformatics tools. Currently working at National Centre for Polar and Ocean Research, with a DST-SERB post-doctoral fellowship his research activities are mainly focused on Arctic fjords and associated terrestrial foreland ecosystems. Dr. Venkatachalam is investigating how glacier retreats influence the microbial food web structure dynamics and associated biogeochemical processes. He has substantial experience in scientific expeditions, including Southern Ocean expeditions, Arctic Svalbard Coastal cruise expedition (Team leader), and Himalayan expeditions. He is also a recipient of three Post-Doctoral Fellowships which include National Post-Doctoral Fellowship by DST SERB, India; Post-Doctoral Fellowship by National Research Foundation, South Africa; and Post-Doctoral Fellowship by Rhodes University, South Africa.

Anita Kamra Verma, Ph.D.

Professor
Kirori Mal College, University of Delhi

Prof. Anita Kamra Verma, has been teaching and research for the past 31 years. While excelling in teaching Physiology, Immunology & Biotechnology, she has the unique distinction of being the first College teacher in Delhi University to set-up an international level Nanobiotech research facility with high-end equipment, an Animal Culture Facility and the only CPCSEA registered Animal Holding Facility (with an MOU for bio-waste disposal). For promoting scientific fervor, Prof. Kamra has organized DST-INSPIRE

Camps as Program Coordinator; signed tripartite MOUs with NII-DBT-KMC, THSTI-DBT-KMC as Nodal Officer for Science Setu; facilitated research activities for faculty as Convener, Research Development Cell; initiated eco-friendly student activities as Convener, Eco-Club; and contributed as member of NAAC, IQAC. Currently, she is the Program Coordinator of DBT Star College Scheme.

She is the recipient of in “Excellence Award for Teachers in service in Colleges” in 2021 from University of Delhi and the “Distinguished Collaborator award (2019)” from University of Central Lancashire (UClan), UK.

She is an accomplished scientist globally known for her significant contribution. Dr. Verma has over 100 publications in international journals, book-chapters focusing on ‘Nanotherapeutics for cancer, arthritis, and Diabetes’. She has more than 1887 citations and an h-index of 24. She supervised 12 Ph.D. and 1 M.Phil. students and completed 14 sponsored research projects funded by various agencies. She has international collaborations with multiple grants from UKIERI, DST and DBT and two Patents on Anti-Cancer drugs.

Her academic strength, demonstrable passion to develop the college as an exemplary research Centre, untiring efforts to inspire students to pursue sciences and her outstanding contributions to the growth of the college, indeed makes her unique among her peers.

Jyoti Prakash Tamang, Ph.D .

Professor,
Sikkim University

Prof. Dr. Jyoti Prakash Tamang is a pioneer researcher in ethnic fermented foods and beverages of India and other Asian countries, which he scientifically studied and reported till date, focusing on food antiquity and culture, gastronomy, metataxonomic, metagenomics, metabolomics, bioinformatics, predictive functionality, starter culture development, food safety, probiotics, whole genome sequencing, nutrition, and health- benefits for last 34 years. The findings of Prof. Tamang have made significant paradigm shift from conventional microbial taxonomy to sequence-based taxonomy providing the information of many functional micro-/mycobiome in ethnic fermented foods and beverages of India. Currently he is the prestigious International Centre for Integrated Mountain Development (ICIMOD) Mountain Chair (www.icimod.org). He has received several national and international awards including Department of Biotechnology-Bio-Science Award in 2005. He has published more than 180 research publications including 7 books from Taylor and Francis (USA) and Springer Nature (Singapore), with cumulative impact factors of 250 and citations of 6000 and h-index of 42 in SCOPUS. He also has one Patent. Professor Tamang held several administrative posts in Sikkim University: first Registrar (2011-2013), Dean, School of Life Sciences (2012-2020) and Acting Vice- Chancellor (2017-18).

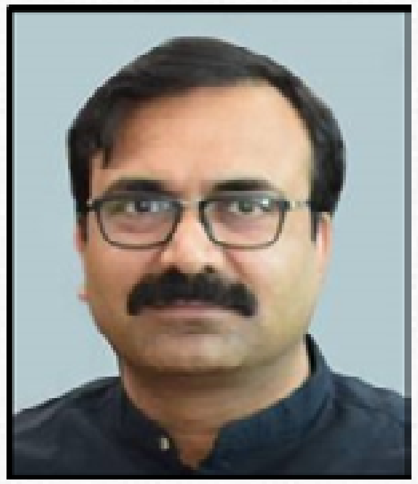
Sanjukta Subudhi Ph.D.

Senior Fellow and Group leader (Microbial Biofuels and Biochemical)
DBT-TERI Centre of Excellence in Advanced Biofuel & Bio-commodities, Advanced Biofuels Program
The Energy and Resources institute, New Delhi

Sanjukta Subudhi is a microbiologist and working as a senior fellow at The Energy and Resources Institute (TERI), New Delhi. She leads the advanced microbial biofuel & biochemical research group at TERI. Research explorations of her group span the domain of; microbial production of clean fuel (bio-hydrogen bio-methane, bio-butanol from 1st, 2nd, and 3rd generation feed stocks) and green chemicals (2,3 Butane Diol, lactic acid, lipase, bioflucculant). She had the opportunity to work in several bilateral and multilateral collaborative research projects. She has over 100 research publications, conference papers, and proceedings to her name, which includes 51 high impact factor peer-reviewed international publications (with RG score of 29.39 and 1061 citations, h-index, 18, I10 index, 23), four patents, and three book chapters. Major research achievements include biohydrogen and bioethanol production from 1st and next generation feed, biomethane from organic matter, microbial production of 2,3 Butane Diol and its downstream purification, algal production of value added biopigments. She is the member of several professional bodies.

Kashyap Kumar Dubey, Ph.D

Associate Professor
School of Biotechnology
Jawaharlal Nehru University, New Delhi



Prof. Dubey is currently working as Associate Professor at School of Biotechnology, JNU New Delhi. Prof. Dubey received his PhD degree in 2008 in the area of Industrial Biotechnology. Dr. Dubey has a research interest in biochemical engineering and wastewater treatment which includes process development of value-added pharmaceutical products (3-demethylated colchicine, betulin, CoQ10, pullulan and lipstatin), through optimization of enzyme reactions and toxicological studies of micro-pollutants.

He is running a research project sanctioned from DST-BRICS, and completed projects funded by DBT (Horizon2020) on Clean Water for Health, BIRAC-DBT and DBT on microbial process development. He has been completed Four major research projects and published 50 research articles in International reputed Journals. He is a Member of Various Scientific societies like IFIBbiop, BRSI, NASc, ISCA, SBC, DST-INSPIRE, MSI, ISCB, and AMI. He has been organised Four National Conferences, Conducted 03 GIAN courses, and 01 STTP. He has delivered several expert lectures at various scientific events. He significantly published in the area of biocommodity engineering and wastewater. His effort has been to develop low-cost technology which would lead to lesser costs.

Utkarsh Sood, Ph.D.

Research Associate,
The Energy and Resources Institute (TERI)

Dr. Utkarsh Sood is working as Research Associate at The Energy and Resources Institute, New Delhi. He is the Director and Co-Founder of PhiXGen Pvt. Ltd. He completed his graduation from Hansraj College and did his Master's in Zoology from the Department of Zoology, University of Delhi. Thereafter, during his doctoral research, he worked on the complete and comparative genomic analysis of clinical and nonclinical isolates of Pseudomonas aeruginosa. He was awarded the Ph.D. degree by University of Delhi in November 2018. He is a young researcher with 25 publications incluidng peer-reviewed research, review articles, and book chapters. He has recently contributed 2 genus chapters in the prestigious Bergey's Manual of Systematics of Archaea and Bacteria. He is now enthusiastically working in the field of comparative genomics, microbiome studies, and secondary metabolites of bacteria.

Vineet Ahuja, MD, DM

Professor, Department of Gastroenterology and Associate Dean, All India Institute of Medical Sciences, New Delhi

Dr. Vineet Ahuja is currently Professor in Department of Gastroenterology and Associate Dean, Research at All India Institute of Medical Sciences, New Delhi. He did MD (Internal Medicine) and DM (Gastroenterology) from Post Graduate Institute of Medical Education & Research (PGIMER), Chandigarh. His areas of interest in research are Inflammatory Bowel Disease, Abdominal Tuberculosis, Gut Microbiome and Gastrointestinal Immunology. He has published 260 International and National Publications and 24 Book chapters having more than 6000 citations. He is serving as Editor of "Tropical Gastroenterology" journal. He is also a member of International Organization for Inflammatory Bowel Disease

Bishwajit Kundu, Ph.D.

Professor
Kusuma School of Biological Sciences, IIT Delhi

Bishwajit Kundu is currently working as Professor at Kusuma School of Biological Sciences, IIT Delhi since 2018. He completed his Ph.D. from Institute of Microbial Technology, Jawaharlal Nehru University. He was Postdoctrol fellow at Case Western Reserve University, CLEVELAND, USA, 2001-2003. There are 50 publications to his credit in peer reviewed and highly indexed International and National Journals and 6 patents to his name. He is very proficient in his administrative work and has handled a number of prestigious positions like Associate Dean, Chairman of Departmental Research committee, DBT Nominee of Institute Biosafety committee of National Institute of Pathology, President Board for sports activities and many more. He leaded a group researchers for the development of in house RT PCR-Based probe free Covid detection kit at very affordable cost which was transferred to the different companies for the mass production. He is invited in a number of National and International academic programs for sharing his knowledge and experiences and has organized various conferences and workshops.

Praveen Gupta, M.B.B.S, M.D., D.M. (Neurology)

Director and Unit Head Neurology
Fortis Memorial Research Institute

Dr. Praveen Gupta is currently the Director and Unit Head Neurology in Fortis Memorial Research Institute since 2014. He served as Corona Warrior in 1st and 2nd wave of the pandemic, managing complicated cases of COVID & Mucor-mycosis. He has been awarded by FORBES as Global Indian Brand Leader along with Ratan Tata, Rahul Bajaj, Shiv Nadar & Kumar Mangalam Birla. He has also been Awarded as the best Neurologist in Delhi and NCR twice by Times Research. He has also received Rastriya Chikitsha Shiromani Award and Dr. B.R. Ambedkar Seva Ratna Awards among many others.

His research interests include Bone Marrow transplant to cure Multiple Sclerosis, Leukodystrophy and other auto immune Neurological disorders. He has been actively involved in treating Epilepsy and Parkinson ’s disease through surgery and Deep Brain Stimulation for Epilepsy Parkinson ’s disease.

He has worked as a Director and Head of Dept. Neurology Artemis Hospital from 2009. He launched the first Stroke Center in Gurugram and was instrumental in starting the first DBS program. He performed the first Solitaire stent to retract clot from the brain in acute stroke patients and has used the first implant pacemaker in brain to treat Epilepsy in Asia.

He has been operating a charitable OPD since his early years of clinical practice. He has been actively involved in various research projects on diabetic neuropathy, Post Herpetic Neuralgia, Intracerebral haemorrhage, stem cell transplantation therapy in muscular dystrophy, cerebral palsy, and motor neuron disease, Multiple Sclerosis to name a few.

Sachin Khurana

Scholar,
Walter And Eliza Hall Institute For Medical Research
Australia

Sachin Khurana is an infectious disease researcher completing his graduate studies at the Walter and Eliza Hall Institute of medical research at the University of Melbourne, Australia. He completed his bachelor with honors in zoology from Sri Venkateswara College at the University of Delhi followed by a master’s degree in zoology from the University of Delhi. During the same time, he got to work at the United Nations funded International Centre for Genetic Engineering and Biotechnology (ICGEB) New Delhi component, where he worked on metagenomic analysis of the midgut of Anopheles stephensi, an Asian malarial vector. Following this short stint, he then formally joined ICGEB New Delhi as a junior research fellow and then as a senior research fellow and worked on elucidating novel protein-protein interactions between *Plasmodium falciparum* and the human host. It is here that he specialized in studying protein-drug and protein-small molecule interactions using surface plasmon resonance, a field which he is very passionate about. In 2018 he joined the infectious diseases and immune defense division at the Walter and Eliza Hall Institute of medical research where he is finishing his graduate studies while working with the model apicomplexan parasite Toxoplasma gondii to search for new drugs and drug targets for this group of parasites while utilizing the latest genome editing tools and advanced microscopy techniques.

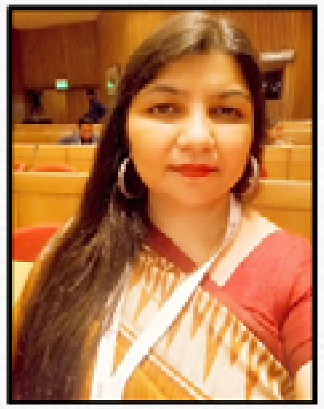
Bhabatosh Das Ph.D.

Associate Professor
Translational Health Science and Technology Institute,
Dept. of Biotechnology, Govt. of India

Dr. Bhabatosh Das is currently working as Associate Professor at Translational Health Science and Technology Institute, Dept. of Biotechnology, Govt. of India. He is a Molecular Biologist and completed his Ph.D from IICB-Kolkata, Post Doc from I2BC-France and was JSPS fellow at Osaka University, Japan. He has been honored and awarded with many prestigious awards like ILSI Young Scientist Award, Bill & Mellinda Gates Foundation Award , Japan Society for the Promotion of Science Award, Young Investigator Award, Probiotic Science Foundation & Yakult India. There are 68 publications on his name in peer reviewed highly indexed International Journals. He has also published 12 book chapters. He is member of a number of National and International academic bodies. His current research focus is oriented to understand the genome and genetics of bacterial pathogens, role of gut microbiota in the emergence and spread of multidrug resistant enteric pathogens and Reverse antibiotic resistance in bacterial pathogens by inducing loss of resistance genes. His research is being funded by various funding agencies of India, USA, Japan and UK.

Charu Dogra Rawat

Associate Professor
Ramjas College, University of Delhi



Dr. Charu Dogra Rawat is Associate Professor at Ramjas College, University of Delhi, heading the Molecular Biology and Genomics laboratory. She is PhD in molecular microbiology from University of Delhi during which she got the opportunity to work as a visiting research scholar at EPFL – École polytechnique fédérale de Lausanne, Switzerland. She pursued postdoctoral research at Jerry L. Pettis Memorial Veterans Hospital in California, USA. She has received prestigious Universitas21 faculty training fellowship to do MS in Bioinformatics from University of Edinburgh, Scotland, UK. She was recommended by University of Delhi as digital literacy champion to undergo further training in digital literacy at Edinburgh College, Scotland under D-LITE (Digital Literacy and

Innovation for Tomorrow's Education) project of UKIERI (UK and India Education Research Initiative). In 2019, she represented University of Delhi in a scientists' delegation to China. She has been awarded Indian Academy of Sciences (INSA) Teachers Award, highest national award for teachers engaged in higher education. She works diligently for the improvement of undergraduate education by exploring, applying and propagating various pedagogical approaches and under COESME, IISER, Pune she has conducted several workshops on research-based pedagogical tools pan-India. She has publications in internationally acclaimed journals and presented papers in many national and international conferences. She is departmental coordinator of DBT-funded Star College project and Principal Investigator of a DBT-funded technology-developing research project. Currently, she's engaged in popularization of microbiology, spreading awareness related to mental health, development of new and effective pedagogical tools and genomics, metagenomics and microbiome research.

Baljeet Kaur Ph.D.

Associate Professor
Hansraj College, University of Delhi

Dr. Baljeet Kaur is working as Associate professor in computer science department, Hansraj College, University of Delhi. She completed her PhD from Utkal University, Bhubanewar, Orissa and post doc from Jawaharlal Nehru University. Her interest interest lies in pattern recognition and machine learning. She has worked extensively with the biological data and will talk on relevance if gene selection in cancer microarray datasets.

ABSTRACTS

Colored scanning electron micrograph of microbes in human gut Photo by Martin Oeggerli

INAUGURAL
ABSTRACTS

Towards Four Dimensional Microbial Systems Biology in the Sea

Edward F. DeLong
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University of Hawai‘i, Manoa, SOEST

Microbial communities 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 perspective 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. We are leveraging both Eulerian and Lagrangian survey strategies that employ robotic sampling techniques, and coupling these surveys with community-wide microbial gene expression analyses in wild planktonic microbial populations, to help answer 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. Over seasonal scales, predictable summer export to the abyss, driven in part by surface water nitrogen-fixing bacteria, help fuel the ocean’s “biological pump”, and deliver nutrients to deep-sea . The coupling of genome-enriched datasets with new observational approaches over nested scales in time and space is advancing our understanding of the inner workings of complex planktonic microbial ecosystems.

The human microbiome in precision medicine

Dr. Jack A Gilbert
Professor, University of California
San Diego, United States

The human microbiome is quickly being recognized as a dynamic part of the human ecosystem, and research is starting to demonstrate that using ecology to understand this ecosystem has profound benefits for patient wellness. The immune system controls our interaction with the microbial world, and yet the microbial communities in our bodies are central to modulating the immune response. Changes in the human microbiome have substantial influence on atopy, neurological disorders, metabolic disorders, and a range of complex conditions and disease states. We will discuss evidence of these mechanisms of interaction and how we have started to disturb the delicate balance of the immune-microbe equilibrium, impacting the development and function of our immune systems. Applying new strategies to identify how the microbial ecosystem correlates with diseases states and treatment efficacy through Microbiome-Wide Association Studies (MWAS) is altering the trajectory of precision medicine and providing a new framework for facilitating patient care. However, to date there are still no FDA approved microbiome related therapies, pointing to concerns about over-promising of microbiome as a real treatment strategy. There is considerable concern about the need to move beyond studies that identify correlations between the microbiome and disease, toward intervention trials that will actually explore specific mechanistic relationships. It truly is time to start delivering on the promise of the microbiome.

The Mars 2020 mission and NASA's search for ancient life

Mitch Shulte
Program Scientist,
NASA Headquarters, Washington, DC

On 30 July 2020, the Perseverance rover was successfully launched, joining the United Arab Emirates Hope Orbiter and the Chinese Space Agency Tianwen-1 orbiter/lander/rover on their respective journeys to Mars, all of which have now safely arrived at Mars. The goals of Perseverance rover, having arrived on 18 February 2021 (US time) are to explore the geological environment of the Jezero crater landing site; to search for ancient signs of life in the martian rock record; to collect and cache carefully selected and documented rock and regolith samples for eventual return to Earth for study in terrestrial laboratories; and to help prepare for future robotic and human exploration of Mars. The scientific instrument suite on board the Perseverance rover was chosen to investigate the surface materials on Mars at a variety of scales, culminating in submillimeter measurements of chemical composition, mineralogy and possible presence of organic material. The instruments will help the Mars 2020 science team determine whether there is evidence in the rock record of Mars for signs of ancient microbial life (potential biosignatures) that may have been present at or near the surface. The Perseverance rover is also equipped with a one of a kind sampling system that will be capable of collecting up to 43 samples of rock and regolith in hermetically sealed sample tubes (with several tubes designated as witness blanks). NASA and the European Space Agency (ESA) are currently formulating plans to return the samples collected during the Mars 2020 mission with a set of missions that would launch no earlier than 2026, with the return of the samples to Earth in ~2030.

Plenary

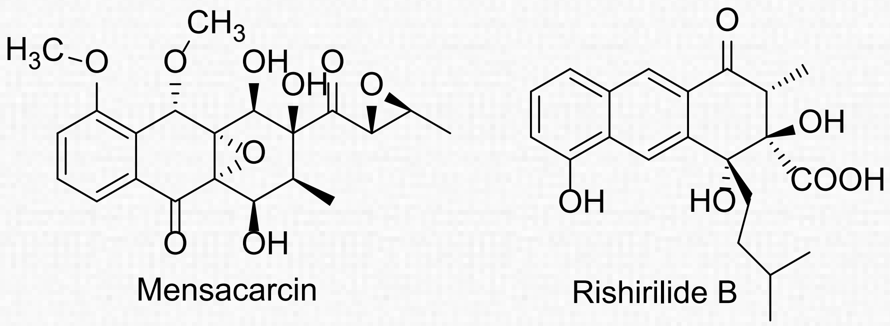
ABSTRACTS

Tailoring enzymes involved in natural product biosynthesis: Studies on the biosynthesis of mensacarcins and rishirilids

Prof. Dr. Andreas Bechthold

Universität Freiburg

The structural diversity of type II polyketides like doxorubicin and tetracycline is largely generated by tailoring enzymes. In Streptomyces bottropensis two PKSII gene clusters have been detected and isolated. Expression of the clusters resulted in the production of mensacarcin and rishirilids. (Scheme 1). We employ gene deletion experiments and in vitro enzyme studies to identify key biosynthetic intermediates and expose intricate redox tailoring steps for the formation of mensacarcins and rishirilides A, B, and D and lupinacidin A.



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Scheme 1: Structure of mensacarcin and rishirilid B

The impact of preexposure prophylaxis on HIV prevention. Meeting the United Nations goal of ending the AIDS pandemic in 2030

David Van De Vijver

Associate Professor, Viroscience department, Erasmus Medical Centre,
Rotterdam, The Netherlands

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 without AIDS-related morbidity when they adhere to antiretroviral drug treatment. Antiretroviral drugs can also 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) with different formulations of antiretroviral drugs can prevent HIV in individuals at high risk of infection. Based on these breakthroughs, the United Nations has included ending the AIDS pandemic as a public health threat, as one of its sustainable development goals in 2030 which aim to achieve a better and sustainable future for all people across the World. This ambitious goal is reached when new HIV infections and AIDS related deaths have declined by 90% between 2010 and 2030.

To support the goal of ending the AIDS pandemic, the World Health Organization (WHO) recommends the use of PrEP by individuals at high risk of infection alongside the use of condoms and achieving viral suppression in individuals living with HIV. In my presentation I will present the data from mathematical modelling studies from Europe and Thailand which show that investing in PrEP is a cost-effective method for reducing the HIV epidemic. In my presentation I will discuss the results of cabotegravir which contrary to daily oral PrEP has to be administered once every eight weeks and which has a superior efficacy in preventing HIV.

ISOTOPE FRACTIONATION CONCEPT FOR CHARACTERIZATION OF DEGRADATION PROCESSES OF HEXACHLOROCYCLOHEXANES IN THE ENVIRONMENT AND ALONG FOOD WEBS

Hans H. Richnow*[+], Xiao Liu[+], Steffen Kümmel[+], Yaqing Liu[+], Langping Wu[+#] and Rup Lal[§]

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Hexachlorocyclohexane (HCH) isomers belong to the persistent organic pollutants banded by the Stockholm conventions. The improper disposal of HCH residues from Lindane production (γ-HCH) causes serious long lasting environmental problems around the globe. HCH isomers dispersed in the environment accumulate in plants and animals along the food web, however HCH are subject of natural attenuation processes particularly biodegradation. There is an urgent need of tracking the source and the fate of HCH in the environment to understand natural degradation processes.

We have develop concepts for multi element compound specific isotope analysis (CSIA) in combination with enantiomer fractionation to characterize the fate of HCH isomers from source to sinks and explored to opportunities to employ CSIA to study uptake and transformation along with the food web.

Carbon and chlorine isotope compositions (δ13C, δ37Cl) of HCHs and the enantiomer fraction (EF) of α-HCH were used as indicators to characterize in-situ degradation in soil, groundwater, and sediment as well as along the food web. The HCHs were detected in plants growing on contaminated soil including a number of crops, which indicates an important transfer pathway of HCHs entering food webs. The EF value of α-HCH and the isotope signature of HCHs indicated that degradation processes occurred in the rhizosphere and in plants potentially attenuating the contamination of HCHs. EF value of α-HCH and the isotope signature of HCHs can also be used for analysis of the exposure of cattle and wild animal by HCHs. We will summarize the current state and recent advances of the stable isotope fractionation concepts to track the reactive transport processes in a complex environment including the food web.

Exploring microbial drivers of halogen cycling in pristine and polluted environments

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A broad range of inorganic and organic halogenated compounds are formed by various natural geochemical, photochemical and biological processes. In addition, halogenated compounds are produced in large quantities for industrial, agricultural and pharmaceutical purposes, which has led to widespread environmental pollution. Naturally occurring organohalogen compounds are synthesized and transformed by diverse groups of (micro)organisms in the presence or absence of oxygen. In turn, anthropogenic halogenated contaminants may be degraded under natural or stimulated conditions. To this end, the widespread occurrence of halogenated compounds in marine and terrestrial environments and various trophic food chains, as well as biotic and abiotic reactions converting halides and organohalogen compounds, suggest a substantial biogeochemical cycling of these compounds. The long-standing presence of chlorine compounds on Earth has driven the evolution of biological mechanisms that gain energy from the metabolism of organic and inorganic halogen compounds. As such, halogenated compounds can be used as electron donors or terminal electron acceptors for microbial growth. In this contribution, latest findings on microbial metabolism of organohalogens in pristine and polluted environments, particularly in pristine marine ecosystems, will be reported, focusing on ecophysiology and molecular basis of halogen cycling in the corresponding organisms.

Supporting women in science careers, why inclusivity is key to success

Hilary Lappin-Scott[*] and Sara Burton
[*]Honorary Distinguished Professor at Cardiff University,
Founder and Director, Lappin-Scott Consulting Ltd.

There are still too few women being supported into senior leadership roles in science careers. Women are still reluctant to become scientists or leave jobs because of a host of factors, such as harassment, feeling ignored or unwelcome, because of lack of support for their caring responsibilities and others. We present some ideas to address the changes needed to build more diverse teams, bringing together people of different backgrounds, lived experiences, values and opinions that have worked elsewhere. This practical experience focuses on many of the challenges women find around recruitment, retention and when trying for promotion or leadership positions.

Stochastic Community Assembly: Does It Matter In Microbial Ecology?

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Institute for Environmental Genomics, and Department of Microbiology and Plant Biology,
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School of Environment, Tsinghua University, Beijing
Earth and Environmental Sciences, Lawrence Berkeley Laboratory, Berkeley, CA

Unraveling the drivers controlling community assembly is a central issue in ecology. Although selection, dispersal, diversification and drift are conceptually accepted as major community assembly processes, defining their relative importance in governing biodiversity is very challenging. Here, I will overview various methods to study community assembly mechanisms by particularly focusing on stochasticity. I will highlight some important recent studies with respect to stochasticity in microbial systems. Particularly, I will present a novel framework to quantitatively infer community assembly mechanisms by phylogenetic bin-based null model analysis (iCAMP). Analyses with simulated microbial communities showed that iCAMP has very high accuracy, precision, sensitivity, and specificity. Application of iCAMP to grassland microbial communities revealed that homogeneous selection and "drift" played dominant roles in controlling grassland soil microbial community assembly in response to experimental warming. Interestingly, warming decreased "drift" over time, but enhanced homogeneous selection. In addition, iCAMP was also used to examine the changes of the assembly mechanisms of forest or groundwater microbial communities along geographical or environmental stress gradients. The general framework developed here provides an effective and robust tool to quantify community assembly processes in microbial ecology, and it should also be useful for plant and animal ecology.

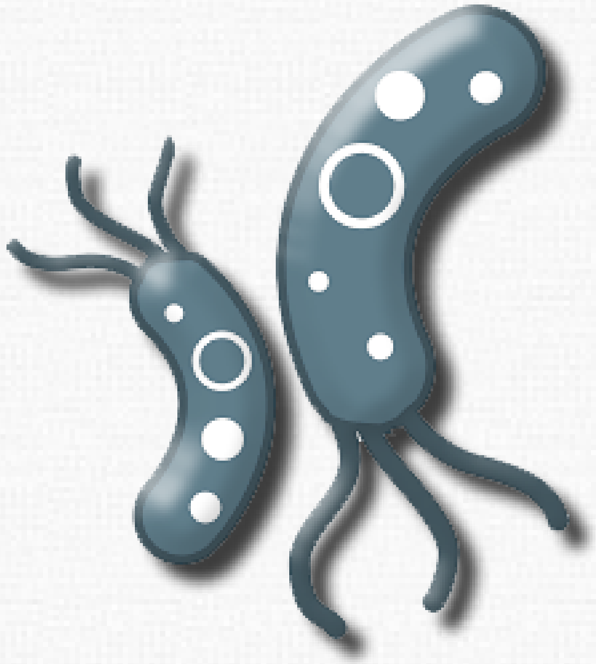
In Extremis: Discovering the Unique Microbial Ecology of Antarctica's Terrestrial Refugia

Stephen Craig Cary
Professor, Department of Biological Sciences, The University of Waikato, New Zealand

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. The 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 these dry arid polar 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 in the past. As the most remote geothermal environments on the planet, they also provide a rare opportunity to address questions around microbial biogeography, the interactions between globally distributed and endemic microbes, and endemism. Despite their biological importance, these extremely remote geothermal locations remain vastly understudied.

Key Note & Invited

ABSTRACTS



MICROBIAL ECOLOGY

Biological species concept in Bacteria

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Although originally thought to evolve clonally ,many studies have revealed that most bacteria exchange DNA .However ,it remains unclear to what extent gene flow shapes the evolution of bacterial genomes .Here ,we analyzed the patterns of gene flow within and between2,600< species of bacteria .Our results show that less than 10% of bacterial species are truly clonal ,indicating that purely asexual organisms are rare in nature .We further demonstrate that the taxonomic criterion of 95% genome sequence identity routinely used to define bacterial species does not accurately represent the levels of divergence imposing an effective barrier to gene flow across bacterial species .Instead ,interruption of gene flow can occur at various sequence identities across lineages ,generally ranging from 90 to 98% genome identity .Our results support a universal mechanism where the availability of identical genomic DNA segments required to initiate homologous recombination is the primary determinant of gene flow and species boundaries in bacteria .However ,we show that these barriers of gene flow remain somewhat porous since many distinct species are capable of maintaining some levels of gene flow in a process similar to introgression in sexual organisms .Overall ,our findings indicate that bacterial evolution and speciation are likely shaped by similar forces driving the evolution of sexual organisms and that gene flow appears to play a predominant role across the Tree of Life.

Key Note

Microbial consortia mediated environmental remediation for textile sector

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Textile industries generate large volumes of colored wastewaters which are difficult to treat using conventional technologies. In view of the environmental sustainability and compatibility with the post treatment polishing stages, a lot of research has focused on biological remediation, which could offer an attractive alternative. However, there has not been much success in translating these results into actual applications. Innovative approaches targeting the ease of applications of microbial interventions are therefore required.

Decolorization task is further complicated by the extreme variability that characterizes industrial effluents due to cocktail of many toxic contaminants. Hence, specialized microbial cultures that can sustain the extremes of environmental conditions are required for efficient removal of such toxic components (Gola et al., 2018). The production of appropriate formulation could simplify storage, handling and dosing in the industrial processes, especially for the unskilled masses in small scale industries (Patent no: 333307). The development of such formulations and learning's originating from the use of these as a tool to decolorize textile effluents shall be discussed. Also, the development of an innovative process based on native consortium for effective decolorization of textile effluents (Samuchiwal et al., 2020) and its long term performance will be covered.

Key Note

Deciphering and understanding the microbial synergy towards poly-aromatic hydrocarbon pollution: A metagenomic approach

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Alang- Sosiya ship breaking yard (ASSBY) is one of the largest ship breaking yard in the world, which covers almost 47% ship breaking of world and 95% ship breaking of India. The ship breaking activities release various types of hazardous materials in the coastal ecosystem, along with the extraction of profitable recyclable materials. The hazardous materials from ship breaking activities include asbestos, coating and paint materials, oil residues, polychlorinated biphenyl (PCBs), petroleum hydrocarbons, polycyclic aromatic hydrocarbons (PAHs), heavy metals, iron dust, glass wool, iso-cyanide gas etc., which destroy the biological balance of marine ecosystem. Owing to the hydrophobic nature of some hazardous materials like oil residues, petroleum hydrocarbons and PAHs, they tend to adsorb strongly and settle down on coastal sediment of ASSBY. The persistent pollutants petroleum hydrocarbons, heavy metals and PAHs are known for their toxicity, mutagenicity and carcinogenicity and they may cause serious health issues to nearby people. For restoration of polluted ecosystem, various remediation approaches can be applied, among all, bioremediation is always proven most suitable due to higher possibility for conversion of xenobiotic pollutants into non-polluted or less harmful compounds. Successful implementation of bioremediation strategies relies on understanding of indigenous microbial assemblages and their functional role regarding the metabolism of xenobiotic pollutants. Due to emerging approaches like culture independent metagenomics, next generation sequencing and advance bioinformatics, in-depth analysis of polluted site microbiome and their functional potential is now possible at higher resolution. Identification of microorganisms having pollutant specific biodegradative abilities is the first and crucial step towards achievement of successful bioremediation.

The present study delineated that ship breaking activities at ASSBY drastically altered microbial diversity and community composition of the polluted sediment as compared to non-polluted sediment. The function profile analysis revealed that microbial communities of polluted sediment of ASSBY distinguished by having stress responsive genes, aromatic hydrocarbons degradative genes and other xenobiotic compounds degradative genes. The presence of antimicrobial resistance genes and heavy metal resistance genes demonstrated the response of microbial communities to cope with heavy pollution in sediment of ASSBY and may help to predict the environmental risk assessment. This study provided the collective knowledge of microbial community composition, microbial biomarkers, functional diversity and resistome profile of polluted site sediment, which may be promising for envisaging and implementation of successful bioremediation strategies for various xenobiotic pollutants.

Biochemistry and genetics of pinoresinol mineralization in bacteria

Gunjan Pandey[1] ,Madhura Shettigar[1,2] and **John G Oakeshott[1]**
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Pinoresinol is an important plant defense compound ,a major food lignan for humans and some other animals ,and the model compound used to study degradation of the β-β ‘linkages in lignin .Our laboratory *Pseudomonas* sp .strain SG-MS2 have been found to mineralize pinoresinol through a novel catabolic pathway .We used comparative genomics ,proteomics, protein semi-purification ,and heterologous expression to identify a novel flavoprotein in strain SG-MS2 that carries out the initial hydroxylation of pinoresinol at the benzylic carbon. The cognate gene is translationally coupled with a downstream cytochrome gene ,and the cytochrome is required for activity .The enzyme is overexpressed in strain SG-MS2 upon exposure to pinoresinol ,along with 45 other proteins 22 ,of which were found to be encoded by genes in an approximately-35.1 kb cluster also containing the flavoprotein and cytochrome genes .While many overexpressed proteins were assigned as enzymes that catalyse pinoresinol catabolic pathway reactions ,some remain as hypothetical proteins with unknown function. The work casts new light on the biology of pinoresinol and its transformation to other bioactive molecules .Potential applications of the findings include new options for deconstructing lignin into useful chemicals and the generation of new phytoestrogenic enterolactones from lignans.

Analytical strategies to understand occurrence, fate and transport of chemical contaminants in the environment

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Chemicals play a pivotal role in our life with several advantages as well as disadvantages to environment and human health. The chemical contaminants which are toxic to plants and animals can cause problems to environment through aquatic and food routes. The interaction of contaminants with model organisms can cause chemical/biochemical transformations thus leads to production of less toxic metabolites and at the same we observe perturbations in the organism. Thus, we need a thorough and complementary analytical strategies to understand the fate of organism, occurrence and transportation of contaminants and their biotransformation. Our group has made efforts to develop and validate various analytical strategies to monitor these chemical contaminants and their biotransformed products as well as to understand their influence on various model organisms. The development of analytical approaches based on various microextractions (MEs) as sample preparation approaches coupled with hyphenated analytical techniques has helped to evaluate multi-class contaminants in environmental, food and biological samples, thus, has helped in monitoring and biomonitoring studies. The solid-phase microextraction, dispersive liquid-liquid extraction and solid-phase extractions with/without molecularly imprinted polymers (MIPs) has helped to handle large number of samples with minimal carryover effects without compromising their sensitivity, selectivity and specificity during the monitoring (environmental and/or bio) studies with acceptable precision and accuracy. Further, the use of mass spectrometry based metabolomics to understand the metabolic perturbations in various model organisms due to exposure of these chemical contaminants has helped to evaluate their toxicological effects. These metabolomics also helped to understand the food safety aspects of fruits after ripened with natural and artificial ripeners.

Alternative tools and tags in Pesticide Toxicology Research - A case study of Ciliates

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This review deals with the potential of certain ciliate protozoa as model organisms in different aspects of ecotoxicology given their species diversity, richness, abundance, cosmopolitan nature, ecology, population growth, toxicity and research as well as the ethical pressures placed on animal-based experimentation. Ciliate protozoa namely *Paramecium caudatum, Tetrahymena pyriformis, vorticella campanula* and *Blepharisma intermedium etc* have been used since a very long time because they show minimum epigenetic variability and a single clone can be preserved for a longer time generation after generation axenically. These are used in determination of effects of insecticides, fungicides, carcinogens, organic chemicals, heavy metals and drugs. Collection, isolation, identification and subsequent biochemical, molecular, proteomic and genomic analysis using different end points was a great success in ciliates and ciliates exhibit high conservation of genes and better matches of coding sequences to those of humans and metazoans, hence can be used as an ideal alternative to eukaryotic organisms for both microscopy and ecotoxicological studies. The above advantages make ciliates extremely flexible and prove as promising models for future research and their use should be embraced

Occurrence of plastics in the marine and terrestrial environment: Assessing diverse plastisphere bacterial communities and their role in biodegradation

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Terrestrial, marine and coastal pollution has become a global concern. Persistent pollutants have been reported from Indian Coasts that includes crude oil, pesticides, plastics and metals. Bacteria that are able to biodegrade different types of plasticizers and plastics have been isolated and characterized. *Sphingobacterium* sp.IITR106, *Achromobacter pulmonis* IITR107, *Dietzia kunjamensis* IITR161, *Alcaligenes faecalis* IITR162, *Pseudomonas stutzeri* IITR163, *Achromobacter mucicolens* IITR164, and *Pseudomonas guguanensis* IITR165 were isolated from dumpsite and marine ecosystem for biodegradation of different plastics, These bacteria were enriched on several plastic compounds such as polyethylene terephthalate (PET), dimethyl phthalate (DMP), dibutyl phthalate (DBP), Monomethyl phthalate (MMT), bis-(2-hydroxyethyl) terephthalate (BHET) and phthalic acid (PA). Out of these few isolates, three different bacteria IITR161, IITR162 and IITR107, responsible for the degradation of plastics were taken for detailed investigation based on their versatile substrate utilization capabilities. They were found to metabolize 500 ppm of DBP, DMP, phthalic acid in 15days under aerobic conditions at 30°C leading to the formation of their mono-phthalate esters. Initial results indicate that *Dietzia kunjamensis* IITR161 comprises hydrolase and esterease enzymes that are involved in catalyzing the degradation activities. Similarly, *Alcaligenes faecalis* IITR162, esterase which is involved in degradation of DBP into MBP and PA were also measured. When cross verified for the presence and activity of the enzyme, it is found that the strain IITR162 convert p-nitrophenol acetate into p-nitrophenol which a key assay to measure the esterase activity. Based on the efficiency of the degradation and other characteristics, these bacteria were subjected to whole genome sequencing to get novel insights on biodegradation of plastics and other aromatic compunds. Similary, a bacterium isolated from a lake ecosystem, identified as *Brucella intermedia* IITR130 was found to biodegrade polyethylene terephthalate (PET). As evident from FTIR and SEM analysis, it was found that the bacterium metabolizes PET-sheet utilizing as carbon in presence of lettuce extract and yeast extract. PET metabolites such as BHET, terephthalic acid were identified using GC-MS and the biochemical investigation is underway to understand the PET-degradation pathway encoded in the bacteria.

Exploring novel avenues in microbial bioremediation: role of computational tools

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The use of computational tools in microbial bioremediation in playing very significant role in addition to techniques of genomics ,gene editing and systems biology .This is an interesting concept and can give breakthrough ideas as these tools are efficient towards understanding the metabolomics of microbial bioremediation .Moreover ,the use of synthetic microbial consortium and concept of’ microbes co-cultivation ‘for bioremediation is an exciting opportunity for gaining new understanding in this area .Our studies gives an insight and crisp overview of heavy metal bioaccumulation using combinatory wet-lab and bio-computational tools .Our studies reported a comparative analysis of heavy metal bioaccumulation by Ochrobactrum intermedium BPS 20-and Ochrobactrum ciceri BPS 26-and their multiple metal resistant potential .It was reported in this study that can resist up to 2400 mg/L and 2000 mg/L of Lead and 850 mg/L and 1200 mg/L of Nickel respectively .On the other hand another strain Bacillus cereus BPS 9-showed a more significant MIC value 2400) ppm (than already reported strains. Further ,our studies conducted through functional analysis through SEED viewer established the presence of genes encoding heavy metal resistant proteins and transporters for the efflux of heavy metals .In summary ,our studies confirmed that these combinatory tools may be crucial towards decoding the important genes and their metabolic networks for achieving efficient bioremediation.

Biomass to Bioenergy

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Our global economic system is dependent on the use of fossil energy sources for the production of fuels and chemicals .However ,fossil fuels are limited resources and its depletion is inevitable .Escalating world population and living standards will lead to higher global energy consumption and demand .It is predicted to increase dramatically over the next half century; at least two-fold ,from the current 12.8 TW to 28 TW by .2050 As a solution to this challenge renewable energy sources) Biomass ,wind ,solar etc (may meet the energy demand in a secure, sustainable and eco-friendly way.

Plant biomass represents sustainable, renewable and alternative feedstock for production of chemicals and energy in replacement for fossil feedstocks in the emerging Bioeconomy. In this regard, efficient and sustainable biomass production systems as well as methods for biomass conversion will be key technologies. Lignocellulosic biomass is recalcitrant in nature and despite recent improvements in enzyme technology it's processing usually requires some physical-chemical pretreatment before efficient biochemical conversion can take place. Intense research is on the way to understand the underlying mechanisms of lignocellulose breakdown by pretreatment that will allow to extract more sugar/energy. The fundamental knowledge of biomass (viz. plant and agricultural residual material), saccharification efficiency, biomethane potential, inoculum and microbial community needed to realize the potential of biomass for energy applications.

Invited

MICROBES IN SUSTAINABLE AGRICULTURE

Microbiome-based Approaches for Sustainable Development

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The microbiome has the potential to advance many of the Sustainable Development Goals laid out by the United Nations, mainly due to the central role of microbes in the provision and regulation of ecosystem services. Microbiomes can contribute to sustainably improving the nutritional value of food, reducing the susceptibility of crops to disease, enhancing crop yields, and improving soil health and fertility. Research into soil microbiomes has shown how some species can enhance plant defences against infection, while some others can produce greenhouse gases. That underlines the need to develop a clear understanding of the impact of soil microbiota. A better understanding of microbiomes associated with the food system will address several critical societal challenges, including food and nutrition security, health and wellbeing, and can even aid in mitigating climate change.

For more than a century, intentional microbiome manipulation in agroecosystems has focused on applying single microorganisms to improve plant growth or control pathogens and pests; however, numerous challenges have prevented their widespread success. In the past few decades, the focus gradually shifted from the individual (reductionist approach) to the community level (holistic approach): from monoculture studies in isolation to consortia cultures to designing synthetic microbial communities and microbiomes in recent years. Despite a recent boom in microbiome research, we are yet to capitalize on microbiome-centric approaches for improving crop health and agroecosystem functioning. Capitalizing on the interconnectedness of plant and soil microbiomes will contribute to developing novel microbial biotechnology and synergistic management practices that positively steer the microbiome to improve crop protection and overall production, while identifying beneficial microbiome-related crop traits can contribute to both traditional and next-generation gene-editing-assisted breeding. The future lies in revolutionizing sustainable agriculture with synthetic biology, customized microbial biotechnology, designing synthetic communities, and precision microbiome management. This lecture will highlight some of the most recent advances in microbiome-based approaches for sustainable development, primarily focusing on crop health and agroecosystem functioning.

Keynote

Plant growth promoting microbes: A tool for healthy agriculture

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Agriculture plays an important role in the evolution and growth of the human race. The microbiome of healthy soil is diverse in nature but in microbiological studies fungi, bacteria and archaea are major microbiomes. These microbes participate in important ecosystem processes. Microbes have an essential role in providing nutrients in the available form to the plant roots (nutrient recycling) and also help in soil formation. Although most of the plant parts are associated with microbes but rhizosphere contains a rich diversity of microbiome because of nutrient rich root exudates and cell debris. The microbes in the soil especially rhizospheric microbes have direct interaction with plant roots where plant growth-promoting microbes improve the plant growth by direct (nitrogen fixation, phosphate solubilization, phytohormones production etc) and indirect mechanisms (siderophore production, enzymes production etc). Some microbes have the ability to generate Induced Systemic Resistance in plants against biotic and abiotic stresses. These microorganisms are known as plant growth promoting microbes (PGPM) and are an excellent substitute for chemical fertilizers and pesticides which have an adverse effect not only on human health but also degrade the soil quality.

Invited

Exploring the unexplored bacterial phyla members of India

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It is an accepted fact that bacteria are useful for human beings and environment in many aspects .Working on the bacterial cultures has now become a fundamental part of various biotechnological processes .Ever since the description of twelve bacterial phyla in ,1987 with the help of phylogenetic analysis of16 S ribosomal RNA gene ,microbial diversity has been thoroughly expanded .While only some of the bacterial phyla members have been cultured in the lab till date ,there are a great number of members of phyla which remains unexplored due to uncultivability .Out of the guesstimated 1300 bacterial phyla ,about 55 phyla members are recognised among which ,large number of the members remain as uncultivated Candidatus phyla .So far ,in India ,we have largely focused working on members of five major phyla which include ;Firmicutes ,Proteobacteria ,Cyanobacteria ,Bacteroidetes and Actinobacteria. To a lesser extent members of the phylum Deinococcus-Thermus .In our laboratory ,we are presently focusing on the cultivation of the members of Planctomycetes ,Verrucomicrobia, Spirochaetes ,Chlorobi and Acidobacteria which are widely distributed in our country in different habitats and exploring their biotechnological potentials.

Contamination of food-chain by human pathogens dwelling in rhizosphere :Life cycle and remedies

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Free-living life cycle of human pathogens in soil is the cause of various food related disease outbreaks. *Salmonella* is an established pathogen of the members of the kingdom Animalia .Reports indicate that the association of *Salmonella* with fresh ,edible plant products occurs at the pre-harvest state ,i.e .in the field .In order to conduct studies on the interaction of human pathogens with plant and soil ,clearance from IBSC was mandatory and all experiments were planned ahead and safety measures were taken .In this study ,we follow the interaction of *Salmonella* Typhimurium with the plants to understand the process of invasion in root via remodelled epidermis and migration in soil via flagella-mediated motility .Biphasic flagellar genes *fliC* and *fljB* were found to be important .We found that genes encoding two-component systems) *envZ/ompR* (and proteins producing extracellular polymeric substances) *csgD* and *bcsA* (are essential for *Salmonella* to adhere to the organic matter in soil and roots .Soil ,as a niche of bacteria ,is influenced by various abiotic factors. We have analysed the role of lactoyl-glutathione lyase in imparting protection to the bacteria against the plant derived antimicrobials under abiotic stress .Our experiments revealed a cross-kingdom invasion by the pathogen via passage through a murine intermediate ,a mechanism for its persistence in the soil and invasion in a non-canonical host .These results form a basis to design strategies to break the life-cycle of *Salmonella* before it reaches its animal host and thus reduce *Salmonella* contamination of food products .Here we discuss a novel approach of using a bio-control plant to reduce the number of bacteria in soil so as to reduce its invasion in plants.

Endophytic fungi and their relevance in abiotic stress management in crop plants

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Microorganisms play an important role in agriculture and beneficial microbes have been used as biofertilizers, biostimulants, and biocontrol agents for many years. Several types of plant-associated microbiomes have been identified and characterized. These microorganisms can be useful in sustainable agriculture and aid in enhancing crop productivity which is essential for meeting the demands for feed and food under fast- changing climatic conditions. Experiments using endophytes, the microorganisms that live inside the host plant and interact closely with the host, indicated that they can regulate several plant traits. Since endophytes can adapt to harsh environmental conditions faster than their host plants and have abilities to activate specific traits in the host, enrichment of such microbes in compatible crops can be an ideal approach to improve stress resilience. We have identified many fungal endophytes from stress- adapted plants and examined the role of the symbiotically associated endophytes in conferring abiotic stress tolerance in horticultural and field crops. Colonization of endophytic fungi activated physiological traits which resulted in a significant improvement in stress tolerance in the crop plants. In this talk, I will be discussing the positive effects of endophytes on crop growth and abiotic stress tolerance. Our results support fact that the endophyte-enrichment technology can be a highly beneficial and eco-friendly approach to boost crop productivity, and the approach can refine agricultural practices in the future.

The Archaea lead in the Ecology of Landfill- Leachate of Pune Municipal Site

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The landfill is a convenient and affordable method of municipal solid waste management. Landfill leachate contains a heavy load of pollutants and pathogens. Discharge of untreated leachate is the leading cause of surface and groundwater contamination and threat to public and environmental health. To develop an efficient leachate treatment technology, an in-depth understanding of landfill chemistry and microbiology is essential. In the current manuscript we conducted a comparative study of three different landfill leachate samples using cultivation based and culture independent molecular studies. We cultivated 85 species of aerobic and anaerobic Bacteria and Archaea from leachate represented by a total of 200 strains using extensive culturomics approaches. Twelve out of 200 cultivated strains showed very low 16S rRNA gene sequence similarity (84-98.6%) with their closest relatives and could be the potential novel taxa, first time cultivated from leachate. Members of the six genera only have 2-5 representatives from past studies from other habitats but first time cultivated from leachate. In addition to bacteria, we also cultivated and characterized different groups of methanogenic Archaea. Our chemistry data indicate that leachate is a highly stressed ecosystem with an assemblage of numerous mixed wastes. Metagenomics analysis showed the dominance of (30-55%) methanogens and haloarchaea,. Our data suggest that Archaea are the significant regulators of leachate ecology, and more in-depth studies with multiple leachate samples are required to understand their role in leachate nutrient cycling and the development of effective leachate treatment technology.

BI-DIRECTIONAL ELUCIDATION OF PROBIOTIC INTERVENTION FOR NEUROLOGICAL MANIFESTATIONS AT GUT-BRAIN AXIS

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Neurological complications occurring due to *Salmonella* infection in some typhoid patients remain a relatively unexplored serious complication. Further, an alarming escalation in antimicrobial resistance and reports pertaining to the inability of existing antibiotics in treating such infections, has worsened the situation resulting in a dearth of effective antimicrobials to combat such infections. In the face of such implications, efforts are being made by the scientific community to evaluate other bio-compatible strategies to which the organisms are unlikely to acquire resistance and along with treating infections, can improve various other aspects of host health. Herein, the use of probiotics presents as a potential treatment alternative. Simultaneously, given the direct association of gut inflammatory diseases with psychiatric as well as functional co-morbidity, the role of microbiota gut-brain axis and the ability of probiotics in modulating this bi-directional communication is being explored in *Salmonella* induced brain infection. Strain specificity of *Salmonella* in causing neurological manifestations has been reported in mouse model using two different strains. In this context, administration of *L. plantarum* (RTA 8) has been found to ameliorate the psychological (depressive-like, anxiety-like and locomotor behaviour), physiological (tight junction protein and mucin gene expression, levels of catecholamines, serotonin, GABA, BDNF, acetylcholinesterase) and pathological (tissue bio-burden, histopathology) condition of the host, thereby preventing serious infection. Thus, it highlights the potential of using probiotics in modulating various facets of the gut-brain axis, thereby providing multidimensional benefits and improving the holistic health status of the host.

Microbial volatile organic compounds (mVOC) for plant health

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Microbial volatile organic compounds (mVOCs) produced by the beneficial microbes are the natural means of combating biotic and abiotic stress, and could be an alternative, sustainable solution for suppression of plant pathogens and induce plant resistance against pathogens as well as enhance plant growth promotion. The microbiome and their metabolites interact with plants and contribute to plant health through hormonal modulation, the supply of mineral nutrition, and pathogen suppression. These microorganisms produce diverse mVOCs, which are specific to species and even strains and are comprised of diterpenes, tetraterpenes, and sesquiterpenes. More importantly, mVOCs are essential for the plants by way of acting as sources of nutrients, such as CO_2, indole, H_2S, and dimethyl disulfide, and health and defense signals. The plant immune responses and plant health promoted by mVOCs are the rapidly expanding field of research. In recent years, many VOC-producing microbes (both rhizosphere and endophytes) that induce ISR against pathogens and pests have attracted the attention of the scientific community. Recently, we have identified several mVOCs of endophytic fungi (*Trichoderma longibrachiatum* EF5), bacteria (*Bacillus altintudinus* FD48) and yeast (*Candida tropicalis*) exerting antagonistic action against various phytopathogens causing diseases in rice and tomato, respectively. In our recent study, mVOC blends of tomato endophytic *Candida tropicalis* TY1 and *Bacillus pumilus* TEB10 were documented during interaction with plant pathogens such as *Pythium aphanidermatum* and *Fusarium lycopersici* and triggers ISR in rice and tomato respectively. In addition, the phyllosphere bacterium *B. altitudinis* FD48 isolated from rice exhibited the signatory volatile compounds including 1-Hexanol, 2,3-butanediol, dimethyl disulfide, benzene, butanoic acid, pentadecane, and acetic acid under drought stress. Further insights on mVOC can be exploited as an alternative for agricultural chemical inputs and it ensuring environmental safety and food security.

Cyanobacterial biofertilizer for sustainability of rice based cropping system

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Cyanobacteria or Blue Green Algae (BGA) biofertilizer now a days forms an essential part of Integrated Nutrient Management (INM) and organic farming. They provide nitrogen to crop plants in a cheap manner besides increasing crop yield by making soil vital, fertile and productive. Cyanobacterial biofertilizer use in rice crop popularly known as 'Algalization' helps in creating an environmentally safe agro- ecosystem that ensures economic viability in paddy cultivation while saving energy intensive inputs. The agricultural importance of these organisms lies in their capacity to fix atmospheric nitrogen, liberation of part of the fixed nitrogen and growth promoting substances as extra metabolites, phosphate solubilisation, addition of organic matter and improving the physico-chemical nature of soil.

The field trials conducted in different locations showed that algal supplementation resulted in saving of about 1/3rd chemical N-fertilizer to obtain similar or enhanced crop yields. The impact of cyanobacterial technology on farmers' field revealed that its use resulted in 25.2 per cent of urea reduction without negotiating the yield of paddy with an overall 3.8 percent increase in the yield and a modest decrease in per acre cultivation cost. A continuous use of cyanobacterial biofertilizer in Rice-Wheat cropping system has also led to gradual improvement in soil nutrient status where the soil organic carbon (OC), available nutrients viz. N, P and K were found to increase when compared with RDF. The soil enzymes activity in terms of soil dehydrogenase and phosphatases were also higher in cyanobacteria biofertilizer treatments.

Although, the cyanobacterial biofertilizer has been recommended mainly in rice crop under flooded conditions that are ideal for their growth, but their effect on succeeding crops like wheat, maize etc. has also been found positive as it helps sustain soil health and productivity. The effective utilization of cyanobacterial biofertilizers will not only provide economic benefits but also improve and maintain soil fertility and sustainability in natural ecosystem on long term basis.

Emerging Signal Molecules for Soil Enrichment and Plant Growth Promotion

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Plant-Microbial symbiotic interaction in the rhizosphere helps bacteria survive in the soil and promote plant growth. Soils are invariably limited in three essential nutritional elements: nitrogen (N), phosphorus (P), and potassium (K). Chemical fertilizers produced at a high cost on an industrial scale prove quite effective in improving plant yield. However, their residual components may continue to persist in soil and contaminate it for an extended period. On the other hand, certain microbes have the unique ability to fix atmospheric nitrogen (N2) and metabolize P and K at ambient temperatures and pressures.

Biological methods have been devised to provide N and P depending upon their s operate their metabolic activities at a unicellular level. However, it has been revealed that a few metabolic activities only prove beneficial to microbes if operated at high cell densities. These cell density-dependent activities termed quorum sensing (QS) operate through specific chemical signals. In Gram-negative bacteria, the most widely reported QS signals are acyl homoserine lactones. In contrast, a novel QS-like system has been elucidated, regulating communication between microbes and plants through strigolactones. These systems regulate bioprocesses, which affect the health of plants, animals, and human beings. This mini-review presents recent developments in the QS and QS-like signal molecules in promoting plant health.

Plant growth-promoting hormones such as strigolactones (SLs) are produced primarily to regulate root and axillary shoot bud development. Under limited phosphate (Pi) and N synthesis, SL exudation is enhanced in the rhizosphere, leading to the optimization of Pi uptake. In non-vascular plants such as Marchantia (liverworts) and Physcomitrella (moss), the exuded SLs above a threshold act as signal molecules regulating the branching of protonemal filaments and colony extension in response to the changes in population density. It helps the host to conserve energy by avoiding growth into regions with Pi depletion. The overall mechanism of communication between signaling molecules and metabolism involves exogenous and endogenous roles. These signal molecules communicate and regulate seed germination, root development, architecture, hair length, and density. These molecules promote arbuscular mycorrhizal (AM) fungal growth, leading to rhizobial symbiosis. Ex-planta (wheat and tomatoes) exposure to SL 2'-epi-GR24, a synthetic analog under Pi starvation, promoted the accumulation of SL and enhanced the expression of related metabolites. Within plants, SLs inhibit side branching to decrease sink tissue and simultaneously expand the root surface to mine Pi while interacting with AM fungi. The role of SLs in establishing communication between parasites and their host plants, such as witchweed and broomrape, has a severe effect on the productivity of economically important crops. The application of naturally occurring SLs (orobanchol and 5-deoxystrigol) and their synthetic analogs (GR7, a GR24 lacking the aromatic A-ring; Nijmegen-1) can help induce suicidal germination of parasitic plant seeds. Despite such promising applications, their applications are limited by a high production cost, low stability, and off-target effects.

Blue strikes again: Re-emergence of chromogenic pseudomonas fluorescens in dairy products, rapid identification and strain characterization in the dairy plant

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In the last two years (2020-2021) it has been reported an increase in the number of blue discoloration cases in dairy products; a phenomenon emerged in Italy mainly in mozzarella cheese in the years 2010-2014, that had a massive economic impact mainly linked to the loss of trust by consumers. Traditional isolation and characterization methods for *Pseudomonas* spp. are time consuming often not compatible with the need of timely answers of the dairy industry. To prevent further cases and monitor the presence of potentially chromogenic *P. fluorescens,* it has been developed a protocol for early detection and typing of strains belonging to the *P. fluorescens* complex in the processing environment. This workflow has been tested in a dairy plant with a history of contamination problems by chromogenic *P. fluorescens*. A weekly monitoring at different stages of the production chain has been planned, and the presence of microbes belonging to the *P. fluorescens* complex has been evaluated by PCR. In case of isolation of putative colonies from positive samples, MLST was carried out. The typing revealed a great diversity of the strains found, mainly of new identification, suggesting the presence of continuous re-introduction through the water supply. However the isolation of the microorganism from the final product was rarely successful, indicating the efficacy of the inactivation strategies implemented by the producer.

Invited

WOMEN IN SCIENCE

Computational redesign of LinA and LinB enzymes

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Both enzymes: lindane dehydrohalogenase (LinA) and haloalkane dehalogenase (LinB) can metabolize well-known pollutants like hexachlorocyclohexanes and hexabromocyclododecanes. They are active toward different isomers either of HCH or HBCD and can be good candidates for bioremediation technology as they have been demonstrated to evolve in bacteria present at the sites rich in various POPs. However, before they are able to be applied in trials using pure enzyme formulations in the field, their potential in such enzyme technology has to be tested at the lab scale. Specific protocols for producing them in a large amount and active form have to be elaborated. They have to provide inexpensive and effective technology to be used on a large scale. Initial attempts in this direction have been undertaken. However, several limitations have been found including those that may change the activity of the enzyme toward their substrates. Therefore it is important to get insight into the studied enzymatic processes at the molecular level and characterize the proteins and the behavior of the ligands in their active sites in such detail that the design of these protocols for proteins to ensure a desired and efficient transformation will be possible.

One way of doing so is to use a computational approach allowing to study the systems of interest in atomistic resolution and to investigate any change taking place due to different ligands, conformation or mutation.

In this talk our attempts to understand and describe the action of LinA and its two variants toward selected HCH isomers as well as efficiency of LinB to degrade β and δ-HCH will be discussed. Based on the computational study results obtained for the wild-type proteins some modifications to the protein sequence will be proposed.

The key role of ciliates in the microbial food web of lakes

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Planktonic ciliates are key organisms in lakes and oceans. Although species identification is standard in any phytoplankton or zooplankton investigation, ciliates are commonly neglected in any lake survey despite their importance in the trophic transfer in aquatic food webs and their good indicator value. In lake plankton, around 150 ciliate species can be found during the course of a year and each one of them has different demands on its environment. In this respect, ciliates need to be identified to the species level because ecologically different, i.e., mixotrophic and heterotrophic species can be found even within one genus. In our studies, we generally follow a ‘bottom-up process’ starting with the morphological identification of a species followed by single-cell sequence analyses and feeding of public databases which in turn form the basis for high-throughput-sequencing approaches. I will present a case study of a potentially new model ciliate species and show why ciliate plankton analyses needed to be based on a combination of morphology, molecular sequences and environmental data. Moreover, an interdisciplinary approach studying these freshwater planktonic protists is necessary to also investigate the nature of symbiotic relationships among ciliates and their algal symbionts. By frequently involving citizens and pupils into our research, we consequently transfer recent findings into classrooms and living rooms to initiate discussions and deposit knowledge on understanding aquatic food webs that form the basis for lake ecosystem functioning.

Vegetables and rhizospheres are reservoirs for the opportunistic pathogen *Pseudomonas aeruginosa*

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World Health Organization) WHO (has declared *Pseudomonas aeruginosa* a serious threat pathogen due to its evolving resistance to multiple antibiotics and its ability to cause high morbidity and mortality .It is a recognized soil pathogen that could easily leach from sewage to water sources .The presence of *P .aeruginosa* associated with agricultural plants was shown back in .1974 However ,the virulence phenotype of the plant-associated *P .aeruginosa* strains has not been characterized extensively .A few human isolates of *P .aeruginosa* are known to infect plants and insects .However ,there is no report on the occurrence of multi-drug resistant *P .aeruginosa* in edible vegetable crops .We hypothesized that highly virulent *P .aeruginosa* strains are associated with vegetables on the farm .This study compared 18*P .aeruginosa* isolates from the rhizosphere and endophytic niches of four vegetable crops)cucumber ,tomato ,eggplant ,and chili (with three known clinical strains .All the isolates were tested for virulence traits ,antibiotics resistance ,motility ,biofilm ,and production of virulence factors) rhamnolipid ,pyocyanin ,hemolysin ,proteases ,and lipases .(The virulence was tested by analyzing their ability to kill the nematode) *Caenorhabditis elegans (*and suppress phytopathogens 'growth) *Pythium aphanidermatum ,Rhizoctonia solani ,Fusarium oxysporum, and Xanthomonas oryzae .(*Hierarchical clustering based on Ward minimum variance with Manhattan distance matrix grouped the strains into three clusters .Strains were exhibiting the highest virulence co-clustered with the human pathogenic isolates .These strains were resistant to cephalosporins ,aminoglycosides ,macrolides ,nitrofurans ,tetracyclines ,and sulfonamides. These extensively drug-resistant) XDR (strains were only susceptible to polymyxin) colistin(and quinolone) cephalosporin .(This study shows that the virulence traits are shared between plant -and human-isolates of *P .aeruginosa* .More importantly ,the occurrence of highly virulent XDR strains in vegetable crops is a serious global threat.

Role of Microbes in Environmental Rejuvenation

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Microbes ensure sustainable remediation of environmental perturbations caused due to anthropogenic activities. Bacteria, in particular, are the world's best biochemists, capable of surviving in harsh environments and hence have been widely reported in bioremediation. However, there are a number of challenges that need to be addressed before bacteria can be used on field scale remediation. Some of them are, contact time, natural vs bioaugmented methods, slow output time, microbial community dynamics etc. Hence, an integrated approach is required using engineering tools along with microbial methods to address rejuvenation of polluted soil or water niches. Polluted niches act as hotspots for the spread of antibiotic resistance genes and these observations make it more imperative to plan knowledge-based remediation strategies. The talk will focus on the challenges and solutions to environmental remediation.

Antimicrobial Resistance and its Impact on United Nation Sustainable Development Goals

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By the beginning of the 21st century, the problem of Antimicrobial Resistance (AMR) has become the most important public health issue and the current COVID19 pandemic has increased the complexity of the problem due to the rampant use of antibiotics. There is a multilateral interdisciplinary interface between the problem of AMR and the achievement of the Sustainable Development Goals. Due to the increasing AMR, there is increased usage of costly last resort antibiotics thereby making the SDG goal 1 (No poverty), 2(Zero hunger)& 3(Good health and well-being) difficult to achieve. Attainment of SDG goal 6(Clean water & Sanitation) & 13 (Climate action) are imperative in reducing the problem of AMR. The life below water (Goal 14) and on land (Goal 15) is also affected by the problem of AMR.
Infection with antibiotic-resistant bacteria may cause severe illness, increased mortality rates, and an increased risk of complications and admission to hospital which lead to a burden on a considerable segment of the society. An antibiotic stewardship or a sustainable approach toward use of antibiotics may help in the reduction of AMR and decrease certain health complications and unwanted healthcare and economic burden. To educate the medical students and to sensitize healthcare professionals we have conducted a series of conferences, CMEs and webinars on antibiotic resistance and antibiotic stewardship. To combat the challenge of AMR, researchers are investigating the alternative to antibiotics. We have been working on different indigenous probiotics which have shown promising results against certain hospital acquired and other pathogens and therefore can be used alone or in combination with certain antibiotics to treat infection. We are also working on bacteriophages and synthetic peptides having potential against pathogens including MDR bacterial strains.

However, there is a need for Global partnership (Goal17) for addressing the problem of AMR and achieving the SDGs simultaneously. It has to be a collaborative effort of medical professionals, scientists, governments, pharmaceuticals, civil society and the general public to work together to address this important public health problem.

Invited

HOST MICROBIOTA INTERACTIONS

Himalayan microbial technologies for society, industry, and the environment

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Life in the Himalayas is adapted to multiple stresses and hostile environmental conditions. Microbes, plants, and animals thriving in such conditions have attained specialized biological functions and adaptive capabilities. Particularly, microbes from such environments can be the source of unique enzymes to perform specialized functions. Intense screening of microbes led to discovery of a unique superoxide dismutase (SOD) enzyme with stability at wide pH and in presence of various inhibitors. Besides, the enzyme was stable even after autoclaving. Realizing its industrial potential, the enzyme technology was transferred to an industry.

Microbes have the capability to improve plant performance, critical to sustain the Himalayan agriculture. For instance, stress-tolerant plant growth promoting rhizobacteria were identified from the rhizosphere of saffron, which have shown growth promotion abilities. Similarly, endophytic microbes of Himalayan medicinal plants such as *Arnebia euchroma* improved plant productivity and adaptability under diverse environmental stresses. Their potential towards production of therapeutically important secondary metabolites is also being investigated. At the societal front, we developed a "Compost Booster", a ready to use formulation for rapid degradation of human/animal waste, and kitchen waste at low temperature conditions. The positive impact of the technology on the environment is reflected as improvement in the management of fecal waste and reduction of foul odour in the night soils, while reducing the impact of chemical fertilizers on the sensitive mountain agroecosystem. Similarly, ethnic fermented foods of Indian Himalayas have great potential due to their nutraceutical and probiotic properties, which are under investigation.

Human Microbiome: Indian Perspective

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The human gut microbiota is "the ecological community of commensal, symbiotic and pathogenic microorganisms that literally share our gastrointestinal tract". Dominated by eubacteria, the metabolic activities performed by the gut microbiome is often as complex as an organ and hence it is now being appreciated and studied in much detail. Increasing evidence suggests that the human gut microbiota changes according to diet, age, lifestyle, climate and geography, genetic make-up, early microbial exposure and health status. Studying the Indian population is relevant given the known dietary and geographical variety, unique family structure and ethnic diversity.

In traditional Indian familial system, where three generations can be studied for changes in the gut microflora with age, it has been shown that the gut microbiota changes according to age within individuals of the same family and a shift in the *Firmicutes/Bacteroidetes* ratio with age is observed, which is different than previously reported in European population. With the incoming wave of lifestyle changes observed now in India and given the availability of sugar-rich diet, the population is at high risk of developing obesity and diabetes. In the case of Diabetes, a consolidated disbiosis of not just eubacterial but also of archaeal and eukaryotic components is seen in the gut microbiota of newly-diagnosed and known-diagnosed diabetic individuals as compared to healthy individuals.

Comparative analysis of gut microbiota of healthy Indian subjects with other populations highlights that the gut microbiomes of Indians is different from that of other Western populations and even cluster separately from Asian populations. The distinctive feature of the healthy Indian gut microbiome is the predominance of genus *Prevotella* and *Megasphaera.*

Taken together, the relevance of studying the Indian microbiome is justified given its unique microbiome features and further studies are necessitated to understand the determinants shaping the Indian microbiome. This will be helpful to develop microbial consortia for prebiotic and probiotic application and devise population specific microbiome therapies.

Soil Microbiome Governs Soil Health and Sustainable Agricultural Systems

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Organisms that reside in the rhizosphere, the topmost soil layer where plant roots interact with microscopic organisms, a motley community, is collectively termed the *Soil Microbiome,* and it functions as the lifeblood of plants – promoting germination, stimulating roots, accelerating growth, and bolstering resistance to disease. Soil microorganisms including bacteria, archaea and fungi play a diverse and often decisive role towards the functioning of ecosystem such as driving the cycling of major elements (e.g. N, C and P). This cycling of elements besides shaping the structure and function of ecosystems also enriches the soil with the abilities that can provide varied services to the people. Soil microbiome along with their allied functions determines the productivity of agro-ecosystems. Sustainable agriculture relies on soil health and the diversity of microbes. Therefore the present day research must focus in managing soil microbiomes. The use of beneficial microorganisms , that improve the health and quality of the plant, and aid in recycling of crop residues are the vital practices for sustainable food production. It is estimated that the majority (≥90%) of the microbial diversity still remains to be explored. This novel unexplored diversity corresponds to treasure troves of improved and innovative biotechnological developments and applications in the fields of agriculture.

Diversity and evolution of chemosensory and flagellar systems amongst Family Vibrionaceae

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Chemosensory systems (CSSs) are advanced, two-component system-based signaling 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 CSS and flagella-system (FS) diversification patterns 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 the 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 different CSS systems, 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; in contrast, 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 characterize further the roles of new CSS, their MCP proteins, and FS proteins in bacterial communication and adaptation.

Phylogenetic Relationships and Potential Functional Attributes of the Genus *Parapedobacter*: A Member of Family *Sphingobacteriaceae*

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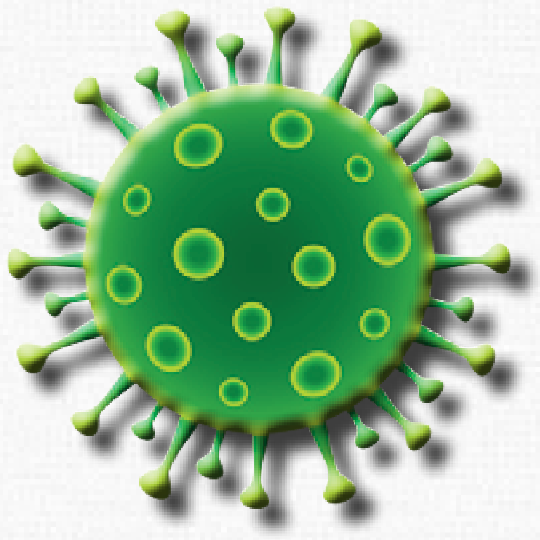
The genus *Parapedobacter* was established to describe a novel genus within the family *Sphingobacteriaceae* and derives its name from *Pedobacter* with which it is shown to be evolutionarily related .Despite this ,they do not share very high16 S rRNA gene sequence similarities .Therefore ,we hypothesized whether these substantial differences at16 S rRNA gene level depict the true phylogeny or these genomes are actually diverged .Thus ,we performed genomic analysis of the four available genomes of *Parapedobacter* to better understand their phylogenomic position within family *Sphingobacteriaceae* .Our results demonstrated that *Parapedobacter* are more closely related to species of *Olivibacter*as opposed to the genus *Pedobacter* .Further ,we aim to study the key differences among these genomes and identified pectinases ,a significant important class of enzymes with the potential industrial application within genomes of *P .luteus* DSM22899 ^{T} and *P .composti* DSM22900 ^{T} .These enzymes ,specifically pectinesterases and pectate lyases are presumed to have largely different catalytic activities based on very low sequence similarities with the already known enzymes and thus may be exploited for industrial applications .We also determined complete Bacteroides Aerotolerance) BAT (operon) *batA, batB ,batC ,batD ,batE* ,hypothetical protein ,*moxR* and *pa3071* (within genome of *P .indicus* RK1^{T} .This expands the definition of genus *Parapedobacter* to containing members that are able to tolerate oxygen stress using encoded oxidative stress responsive systems .By conducting a signal propagation network analysis ,we determined that BatD ,BatE and hypothetical proteins are the major controlling hubs that drive the expression of BAT operon .As a key metabolic difference ,we also annotated complete *iol* operon within *P .indicus* RK1^{T} genome, for utilization of all three stereo-isomers of inositol namely ,myo-inositol ,scyllo-inositol and 1D-chiro-inositol which are abundant source of organic phosphate found in soils .The results suggest that genus *Parapedobacter* hold promising applications owing to their environmentally relevant genomic adaptations which may be exploited in future.

Invited



SARS COV-2

Reading and writing the genome with precision

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The advent of CRISPR-Cas (Clustered regularly interspaced short palindromic repeats-CRISPR associated) makes it feasible to target/edit the genome with precision. Most of the CRSIPR-Cas systems show a trans nuclease activity upon binding their specific target, which is absent in FnCas9 (Cas9 derived from Francisella novicida). This high specificity along with an extremely high mismatch sensitivity (binding is abolished if there is more than a single base pair mismatch between guide RNA and the substrate DNA) of FnCas9 makes it possible to target and edit SNPs with precision. The proof-of-concept for which has been shown by the correction of the Sickle Cell Disease (SCD) point mutation (in patient derived iPSCs, induced pluripotent stem cells) and the detection of SCD/COVID-19 by FELUDA (FnCas9 linked uniform detection assay is a robust, rapid, and inexpensive point-of-care test).

Keynote

Relevant Gene Selection in Cancer Microarray Datasets

Baljeet Kaur
Hansraj College, University of Delhi

Cancer diagnosis can be improved by accurate classification of the gene microarray data. In general, the microarray data is characterized by a large number of genes and a small number of available samples. Hence it suffers from the limitation called the curse of dimensionality. This problem can be overcome by identifying a smaller number of genes accountable for a given disease. Since such relevant genes are only a handful, there is a need to identify them. Feature selection refers to reducing the dimensionality of the feature space by discarding redundant and irrelevant features. This leads to saving the measurement cost as well as reducing the complexity of building the decision model. When feature selection is applied to the cancer microarray dataset, it selects the relevant and non redundant gene set that is discriminatory and helps build a high performance prediction model. The selected genes retain their original physical interpretation. In addition, the retained genes may be important for understanding the physical process related to these genes.

I will be discussing the important feature selection techniques that have been successfully applied to various cancer microarray datasets by our research group to improve the performance of cancer prediction machine learning algorithms.

Invited

Pharmacological modulation of autophagy as a potential therapeutic for Japanese encephalitis

Manjula Kalia

Regional Centre for Biotechnology, NCR Biotech Science Cluster, Faridabad, Haryana, India

Japanese encephalitis (JE) is the leading global cause of viral encephalitis with a significant disease burden in India. One-third of JE infections are fatal, and one-third develop permanent neurological sequelae. There is no specific treatment and clinical management is only supportive. Previous studies from our laboratory have established that a cellular homeostatic process Autophagy, becomes dysfunctional during JE infection and that autophagy enhancement through drugs is likely to be neuroprotective. Recent studies have shown the promise of using autophagy inducers to treat neurodegenerative disease conditions. Several FDA approved drugs have been shown to enhance autophagy, and have the potential to be repurposed. We are currently testing novel compounds and FDA approved drugs for their potential to modulate autophagy. One of the critical aspects of studying autophagy is the measurement of its degradative capacity, also known as autophagy flux. The measurement of autophagic flux (rate of degradation) is important to identify novel autophagy inducers and inhibitors. We have established a stable mammalian cell line expressing the fluorescent probe GFPLC3-RFP to evaluate autophagy flux using a high throughput imaging platform. We have utilized this assay to screen a drug library comprising of 2560 compounds to identify autophagy modulators. In addition to known autophagy effectors we have identified several novel autophagy inducers and inhibitors. These are currently being tested for their potential to prevent neuroinflammation and neuronal cell death, and enhancing immune responses *in vitro* and in mouse model of JE. We aim to provide proof of concept for testing these drugs for JE therapy.

Combating SARS-CoV 2-using drugs and phytocompounds

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It's been almost two years since we heard the term COVID caused by novel coronavirus SARS-CoV-2, the virus which originated from Wuhan City of China. Since then, scientists are looking for several ways to combat this disease, either by prevention using vaccination, lockdown and social distancing or by curing using several drugs. Many mutations have been traced in this virus that have led to emergence of several variants, especially mutations in RBD region of Spike protein has increased pathogenicity and transmissibility of some of these variants. Though many vaccines are now licensed, yet some Variants of Concern (VOCs) have now raised doubts regarding the efficacy of the same.

Nevertheless, several drugs have been tested using *in silico* and *in vitro* studies against SARS-CoV-2, but these drugs are not free of side effects and comprise of toxicity or immunogenicity. In our present study, we tried to find the potential existing drugs that are used against other RNA viruses. And as phytocompounds are usually free of toxicity and other side effects, Emodin, Artemisinin, Apigenin like phytocompounds have also been docked against SARS-CoV-2. A comparative analysis of the best drugs and phytocompounds was also conducted on all the VOCs categorized by WHO. Hence, we propose that some drugs and phytocompounds can be a conceivable solution for curing COVID.

Host-pathogen interactions during SARS-CoV2 infection: insights from virus-host RNA-protein interactome studies

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Severe acute respiratory syndrome-coronavirus-2 (SARS-CoV-2) is a positive-strand RNA virus, which is responsible for the ongoing COVID-19 pandemic. Replication of a positive-strand RNA virus involves an RNA-protein complex consisting of viral genomic RNA, host RNA(s), virus-encoded proteins and host proteins. Dissecting out individual components of the replication complex may help in decoding the mechanism of viral replication. SARS-CoV-2 genome is capped at the 5'-end, followed by an untranslated region (UTR). There is poly-A tail at 3'-end, preceded by an UTR. Self-interaction between the RNA regulatory elements present within 5'- and 3'-UTRs as well as their interaction with host/virus-encoded proteins mediate the function of 5'- and 3'-UTRs. Using RNA-protein interaction detection (RaPID) assay coupled to liquid chromatography with tandem mass-spectrometry, we identified host interaction partners of SARS-CoV-2 5'- and 3'-UTRs and generated an RNA-protein interaction network. By combining these data with the previously known protein-protein interaction data proposed to be involved in virus replication, we generated the RNA-protein-protein interaction (RPPI) network, likely to be involved in controlling SARS-CoV-2 replication. In silico analysis of the RPPI network revealed the enrichment of factors involved in translation initiation and RNA metabolism. In addition, analysis of one of the interaction partners of the 5'-UTR (Lamp2a) demonstrated its role in reducing the viral RNA level in SARS-CoV-2 infected cells. Collectively, our study provides a resource of SARS-CoV-2 UTR-binding proteins and identifies an important role of host Lamp2a protein during viral infection.

Advances in the research of the SARS-CoV-2 molecular structure and pathogenesis from a systems biology approach

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Experimental analysis of the interaction of viral and host proteins, or interactome has been a fundamental contribution to understand the form in which SARS-CoV-2 virus takes control of the host molecular network to produce new virions and propagate the infection. This allows the construction of the viral network representation of the interactome and its statistical analysis. Formulation of network models of this interactome is a basic tool to identify drug targets capable of interrupt the viral replication cycle, and for the design of novel therapeutic agents. SARS-CoV-2 is a free-scale hierarchical modular structure in which the open reading frame 8 protein, nucleocapsid protein (N), and non-structural protein 7 (Nsp7) are the central hubs. This kind of organization confers an extra level of complexity to this molecular network allowing it to resist the attack of drugs on single nodes. However, simultaneous suppression of these three hubs can effectively disrupt the network. Systems biology approach to the analysis of the SARS-CoV-2 interactome reveals the existence of key nodes (open reading frame 8 protein (orf8), Membrane protein (M), open reading frame 9b protein (orf9b), Nucleocapsid protein (N), open reading frame 10 protein (orf10), Envelope protein (E), open reading frame 6 protein (orf6), open reading frame 7 protein (orf7) and Spike protein (S)) that belong to high modularity classes and control the flow of information during infection. These proteins are possible targets for new drugs through which most of the information required for the production of new virus must flow. A therapeutic attack on these hubs can increase the probability to defeat viral infection as an alternative to a vaccine.

Multi-omics analysis to understand the host-metabolic reprograming during SARS-CoV-2 infection associated with disease severity

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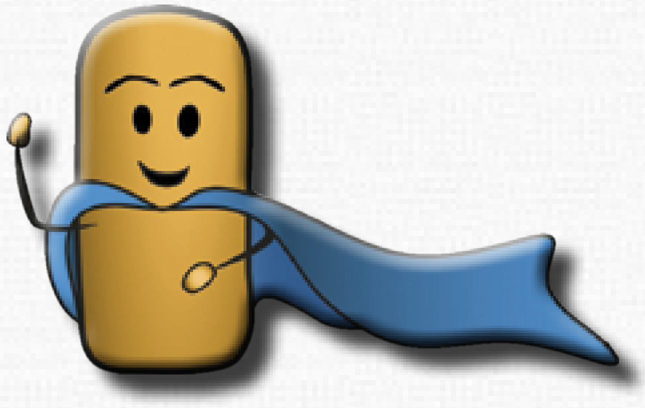
Viruses are known to exploit the host metabolic machinery to meet their biosynthetic demands for optimal replication capacity. This cellular exploration is highly connected with the initial host-viral response, thereby determining the disease pathogenesis. Viral replication is dependent on extracellular carbon sources such as glucose and glutamine. It induces a plethora of metabolic alterations in host-cell including host central carbon metabolism, nucleotide, fatty acids and lipid synthesis that modulate viral pathogenesis and host-response. Recent using in vitro multi-omics studies, we have shown that the severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) dysregulates PI3K/Akt/mTOR and HIF-1 signaling in infected cells. We used patient-derived multi-omics data and in vitro infection assays, to understand the role of key metabolic pathways that can regulate SARS-CoV-2 reproduction and their association with disease severity. COVID-19 disease severity was characterized by increased plasma glucose and mannose levels and monocytes showed altered expression patterns of carbohydrate and amino acid transporters, GLUT1 and xCT respectively. In in vitro lung epithelial cells (Calu-3) infection model we found that glycolysis and glutaminolysis are essential for virus replication and blocking these metabolic pathways caused significant reduction in virus production. Further personalized genome scale metabolic modeling identified role of mitochrondrial metabolites and transporters in COVID-19 disease severity. Taken together, our study highlights that the virus utilizes and rewires pathways governing central carbon metabolism leading to metabolic toxicity. Thus, the host metabolic perturbation could be an attractive strategy to limit the viral replication and disease severity.

Invited



MICROBIOLOGY OF EXTREME ENVIRONMENTS

Archaea as an option for plant growth promotion and abiotic stress management

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Microorganisms, particularly eubacteria and fungi are known to play an important role in biogeochemical cycling and making available important nutrients like nitrogen (N), Phosphorus (P) and potassium (K) to the plants through fixation, solubilisation or mobilization of nutrients. Archaea represents the third domain of life and inhabits extreme environments. It comprises more than 20% of the world' biomass and is among the most primitive and ancient life forms on earth. However, their role in biogeochemical cycling and in the sustenance of vegetation in extreme environments has not been given much focus. Despite the fact that archaea were recognized as a separate kingdom more than 30 years ago, virtually nothing is known about their activities in most ecosystems. They are significant contributors to the global carbon and nitrogen cycles; still, their involvement in these processes in terrestrial environments is to a large extent unknown. Likewise, there are very few reports on the characterization of these archaea for their plant growth promoting traits so as to help the vegetation to survive better in these extreme environments characterized by nutrient deficient milieu. Halophilic archaea were isolated from the hypersaline environment of Rann of Kutch, Gujarat, India. 16S rRNA sequence comparison and phylogenetic analysis demonstrated that only euryarchaeotal archaea were present at Rann of Kutch. Among 157 isolates, sixteen distinct species of ten genera namely Haloarcula, Halobacterium, Halococcus, Haloferax, Halolamina, Halostagnicola, Haloterrigena, Natrialba, Natrinema and Natronoarchaeum were identified. Among 157 archaeal isolates, twenty exhibited phosphate solubilization both in plates and broth. The ability of archaeal isolates to solubilise tricalcium phosphate ranged from 51.92 ± 0.8 to 1986.86 ± 1.8 $\mu g\ mg^{-1}$ protein. In addition, isolates could solubilize potassium; produce IAA, Zeatin and siderophore. An archaea, Halolamina pelagica strain CDKAB1 was selected and used as seed inoculant for the wheat cultivar KRL 213 grown in saline soils of Rann of Kutch having EC of 7.36 $dS\ m^{-1}$. The shoot and root length of plants inoculated with CDKAB1 increased by 9.2% and 44.7% respectively. A significant increase of 45.37% in the plant biomass was recorded in plants inoculated with CDKAB1 as compared to control. The degree of membrane damage due to stress is higher in the control as compared to treatment with CDKAB1. The plants inoculated with archaea CDKAB1 showed a significant increase in phosphorus and potassium uptake and helped wheat and mustard plants to grow under drought conditions.

Exploiting Microbial Factories for Nanoparticle Synthesis: Novel Nano-biotechnological based Sustainable Bioremediation of Environmental Contaminants

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Modernization has thrown humanity and other forms of life on our planet into innumerable problems. Climate change, indiscriminate use of pesticides and fertilizers, environmental degradation are a few of the shared global problems that have intensified in the face of population growth and food shortages. Conventional physical and chemical procedures for development of metal nanoparticles have become outdated due to extensive energy expensive production method, requiring hazardous materials, advanced equipment. This has a negative impact on the environment by generation of toxic by-products that causes significant risks to the human health and environment.

Nano-biotechnology along with sustainable chemistry has immense potential to replicate innovative and critical components to support the surrounding environment, human health, and industry sustainably. Different unconventional methods were being used in green chemistry to synthesize gold and silver nanoparticles from various microbes. The production of nanoparticles by physical and chemical methods research activities in the context of nanotechnology have shifted towards environmentally friendly and economically viable 'green' synthesis to support the increasing use of nanoparticles in various industries. Green synthesis, as part of bio-inspired protocols, provides reliable and sustainable methods for the biosynthesis of nanoparticles by a wide range of microorganisms rather than current synthetic processes. Bacteria are known as potential bio-resources for generation of nanoparticles such as gold, silver, platinum, palladium, titanium, titanium dioxide, magnetite cadmium sulfide and others Nanomaterials synthesized through microbes can be used as a pollution abatement tool due to the multiple functional groups that can easily target pollutants for efficient bioremediation thereby promoting environmental clean-up. The objective of the present talk is to highlight the significance of micro-organisms like bacteria, actinomycetes, filamentous fungi, yeast, algae and viruses for nanoparticles synthesis and advantages of microbial approaches for elimination of heavy metals, dyes and wastewater treatment.

Insights Into The Lifestyle Of A Thermophilic Genus *Thermus*

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Thermophiles, in general, have been recognized to hold great potential as a source of various industrial and biotechnological enzymes. Among thermophiles, the genus *Thermus* has occupied a centre stage in biotechnology since its discovery. *Thermus thermophilus* is a model organism, due to easy handling and well-developed manipulation techniques. Establishing a better understanding of their genomes can provide a glimpse of the lifestyle and community interactions of these thermophiles. *Thermus* spp. are known to harbour small and dynamic genomes. Comparative genomic analysis of 17 strains of *Thermus*, including the only Indian species *T. parvatiensis*, isolated from Manikaran hot water springs in the Himalayan region of Himachal Pradesh was undertaken. The genome of *T. parvatiensis* (2.01 Mbp) was sequenced and annotated, which revealed the presence of a megaplasmid pTP143 (143 Kbp). Phylogenomic placements of the members was accessed using multiple genome-based parameters to resolve phylogenetic relations among them. The role of bacteriophages in thermophilic microbial communities has been recognized in carrying out gene shuffling and modulating host populations, therefore, their diversity was elucidated in this group by the analysis of CRISPR spacers found incorporated in their genomes. Amenability to phage invasion was also found correlated with natural competence in this genus which is responsible for its easy manipulation. This study provided crucial insights into the genome construct, dynamics, habitat-specific gene repertoire and inter-species relationships among the members of *Thermus*.

Exploration of extremophiles for potential bioremediation & biotechnological applications

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With the capability to survive, adapt and thrive in diverse conditions such as extremes of temperature, pH, pressure, salinity, UV radiation, etc., extremophiles possess robust enzymatic and bio-catalytic systems which are useful in a variety of industrial applications. The marine biosphere is one of the richest and unexplored biospheres on the Earth and is a major source of natural compounds with potential in biotechnology. The search for extremophiles for industrial and biotechnological applications has gained importance in recent years. The Southern Ocean, which harbors rich microbial diversity, seems to have a promising future in the development of novel biologically active substances. In the present investigation, 80 samples (water, sediment, and algal mats) were collected during the Expedition to the Southern Ocean and Antarctica. Water and sediment samples were collected from different locations of different islands/ peninsulas like Bharti Station, Fisher Island, McLeod Island, Broknes peninsula, and Stornes peninsula. Seawater samples were collected in sterilized bottles from different depths using CTD operations. On-board culturing of microorganisms were done using selective media for investigating their roles in bioremediation and other biotechnological applications. Various extremozymes are being isolated and studied for their potential uses. Extremophillic microbes can be used to actively degrade xenobiotics and convert them into less harmful substances. This presentation gives a detailed review of exploring the roles of extremophiles in bioremediation and other biotechnological applications.

Exploration of Himalayan microbes for the improvement of hill agriculture

Dr. Rakshak Kumar
CSIR - Institute of Himalayan Bioresource Technology,
Palampur, India

Commercial biofertilizers tend to be ineffective in cold mountainous regions due to reduced metabolic activity of the microbial inoculants under low temperature. Cold-adapted glacier bacteria with plant growth-promoting (PGP) properties may prove significant in developing cold-active biofertilizers for improving mountain agriculture. With this perspective, the cultivable bacterial diversity was documented from East Rathong glacier ecosystem lying above 3900 masl of Sikkim Himalaya. Eastern Himalaya: A total of 120 bacterial isolates affiliated to *Gammaproteobacteria* (53.33%), *Bacteroidetes* (16.66%), *Actinobacteria* (15.83%), *Betaproteobacteria* (6.66%), *Alphaproteobacteria* (4.16%), and *Firmicutes* (3.33%) were recovered. Fifty-two isolates showed multiple *in vitro* PGP activities of phosphate solubilization (9-100 µg/mL), siderophore production (0.3-100 psu) and phytohormone (IAA) production (0.3-139 µg/mL) at 15 °C. Western Himalaya.

Genome analysis of four representative bacteria of diverse genera predicted many genes involved in the bacterial PGP activity. Comparative genome study highlighted the presence of PGP-associated unique genes for glucose dehydrogenase, siderophore receptor, tryptophan synthase, phosphate metabolism (PhoH, P, Q, R, U), nitrate and nitrite reductase, TonB-dependent receptor, spermidine/putrescine ABC transporter etc. in the representative bacteria. Overall, this study signifies the psychrotrophic bacterial diversity from an extreme glacier environment as potential tools for improving plant growth under cold environmental stress.

Microbial ecology of Arctic fjords and associated glacier foreland ecosystems in the changing climatic era

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The Arctic region is known as one of the fastest-warming regions of the world, and current predictions indicate that the ongoing environmental changes are greater than any other part of the Earth. The glaciers around Svalbard Archipelago have been rapidly retreating for the past two decades, and recent observations suggest the increased influence of Atlantic water masses in the Arctic shelves. These unprecedented changes have already proven to profoundly impact the ocean biogeochemical process, microbial food web structure, and biodiversity changes. Monitoring and documenting these changes in the Arctic marine and terrestrial environments are critical to forecast and respond to the changes. Our research group is mainly focused on investigating How microbial ecosystems are responding to physical oceanographic perturbations across different Arctic fjords, the influence of environmental variables and their relationship between community assembly, distribution-dispersal patterns and associated biogeochemical processes, Microbial succession and colonization across different deglaciation stages of foreland systems. In our approach, we use both 16S rRNA gene-based amplicon sequencing and shotgun metagenomics techniques to delineate the microbial community structure and its functions in their relevant ecosystems. Our recent observations shows that fjords host distinct microbial populations among the different Arctic fjords located in the western and northern region of Svalbard.

TRANSLATIONAL & INDUSTRIAL MICROBIOLOGY

Process development and scale up for production of microbial exopolysaccharides :Petri plate to pilot plant

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Polysaccharides are natural and biodegradable polymers that envelop the surface of most cells and have variety of biological functions. Recently there has been an increasing interest in extracellular microbial polysaccharides for food, pharmaceutical, and medicinal use. Xanthan, gellan, curdlan and dextran are the major commercially available bacterial polysaccharides. Few fungal exopolysaccharides are also well known for their unique physicochemical properties and industrial potential.

Pullulan is one such commercially important fungal exopolysaccharide. Due to its unique physicochemical properties, pullulan has found applications in diverse industrial sectors. Pullulan capsules may be used for pharmaceutical and nutraceutical products. Its non-animal origin and GRAS status ensures safety and acceptability across diverse consumer groups. Despite large number of valuable applications, major constraints associated with fermentative production of pullulan are formation of melanin pigment, low yield and high cost associated with pullulan production. Hence, it would be highly desirable to develop a cost effective technology for pullulan production.

In CSIR-IMTECH, we have developed a process for pullulan production using an osmotolerant strain of Aureobasidium pullulans. Initially, the process was optimized in 5L fermenter and later it has been scaled up to 500 L fermenter. It was possible to obtain more than 80g/L pullulan after process optimization and scale up. The yield and productivity of our process is higher as compared to published literature. Moreover, the process of CSIR-IMTECH has been developed using inexpensive agri-industrial residues and would result in significant reduction in the cost of production. Hence, our process is actually about creating wealth from waste

Fermentative production of 2,3 Butane Diol :A sustainable pathway for renewable chemical production

Sanjukta Subudhi*, Divya Mudgil & Koel Saha

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Current market demand of industry platform chemicals are mainly fulfilled through use of conventionally derived fossil based chemicals produced through energy intensive chemical routes. These processes are not environmentally sustainable. Thus, bio-based production of industry platform chemicals are gaining global attention. 2,3-Butane Diol (2,3-BDO) is one of the value added specialty industry platform chemical that has found application in various industries; pharmaceutical, cosmetics, food, agriculture, polymer, synthetic rubber, owing to its unique stereoisomerism. Levo isomer of 2,3-BDO has very low freezing point (-60 ºC), making it a suitable antifreeze. Current market demand for 2,3-BDO is fulfilled through use of traditionally derived fossil based 2,3-BDO.

Biotechnological production of renewable 2,3-BDO has got environmental as well as economic advantages over the conventional 2,3-BDO. Biobased 2,3-BDO production process is yet to be commercialized. Major drivers of this process are; upstream production, downstream purification and application. Upstream production process has been widely explored globally. However, the downstream recovery process still requires intensive investigation to make the process cost economically viable. Major challenge is high boiling point of 2,3-BDO. Another important factor contributing to the cost of biobased 2,3-BDO production is; feed. Hence, it is essential to explore for use of low cost commercial grade feed and/or co-product such as glycerol from other biodiesel production processes, molasses, to make the overall process cost economically viable.

This presentation will highlight on the research outcome with respect to the development of a bioprocess for 2,3-BDO production using a select non-pathogenic host strain; ‘*Enterobacter roggenkampii* strain TERI-CT’ and its downstream purification form the fermentation broth.

Integrative Metagenomics and Metabolomics of Some Himalayan Fermented Foods; Microbial Communities and Health Benefits

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The Himalayan regions of India, Nepal and Bhutan have more than 200 varieties of unsurpassed ethnic fermented foods and alcoholic beverages, which are region- and community-specific, unique and some are exotic and rare. The Himalayan people have invented the indigenous knowledge of utilization of unseen microorganisms, both culturable and unculturable, present in and around the environment for preservation and fermentation of perishable bio-resources to obtain the organoleptically desirable and culturally acceptable ethnic fermented food and alcoholic beverages. Sequence-based metataxonomic studies using high-throughput and shotgun sequences have revealed huge microbial community structures in some Himalayan fermented foods and amylolytic starters. Most of the beneficial microorganisms isolated from some ethnic fermented foods are listed in microbial food cultures (MFC) safe inventory. The integrative metagenomes and metabolomics studies of some Himalayan fermented foods have detected many untargeted metabolites including bioactive compounds, immunomodulators, vitamins, etc, which are considered as the prime health-promoters to the consumers. The KEGG annotation of predictive functionalities generated by the machine learning tool, have been validated by the real time experiments of metabolomics.

Biofoundry of lipstatin from Petriplate to Bioreactor

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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 leads 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.

Scale-up and commercialization of 24-desmethyl rifampicin effective against resistant strains of rifamycin *Mycobacterium tuberculosis*

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Rifamycin has been used as a wonder drug for treating tuberculosis caused by *Mycobacterium tuberculosis* (Mtb) since its discovery in the 1950s. However, with the advent of antimicrobial resistance, the strains of Mtb have developed resistance against the rifamycin produced by *Amycolatopsis mediterranei.* Our group is using a mutant producer strain of *A. mediterranei* generated using the combinatorial biosynthesis approach. The mutant strain produces an effective analog known as 24 desmethyl rifamycin having an activity of almost 50-fold higher when tested against the resistant strains of Mtb. We are now focussing on scaling up the production and purification of 24 desmethyl rifamycin. As the first step, the fermentation media and conditions had been standardized and now, we are also working to develop a downstream purification process. The results are encouraging as the production of the molecule has increased and the production time has been decreased. The research findings and results will be presented during the lecture.

CLINICAL MICROBIOLOGY

Understanding environmental dimensions of antibiotic resistance

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Antimicrobial resistance (AMR) is one of the most critical epidemiological predicaments of the 21st century, and there is increasing evidence that environmental hotspots contribute to this phenomenon. This presentation specifically focuses on the potential contribution of treated wastewater irrigation on AMR in irrigated soil and crops. Culture-based and shotgun metagenomic analyses indicated that treated wastewater irrigation does not significantly disseminate antibiotic resistance to soil. However, following short-term soil inoculation in copiotrophic media, these methods revealed significant differences between freshwater and treated wastewater irrigated soils when low-quality wastewater was used for irrigation. This suggests potential epidemiological ramifications if soil is ingested and exposed to "gut like" conditions. Collectively, we demonstrate how coupling culture-based and metagenomic approaches can uncover environmental reservoirs of antibiotic resistance, and recommend applying these methods within the framework of future "*farm-to-fork- one health*" evaluations.

The mysterious deep subsurface biosphere: What sustains one of the largest, slowest ecosystems on Earth?

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The oceanic subsurface contains a vast microbial ecosystem whose metabolic processes drive key biogeochemical cycles. These microbes are often from evolutionary branches on the tree of life that have never been characterized or described in a laboratory. Therefore, new methods have had to be developed to learn about these elusive communities in deep subsurface sediments. Methods such as direct identification of a suite of biomolecules (DNA, RNA, proteins, lipids, and metabolites), coupled to isotopic tracer incorporation and geochemical measurements have produced a more in-depth view of the role that these microbes play in Earth systems. From this work, a picture has emerged of a diverse ecosystem that may be growing orders of magnitude more slowly than life at the surface. Although it is slow, this life is metabolically active, contributing to the breakdown of ancient organic matter in ways that differ from those found in surface organisms.

Recent work has identified zones where microbes have enough energetic resources to grow faster than the cellular decay rate. This suggests a model for adaptive selection to ultra-slow growth in long-term burial in marine sediments. Rather than simply being accidentally alive for thousands of years while riding a one-way conveyer belt to their deaths, it is possible that sediment microbes are adapted to this subsurface niche space. The payoff for long-term ultra-low activity is that rare events such as slumping, turbidite flows, or mud volcanoes enable a return to shallow sediments where higher quality substrates enable natural selection to occur.

Biosynthetic studies of microbial-derived α-glucosidase inhibitors

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α-Glucosidase inhibitors have been used clinically to treat type-2 diabetes. They inhibit glycosidase enzymes that digest carbohydrates in the intestines, resulting in reduced glucose absorption and improved post-prandial blood sugar level. In addition to some plants, many bacteria produce specialized metabolites with α-glucosidase inhibitory activity. Metabolites with such biological activity include the iminosugars, e.g., nojirimycin and deoxynojirimycin, and the pseudo-oligosaccharides, e.g., acarbose. Nojirimycin and deoxynojirimycin are mainly produced by strains of Bacillus and Streptomyces, whereas acarbose and its analogues are produced by several strains of Actinoplanes and Streptomyces. Another α-glucosidase inhibitor that is used as an antidiabetic drug is voglibose, a semi-synthetic product of valienamine, which is derived from the crop protectant validamycin A. Over the past decades, efforts have been made to understand how these interesting sugar-like compounds are made in nature. Isotope incorporation experiments, genetic inactivation, enzymology, and synthetic biology are among the approaches used to elucidate their biosynthetic pathways. Results from the studies as well as the proposed ecological functions of these specialized metabolites will be discussed.

Genomics and genetics of antimicrobial resistance in human associated bacteria

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Antimicrobial resistance (AMR) in clinically important microbial species has become a global concern. However, our knowledge about the genetic nature of AMR genes, its linkage with mobile genetic elements, source and acquisition process, and stability of the genetic elements linked with AMR genes are limited. We recently sequenced the whole genome of several human associated commensal and pathogenic enteric bacteria isolated from different parts of India. Our findings provided insights into the genome of Indian isolates and identified several acquired traits including plasmids, transposons, integrating conjugative elements (ICEs), pathogenicity islands (PIs), prophages, and gene cassettes that confer AMR and fitness to the enteric bacteria. For a comprehensive understanding of dynamics of MGEs in the bacterial genome, we engineered the genome of *Vibrio cholerae* and examined *in vitro* and *in vivo* stability of genomic islands (GIs), ICEs and prophages. The new knowledge generated from this study would help in better understanding of bacterial evolution and management of enteric diseases by providing clinical guidance on preferred treatment regimen.

Enzyme engineering through iterative learning: the case of L-asparaginases

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L –asparaginase is an amidohydrolase long known for its antileukemic activity. Currently available L-asparaginase suffers serious drawback of having low half-life and associated glutaminase activity. A top down approach was taken where a thermophilic L-asparaginase with a stable scaffold was successfully converted into a mesophilic type which became commercially viable. We changed its properties through iterative learning from its structure and biochemistry. This talk is about how a protein engineering attempt unfolded several surprising realms of asparaginases. This study illuminates on many parallel leads, each with potential industrial and therapeutic applications.

Gut microbiology in multiple sclerosis

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Multiple sclerosis (MS) is an autoimmune central nervous system (CNS) disease, and experimental autoimmune encephalomyelitis (EAE) is an animal model of MS. The etiology and pathogenesis of MS and EAE remain unknown. Recently, studies have focused on the microbes that colonize the skin and mucosal surfaces and mainly those that may be found in the gastrointestinal (GI) tract . Gut microbiome is immunogenic and protective. It has been shown that an imbalance in the gut microbiota, called "dysbiosis," is associated with various diseases, ranging from intestinal diseases, like colorectal cancer, irritable bowel syndrome, and inflammatory bowel disease (IBD), to other systemic diseases such as obesity, malnutrition, diabetes, metabolic syndrome, and rheumatoid arthritis (RA). In the field of neurology, attention is also focused on the role of the gut microbiota in CNS diseases, such as Alzheimer's disease and Parkinson's disease (PD). Gut microbiome can worsen EAE as segmental fila-mental bacteria induce T17 cells . Disease modifying agents for MS may act by altering gut microbiome. The mechanisms with which gut microbiome may impact MS pathogenesis are molecular mimickers which increase T17 helper cells and bring about decrease in immunosuppressive cells. The research in role of gut microbiome opens new vistas for understanding pathogenesis and creating new treatment paradigms for MS.

Parasites are Beautiful: Microscopy based approaches to study parasitic diseases

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Every year parasitic diseases of humans lead to loss of countless human lives and those infecting livestock lead to enormous economic damage. Eradication of parasites has been seldom effective and has fuelled research for the development of better anti parasitic treatments. Apicomplexan parasites like *Toxoplasma* and *Plasmodium* have a specialised replicative niche known as the parasitophorous vacuole that is selectively permeable and limits the transport of materials or drugs into the parasite. They also harbour specialised drug efflux or evasion mechanisms that pump out compounds that are able to permeate the parasites thus rendering them ineffective and giving rise to drug resistance. Augmenting current therapies is thus the need of the hour along with developing new therapies for which we need to identify new drug targets. We can now utilise CRISPR-Cas9 based gene editing tools to identify potential candidates and study their effect on parasite viability and infectivity. Fusing the protein of interest with a fluorescent tag helps to track the localisation of the protein and accompanied with microscopy-based tools has proven to be extremely useful in developing specialised compounds that can target the protein with ease. Coupling CRISPR-Cas9 based tools with super resolution structured illumination microscopy provides a rather effective opportunity to identify potential druggable targets for apicomoplexan parasites which will eventually aid in generating a new class of drugs that can penetrate the selectively permeable membrane of these parasites and eventually save human lives.

Unique gate dynamics of topoisomerase I in the presence of PPEF which combats WHO listed priority pathogens *in vitro* and *in vivo*

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New therapeutic agents are required on a priority basis to replace existing drugs to deal with antimicrobial resistance. DNA topoisomerases are well-validated targets for antimicrobial therapies, even though DNA gyrase has been largely exploited as a drug target, due to multiple mutations, hence the gyrase is not an ideal target. In this study, bacterial topoisomerase IA has been evaluated as a drug target. Our study narrowed down to two broad-spectrum antibacterial agents; PPEF and BPVF targeting topoisomerase IA and III and killing 08 MDR pathogens. WHO expert group (Bull World Health Organ 2020 ; 98:151) assessed the novelty of the antibacterials using four criteria: absence of known cross-resistance, new class, new target, and the new mode of action. PPEF and BPVF fulfill three of the above criteria. PPEF and BPVF showed significant efficacy in sepsis mice with no toxicity. Our study provide lead antibiotics to combat drug-resistant pathogens. Using this hypothesis, two bisbenzimidazoles, PPEF and BPVF were synthesized, which selectively inhibit topo IA and topo III enzymes in bacteria. PPEF displayed high efficacy against ~455 MDR bacteria. PPEF induces transcription repressor genes. Both the compounds demonstrated efficacy against mice infected with MDR, *Escherichia coli*, and methicillin-resistant *Staphylococcus aureus* without toxicity. Further, to understand the molecular mechanism of inhibition of topo IA with PPEF accelerated molecular dynamic simulations were carried out and the results suggest that binding of PPEF preferentially stabilizes the (gate) closed confirmation topo IA by about -6 kcal mol^{-1} and consequently destabilizes the binding ssDNA. The gate opening dynamics model of topo IA may be used as a tool to screen topo IA inhibitors.

Human Gut Microbiota and Microbiome Manipulation therapies

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Trillions of microorganisms, including bacteria, viruses, archaea, and fungi, inhabit the human gut, collectively known as microbiota. With almost equivalent number of microbial cells and 100 times more genes than the human genome, the human gut microbiota is considered as another genetically distinct organ or a second metabolic organ with diverse functions. Traditional culture-based methods could not characterize vast bacterial communities and many microbes require anaerobic conditions to grow. These difficulties have been overcome by nucleic acid amplification methods. The change in quality and quantity of gut microbial flora, or "dysbiosis" have been associated with various gastro-intestinal and non-gastrointestinal disorders. Microbiota manipulation has attracted researchers and various strategies have been developed in an attempt to restore healthy microbiota. Modalities of gut microbiome manipulation includes prebiotics, probiotics and fecal microbiota transplantation (FMT). FMT is one of the most effective microbiome therapeutic strategy. It has gained popularity in recent decades and has been proven to be effective in recurrent *C.difficile* infections (CDI), inflammatory bowel disease (IBD) and its role has been explored in various gastrointestinal and non-gastrointestinal diseases

MICROBIOLOGY FOR SCIENCE & SOCIETY

Diet from a poospective :The Microsetta Initiative

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The Microsetta Initiative, a microbiome citizen science effort initiated at the University of Colorado Boulder in November of 2012, has enabled over 25,000 people to take part in microbiome research to date. Participants receive an educational and non-actionable report about their microbiome and the Microsetta Consortium de-identifies and aggregates these data, including rich questionnaire responses, into the public domain for anyone to reuse. Our analysis of this resource revealed numerous strong and novel associations with microbiome data, such as the number of different plants consumed correlating with microbial diversity. To explore these associations further, we performed untargeted mass spectrometry on a subset of samples and uncovered a suite of novel molecules associated with the faecal microbiome related to hosting lifestyle. Highlighting the potential for data reuse, we re-evaluated the dataset to explore the impact of fermented food consumption, observing a subtle but significant association with microbes used in fermented products. We further integrate the data as a whole with n=1 individual longitudinal trajectories to emphasize how data reuse can provide a contextual landscape for interpretation of the impact of life events. Finally, we explore a glaring gap in microbiome research: studies often focus analytic efforts on western individuals, limiting the scope and applicability of microbiome associations. Our collaborative effort aims to address this by bringing the Microsetta infrastructure to the worlds population.

The International Microbiology Literacy Initiative

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Microbial activities pervasively influence our personal lives, sustainable development, economic development and global crises (witness the current COVID-19 pandemic). In order to take appropriate, evidence-based decisions in many spheres at all levels, an understanding of relevant aspects of microbiology, including microbiomes, is essential. There is an urgent need for microbiology literacy in society. The case for microbiology literacy has been made in an Editorial published in 2019:
(https://sfamjournals.onlinelibrary.wiley.com/doi/epdf/10.1111/1462-2920.14611).
This Editorial has in the meantime been translated into the major international languages. The International Microbiology Literacy Initiative was launched with the goal of creating microbiology literacy through the development of a microbiology school curriculum and supporting resources, all of which will be made freely available. The aim of the Initiative is not to create microbiologists, but rather to engender new adult generations that know enough about relevant microbiological processes to be able to take informed evidence-based decisions at personal, family, community, national and international levels. To do this, the IMLI seeks to generate curiosity and excitement about microbes and their activities in children, and to inform them how microbes affect us in our everyday lives and how important such activities are for our wellbeing and that of the planet. The relevance of microbes and their activities to sustainability, to attainment of the Sustainable Development Goals, and to Grand Challenges, are revealed and proposed for class discussions.

The use of comics for microbial literacy in children

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Throughout history, bacteria have been mainly associated with human and animal diseases. As microbiologists, we all know the relevance and impact of microbes in our daily lives. Even more, the COVID-19 pandemic put in evidence that microbiology literacy to our society is mandatory. One of the most challenging microbiology problems is that we cannot see microbes and viruses by eye. It is also more complicated for children as we still do not have specific microbiology curricula for them according to their age and needed. In this context, as microbiologists, we need to explore different strategies to communicate the discipline. Convinced of the importance that science education has on children, we have been involved in a project using comics as a tool for microbial literacy, mainly for children and the general public. Here, I will tell you our experience with the development of comics to teach microbiology. The use of different strategies for teaching microbiology will empower children and, as a consequence, parents and finally the general society to make an informed decision, to have arguments for and against misinformation and fake news.

Bringing Evidence-Based Microbiology to the Community Level in Lower Nyakach, Kenya, to Eliminate Waterborne Disease

Bob Metcalf
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A major obstacle in addressing waterborne disease at the community level in low-income countries is because standard water testing methods require materials and facilities that are neither available nor affordable and are totally unsuited for community use. Also, because disease microbes are invisible to the naked eye, it is difficult for people to understand their drinking water sources may be contaminated and result in disease.

Water testing challenges at the community level have been overcome by using two internationally approved tests for *Escherichia coli* from the water and food industries: the Colilert 10 ml presence/absence test and the *E.coli*/Coliform Count Petrifilm, a quantitative test for 1ml. Overnight results from these tests identify WHO disease risk categories of low, moderate, high and very high.

Using these methods with a brief training session, community-based organizations can become competent to perform and interpret the tests, educate their communities, and develop strategies to eliminate waterborne disease.

Microbiome and Human Health: Societal Perspective

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Recent advancements in human microbiome research have completely changed our understanding to deal with human diseases for maintaining good health. Keeping this in view, we have started a rigorous campaign to take these researches to the society particularly among children. Recent technological advances and our efforts to spread this message to the society and the remotest parts of India will be presented.

Visualizing the invisible: class excursions to ignite children's enthusiasm for microbes

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As argued previously, because of the great influence of microbes on our lives, their roles must be taken into account in many of the decisions we face, and so society must become microbiology-literate (Timmis et al. 2019. Environ Microbiol 21: 1513-1528). However, a significant barrier to attaining widespread appreciation of microbial contributions to our well-being and that of the planet is the fact that microbes are seldom visible, and it is disease, rather than all of the positive activities mediated by microbes, that colours public perception of microbes. It is imperative to render microbes visible and enable automatic mental associations between everyday information inputs, as well as visual, olfactory and tactile experiences, on the one hand, and the responsible microbes or microbial communities, on the other hand. Microbes can be brought to life by exposing children directly and personally to natural and managed microbial processes, and the results of their actions, through carefully planned class excursions to local venues. This presentation highlights the many ways by which microbiology-centric class excursions can be embedded in curricula, and thus how microbes become more relevant for children, and collaterally their families (McGenity et al. 2021. Microbial Biotechnol 13: 844-887). Several examples are provided, relating to the topics of: food (a favourite pre-occupation of most children), agriculture (together with horticulture and aquaculture), health and medicine, the environment and biotechnology. And, although not all of the microbially relevant infrastructure will be within reach of schools, there is usually access to a market, local food store, wastewater treatment plant, farm, surface water body, etc., all of which can provide opportunities to explore microbiology in action. If children sometimes consider the present to be mundane, even boring, they are usually excited with both the past and the future so, where possible, visits to local museums (the past) and research institutions advancing knowledge frontiers (the future) are strongly recommended, as is a tapping into the natural enthusiasm of local researchers to leverage the educational value of excursions and virtual excursions. Via this presentation and the associated publication (McGenity et al. 2021. Microbial Biotechnol 13: 844-887) we strive to extend the vistas of current class excursions and to: (i) inspire teachers and school managers to incorporate more microbiology excursions into curricula; (ii) encourage microbiologists to support school excursions and generally get involved in bringing microbes to life for children; (iii) urge leaders of organizations (biopharma, food industries, universities, etc.) to give school outreach activities a more prominent place in their mission portfolios, and (iv) convey to policymakers the benefits of providing schools with funds, materials and flexibility for educational endeavours beyond the classroom.

Keynote

Inquiry, Inclusivity and InReach- the 3-Is in the Microbiology Education

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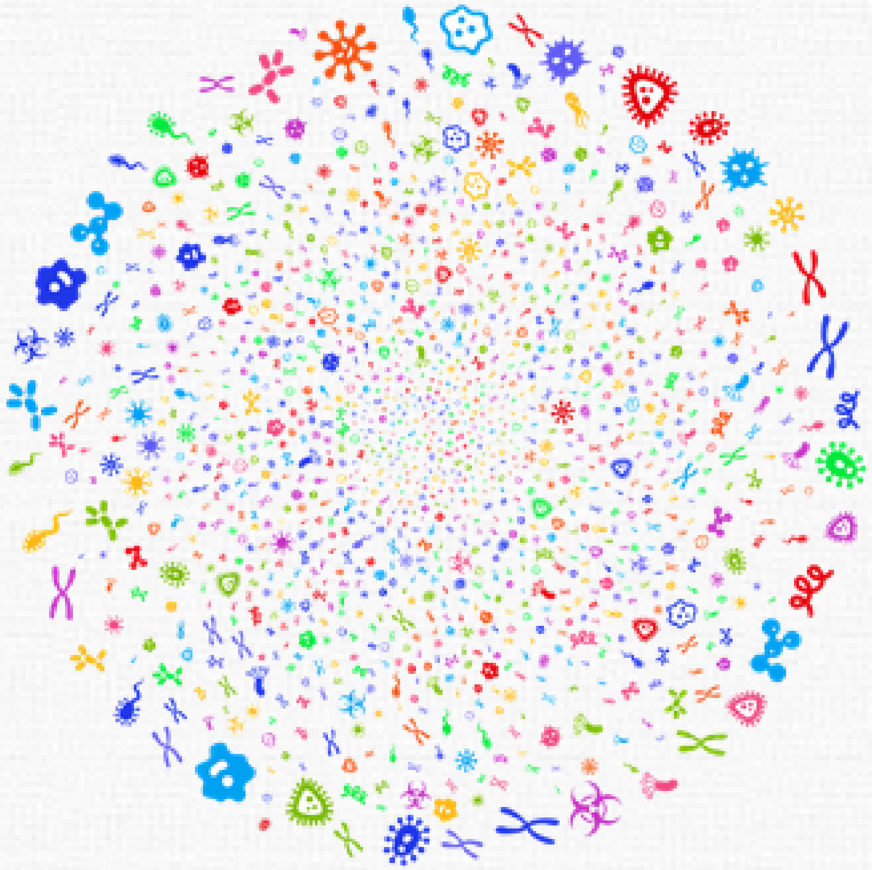
COVID-19 pandemic brought to forefront many aspects of microbiology research and development. All individuals, with or without biology academic backgrounds, were pushed towards understanding the biology of the virus, epidemiology of the disease, preventive measures, treatment strategies, development of vaccines etc. In the process, information with no or false scientific basis was also widely circulated. This highlighted the urgent need of basic microbiology education to be imparted to all sections of the society. Enabling widespread dissemination of microbiology education involve generation of microbiology resource material, conduction of awareness/literacy sessions and outreach programs, inclusion of microbial literacy in curricula, etc. However, certain aspects need to be kept in mind before these measures can be employed effectively. The element of 'inquiry' inculcates higher order thinking skills of evaluating, analysing and creating knowledge and thus, 'inquiry' needs to be incorporated in the resource material for general masses or education curricula at various levels. Similarly, owing to the large diversity in the society, 'inclusivity' should be considered before conducting awareness sessions, outreach programs and the likes. Whereas outreach programs enable the understanding and knowledge to reach out beyond the limits of the expert community to the larger and generally remote society, 'inreach' programs can also be designed to enrich expert communities and ensure spread of microbiology education in the society just like the pandemic. Strategies and examples of the three Is – Inquiry, Inclusivity and InReach will be discussed for the meaningful dissemination of microbiology education for producing 'microbiology literates' in the society.

Invited



Oral Presentation

ABSTRACT

MICROBIAL INTERACTION TO INTENSIFY THE BIOCHEMICAL COMPOSITION OF ECHINACEA PLANT

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Gardens are obviously beautifying with diversity of ornamental plants. It's being an inessential enhancement when a flowering ornamental plant would be a medicinal plant too. *Hibiscus*, Chamomile, *Lavandula*, *Fuchsia*, *Impatiens*, *Cichorium*, *Tagetes*, etc. are those plants which are ornamental as well as medicinal and are used since time immemorial. The ornamental as well as medicinal plant *Echinacea* is used for the experiment. A very good use of the flower is in beverages especially in teas that strengthen the immune system, accelerate recovery from the common cold, fights infection, relieves upper respiratory issues, etc. We have inoculated three species of *Echinacea* (*E. purpurea*, *E. angustifolia* and *E. pallida*) with the dominant Arbuscular Mycorrhizal Fungi (AMF), *Glomus mosseae* and *Gigaspora gigantean* along with Mycorrhizal Helper Bacteria because of phosphate solubilizing capability and that's why also known as Plant Growth Promoting Bacteria (PGPB), *Pseudomonas fluorescence* and *Bacillus subtilis*. The physical, physiological, biochemical and mycorrhizal characterization were assessed. Root essential oil, Ferric Reducing Antioxidant, ABTS Antioxidant, Total phenolics, AMF Spore no., AMF Root Colonization are higher under mycorrhizal association than the control plants of different *Echinacea* species. It was found that inoculation of microbes on *E. purpurea* showed superior results than *E. pallida* and *E. angustifolia* as the AMF Spore no. (231.30) and AMF Root Colonization (78.70%) were greater in *E. purpurea*. *E. pallida* was found with the lowest physiological and mycorrhization characteristics.

Keywords - Arbuscular Mycorrhizal Fungi (AMF), Mycorrhizal Helper Bacteria, essential oil, antioxidant, etc.

ENDOPHYTIC FUNGAL ASSOCIATES OF SELECTED WILD ORCHIDS OF KERALA

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Endophytes are those microorganisms that inhabit the internal tissues of plants and perform a plethora of plant beneficial activities. They also act as a repository of pharmacologically important bioactive chemical compounds of industrial application. Endophytic fungal isolates can be assessed for the production of industrially important enzymes, as they exhibit wide range of enzyme activities for supporting their host. In the present study, absorption roots of four epiphytic wild orchids viz.: *Cleisostoma tenuifolium* (L.) Garay, *Rhynchostylis retusa* (L.) Blume, *Bulbophyllum* sp. and *Dendrobium ovatum* L. Kraenzl., were collected from different parts of Kerala state. Thin hand sections of the absorption roots stained using lactophenol cotton blue showed the presence of deeply stained pelotons in the cortical cells of the absorption roots, which is an indication of the presence of fungal associates. Of the four strains examined, a high infection percentage was observed in the absorption roots of *Rhynchostylis retusa* (L.) Blume and *Dendrobium ovatum* L. Kraenzl. The percentage infection was observed to be higher in the roots collected from humid areas, indicative of the influence of climatic conditions on the endophytic inhabitants. The number of velamen layers was also noted to be higher in species that were collected from dry areas when compared with that of orchids from humid areas. Orchids can be considered as the indicators of the health of an ecosystem as their survival is dependent of the active presence of many other life forms. The study revealed the presence of a rich fungal diversity, associated with the absorption roots of wild orchids, that can be harnessed for many industrial applications. The integration of these diverse fungal associates in the conservation biology of the holobiont can show a tremendous impact on conservation efforts since, a healthy microbiome is an indication of healthy organism.

Key words: Orchids, Endophytes, Absorption roots, Fungal associates

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ABSTRACT CODE: OF3

INSIGHTS INTO DRUG RESISTANCE AND POTENTIAL DRUG TARGETS IN MYCOBACTERIUM TUBERCULOSIS: A COMPARATIVE GENOMICS STUDY

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Mycobacterium tuberculosis is a causative agent of airborne infectious disease tuberculosis (TB).The identification of multi-drug 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. Each year millions of people worldwide suffer from tuberculosis (TB) which raises the need to determine effective cure against the disease. Here, we analyzed genomes of 174 strains of *M. tuberculosis* in the light of evolutionary divergence of molecular drug target (MDT) genes. Phylogenomic clustering of *Mycobacterium* has shown temporal type of clustering. 51 MDT genes were categorised into, diversifying (D, $dN/dS>0.70$), moderately diversifying (MD, $dN/dS=0.35-0.70$) and stabilized (S, $dN/dS<0.35$) genes. Among 51 TDR genes, *rpsL, gidB, pncA* and *ahpC* were observed having diversifying selection while *Rv0488, kasA, ndh, ethR, ethA*, *embR* and *ddn* were found under least selection pressure thus stablized. Sequence Similarity Networks (SSN) also showed substantial difference between diversifying and stabilizing protein clusters. We also performed protein-protein interactions (PPI) of diversifying and stabilized proteins with host proteins i.e., human proteins. This highlighted 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, its homology with a human mitochondrial beta-ketoacyl synthase protein requires further investigation before designing drug strategies against KasA.

Keywords: Mycobacterium tuberculosis, molecular drug target, KasA

ABSTRACT CODE: OF4

WHAT ELSE WE HAVE BESIDES VACCINES?- EDTA CHELATION THERAPY!

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Ever since after its emergence, SARS-CoV-2 has been continuously mutating and resulting into several pathogenic SARS-CoV-2 substrain. This has posed a serious challenge in front of researchers and vaccine manufacturers to develop a vaccine to control infections arising from all substrains and give protection to humans all over the world. So far, vaccines developed by any country, although highly efficacious, have been designed keeping in mind the indigenous priorities and safety of people belonging to some countries. Considering the requirement of high-throughput infrastructure facility, highly trained manpower, logistic supports and approvals, designing and development of vaccine and to launch it is very challenging for any researcher. Herein, I have performed some basic bioinformatics techniques and employed some structural biology approaches and have uncovered a novel treatment therapy for all control infections arising from possible substrains of SARS-CoV-2. The designed treatment therapy is based on Nebulier/Inhaler based EDTA Chelation. The suggested therapy presents a simple, novel, quick, safe, affordable and effective solution to control SARS-CoV-2 infection and treat COVID 19.

Keywords: EDTA Chelation Therapy, Coronovirus, SARS-CoV-2, SARS-CoV, Integrins, COVID-19, Spike Protein

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ABSTRACT CODE: OF5

BACTERIOPHAGES AS JEYKLL AND HYDE IN MULTIDRUG-RESISTANT BACTERIA

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The rise in antimicrobial resistance and emergence of multidrug resistance has raised the need for alternative strategies to treat bacterial infections. Scepticism in the ability of phages as agents of horizontal gene transfer has hindered phage therapy. The study aimed to weigh the odds of phage therapy(Dr Jekyll) versus phage mediated antibiotic resistance(Hyde).

Multi-drug resistant *Escherichia coli* (MDR-EC) from the environment (n=30) and clinical sources (n=30) were chosen for this study.

Bacteriophages as Dr Jekyll : Bacteriophages were isolated from environmental samples by the soft agar overlay technique. Plaques were purified by three consecutive rounds of plaque purification. The host range, viable cell reduction assay and antibiofilm ability were determined. MDR-EC were susceptible to the isolated phages.0.01 multiplicity of infection was effective in reducing the viable cells by more than 99.9% in 2 hours and reducing the biofilm formed ($p<0.01$).The nucleic acid from the phages were extracted and screeded for the resistance genes bla_{TEM} and $bla_{\text{CTX-M}}$ by the polymerase chain reaction. Of 52 lytic coliphages isolated, 11 harboured the gene $bla_{\text{CTX-M}}$. Four of these lysates were able to transfer the resistance via generalised transduction.

Bacteriophages as Hyde: Prophages of MDR-EC were induced by mitomycin C induction followed by DNA extraction. Prophage DNA was screened for bla_{TEM} and $\text{bla}_{\text{CTX-M.}}$ Forty-six isolates harboured bla_{TEM} or $bla_{\text{CTX-M}}$ while ten isolates concomitantly carried both bla_{TEM} and $bla_{\text{CTX-M}}$ .The $bla_{\text{CTX-M}}$ genes were present in the prophage fractions in ١٣ isolates and bla_{TEM} in twelve . Of 19 induced phage lysates tested for transduction, four were able to confer beta lactam resistance in the lysogens.

Phages and prophage elements can carry resistance genes, however, the proportion of these phages that are able to transfer the resistance are relatively low compared to the lytic ability of phages. Hence, judicious use of phages could be instrumental in circumventing the raging antimicrobial resistance era.

ABSTRACT CODE: OF6

2,5-DISUBSTITUTED-1,3,4-OXADIAZOLES AS NOVEL ANTIMICROBIAL AGENT

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The increase of drug resistance to most of commonly used antibiotics, as well as the importance of oxadiazole as an antibacterial agent, motivated us to develop a few novel oxadiazole analogues that had previously been undocumented for their antimicrobial properties. IR and NMR spectroscopy were used to confirm the compounds' structures. The antimicrobial properties of the compounds were investigated using the disc diffusion method against bacterial strains such as Proteus mirabilis (MTCC-425), Pseudomonas aeruginosa (MTCC-424), Bacillus subtilis (MTCC-639) and Staphylococcus aureus (MTCC-96), as well as fungal strains such as Aspergillus niger (MTCC-1334) and Candida albicans (MT Some of the compounds were shown to have considerable antibacterial and antifungal properties. The relationship between structure and activity among the synthesized oxadiazoles has also been studied.

Keywords: Antimicrobial activity, Disk diffusion method, Oxadiazoles.

ABSTRACT CODE: OF7

TARGETING STRUCTURAL PROTEINS IN BIOFILM MATRIXOME FOR DEVELOPMENT OF ANTI-BIOFILM THERAPEUTICS: OPPORTUNITIES AND CHALLENGES

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Biofilms are communities of microorganisms firmly adhered to a surface and covered under a highly hydrophobic extracellular matrix (ECM). Biofilms have been characterized for heightened resistance against disinfectants, antibiotics, antimicrobial peptides, and host immune systems. Therefore, biofilm-associated microbial infections are exceptionally difficult to treat with conventional antimicrobial and lead to chronic infections. According to the National Institute of Health (NIH), USA, ~ 80% of all chronic infections are caused by biofilm-forming microorganisms. There is a pressing need to discover, develop, and implement anti-biofilm therapeutics to manage biofilm-associated microbial infections effectively. It is being proposed that targeting biofilm Matrixome could be the way forward to discover and develop specific antibiofilm therapeutics. Few studies have shown promising results with the degradation of polysaccharides and DNA present within the Matrixome. Relatively fewer studies have reported targeted inhibition of structural proteins associated with biofilm Matrixome; nevertheless, results obtained with these studies are quite promising and accentuate that targeting structural protein within bacterial matrixome could lead to effective and precise 'anti-biofilm therapeutics.' This deliberation aims to present an overview of the unique opportunities and challenges associated with targeting structural proteins in the biofilm matrixome as the approach to discovering and developing anti-biofilm therapeutics.

ABSTRACT CODE: OF8

EDIBLE MUSHROOMS – FROM LAB TO FIELD

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Mushrooms are macro-fungus, which can be seen from naked eyes belongs to Ascomycota and Basidiomycota phylum. About 10 types of mushrooms are commonly used for edible purpose. Various types of dishes are prepared all over the world. Among those, oyster mushroom is edible and has excellent taste and flavor. They are like antimicrobial, anti-cancerous and anti-cholesterol in nature. They are rich source of nutrients as they are rich in proteins, iron, calcium, phosphorus and are a rich source of Vitamin D. Cultivation of Oyster mushroom is a profitable agro-business, as it can be grown on agricultural waste such as- wheat, rice husk, leaves, saw dust, bean hulls etc. Waste can be recycled in to food and environment can be pollution free. Cultivation of mushroom can generate more employment, promote sustainable agriculture and can be a low input and high output business.

Keywords: Mushroom, agro- business

ABSTRACT CODE: OF9

MICROBIAL BIOCONTROL STRATEGIES OF PLANT PATHOGEN

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To address food security, agricultural yields must quickly increase to keep pace with the world's rising population. There is presently a tremendous effort to develop low-input, more sustainable agricultural techniques, including alternatives to chemicals for pest and disease control, which is a major cause of productivity losses. Researchers are focused on potential biological control microbes as feasible options for the management of pests and plant pathogens due to the negative effects of some pesticides on human health, the environment and living organisms. A growing body of evidence shows that leaf and root-associated microbiomes have the potential to improve plant efficiency and output in cropping systems. It's critical to comprehend the role of these bacteria in encouraging development and managing illnesses, as well as their use as biofertilizers and biopesticides, which have had mixed results in the field. Biocontrol bacteria alter plant defense mechanisms, deploy biocontrol actions in plants, and offer novel ways for controlling plant diseases, according to this review. There are now initiatives to improve, facilitate, and maintain long-term plant colonisation in addition to just introducing particular biocontrol bacteria. New techniques to employ "plant-optimized microbiomes" (microbiome engineering) and understanding the genetic basis of positive plant-microbe interactions to enable breeding of "microbe-optimized crops" have piqued interest

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Keywords: biocontrol bacteria, plant-optimized microbiomes

ABSTRACT CODE: OF10

JASMONATES MEDIATED PLANT–MICROBE INTERACTION: A STEP TOWARDS SUSTAINABLE AGRICULTURE

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In nature plants are exposed to several biotic and abiotic stresses. Plants being sessile respond to these environmental cues through various physio–biochemical processes and structural modifications. Within their environment plants encounter a tremendous range of microorganisms which includes both the disease causing pathogens as well as growth promoting beneficial microorganisms. Plants have a complex and highly flexible innate immune response to recognize and respond to these invading microorganisms. A volatile lipid based phytohormone jasmonates (JAs) including jasmonic acid and its derivatives have emerged as an important signalling molecule in plants for regulating the plant–microbe interactions. There is a complex interplay of JAs with other signalling molecules like salicyclic acid (SA) and ethylene (ET) to provide plants with a strong regulatory mechanism. Besides playing significant role in plant defence JAs are also involved in many growth and development activities in reproductive as well as vegetative parts of plants including roots. A complete understanding of the role of JAs in inherent and induced resistance to pathogens and in plant growth and development provide us a tool to establish strategies for sustainable agriculture.

Key words: Signalling molecule, phytohormones, Jasmonates, sustainable agriculture,

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ABSTRACT CODE: OF11

MICROBES AS BIOCONTROL AGENTS FOR SUSTAINABLE AGRICULTURE: ITS STATUS AND FUTURE PROSPECTS IN INDIA

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Maintaining the agricultural production at a level to sustain the food needs and food security of the world population is going to be a challenge in the future due to the rapid increase in population. Therefore, necessitating the protection of agricultural crops from pests and diseases which cause considerable economic losses of up to 20-40%. To prevent this loss in the middle of 20th century injudicious use of cheap synthetic chemicals was widely practiced. After the publication of 'Silent Spring' in 1962 by Rachael Carson, highlighting the demerits of use of chemical pesticides, other alternative methods of control such as 'Biological Control' gained significance. This is a method for the management of insects, weeds and diseases using natural enemies. Some of the important microbes as potential biocontrol agents are bacteria, fungi, viruses, protozoa and nematodes. Yet, till date, the biological control practices are underutilized and not universally accepted. An International Organization for Biological Control (IOBC) initiative, aims at identifying the limitations of biological control and recommend ways of its mitigation. Some key factors identified by them are risk averseness, cumbersome regulatory processes, non-accessibility to biocontrol agents, insufficient knowledge dissemination to public, farmers and stakeholders of the benefit of biocontrol and fragmentation of biocontrol discipline. Due to the universal acknowledgement of the fact now that the use of chemical pesticides needs to be reduced, the impetus of biocontrol methods has gained importance. India has taken some major initiatives and invested widely in the biological control research, training and adoption. However, biocontrol practices need more support and boost in terms of funding for research and implementation. The IOBC should play a significant role in the implementation and facilitation of the development of biocontrol strategies worldwide.

Keywords- Biological control, bacteria, fungi, virus, protozoa, nematodes, IOBC.

ABSTRACT CODE: OF12

ROLE OF MICROBES IN SUSTAINABLE AGRICULTURE AND ENVIRONMENT MITIGATION

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Anthropogenic activities such as intensive agricultural methods, use of agrochemicals, burning of crop residues etc., have drastically affected the environment and biodiversity. Burning of crop residues results in emission of Greenhouse gases, various hydrocarbons and particulate matter. Improper crop residue management practices and irrational use of chemical fertilizers and pesticides have deteriorated the soil health by destroying the micro-organisms which contribute to soil fertility, and loss of biomass. At present, there is a growing concern about environmental hazards and threat to sustainable agriculture. Biofertilizers have emerged as eco-friendly substitute for agrochemicals and can minimize environmental toxicity and long residual retention of chemicals. Soil microbes, particularly bacteria and fungi play a vital role in decomposing soil organic matter containing cellulose, hemicellulose and lignin and recycle the organic residues. They mobilize nutritionally important elements from non-usable form to usable form through biological processes such as Nitrogen fixation, Potassium and Phosphate solubilization. Plant growth promoting rhizobacteria (PGPR) promote plant growth by producing phytohormones, and some of the species of PGPR, besides other microbes, effectively mitigate abiotic stresses, such as draught, salinity, nutrient imbalance and temperature fluctuations etc. Microbial management of agricultural waste seems to be a promising approach to manage soil fertility, meet global food requirement and mitigate the environmental impacts of crop residue burning. Though Bio-fertilizers are economical, ecofriendly, but they pose some constraints and limitations. More research needs to be carried out to overcome these limitations and elevate agriculture sustainability worldwide.

Key words: agricultural waste, Bio-fertilizers, nutrient availability and environmental degradation.

ABSTRACT CODE: OF13

APPLICATIONS OF PGPR FOR CLIMATE FRIENDLY SUSTAINABLE AGRICULTURE

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Feeding a growing (and high nutrient consuming) world population amidst the twin challenges of preventing soil fertility loss and natural biota damage because of excessive chemical usage and climate change inflicted crop yield drop in many breadbasket regions of the world. It has forced scientists and policy makers to look at long ignored sustainable agriculture practices. If famine like situations and further environmental damage have to be avoided in future, all methods of sustainable food production practices have to be put in place urgently.

One important category of inputs towards long term sustainable agriculture is the active use of naturally occurring micro-organisms. Microorganisms are the “green” option as biofertilizers, biopesticides, biocontrol agents, biostimulants and bioremediators etc.

Plant Growth Promoting Rhizobacteria (PGPR) represent one such microbial group with ability to colonize plant roots, influence plant growth through various direct and indirect mechanisms and act as a defence against diseases and pests. The direct mechanisms include Nitrogen fixation, Phosphate and Potassium solubilization, Phytohormone production, Siderophore production while the indirect mechanisms include Antibiotic and hydrolytic enzymes production and Induced Systemic Resistance, etc.

Various microbial biotechnologies have been suggested for the better understanding of PGPR mediated mechanisms in plants. Multipurpose PGPR based formulations have been used in Composting, organic farming, biofilm production, bioleaching, microbial consortia microbial exudation, rhizomicrobiome, nano pesticides etc. By translating and assimilating the current knowledge and techniques of various aspects of PGPR into crop production practices will solve many of the sustainability questions in production of food and non-food crops.

Keywords: soil fertility, climate change, sustainable agriculture, Plant Growth Promoting Rhizobacteria (PGPR), microbial biotechnologies, crop production practices

ABSTRACT CODE: OF14

AGRICULTURAL MICROBIOLOGY AS A SUSTAINABLE MANAGEMENT STRATEGY IN APPLE ORCHARDS

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Sustainable horticultural practices address the global issues of food security, pest and disease management, soil health, water pollution, depletion of biodiversity etc. with eco–friendly approaches. Increasingly, adoption of such strategies is benefitting agricultural production including that in orchards. Even though several Integrated Pest Management, disease and weed management strategies have been in use in apple orchards, they are still not the most favored methods of control. On the other hand, horticulturists can exploit naturally occurring microbial populations in the soil to improve the quality and quantity of organic apples since microbes are an integral part of soil biodiversity and impact various parameters like pH, geochemical cycles, soil structure, water retention, resistance and resilience of plants and other functional soil properties. Mutually beneficial interactions like plant-arbuscular mycorrhiza, legume-rhizobia interactions, plant growth-promoting rhizobacteria (PGPR), endophytic and epiphytic interactions like root-associated or phyllosphere communities can be employed to help in further development of agricultural systems sustained by microbes. Microbial systems not only reduce dependence on inorganic fertilizers and minimize ecotoxicity but also aid plants in their fight against pathogens, carry out nitrogen fixation and help in superior utilization of nutrients like phosphorus, potassium etc to counter nutritional imbalances thereby leading to proper tree growth and improved photosynthesis in organic apple systems.

Keywords: Sustainable horticultural practices, plant growth-promoting rhizobacteria (PGPR)

ABSTRACT CODE: OF15

AMLA ENDOPHYTES: A POSSIBLE MICROBES FOR SUSTAINABLE AGRICULTURE

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In urge of high agriculture yield in crop production, chemical fertilizers and pesticides are being exposed to soil in considerably high amount. Supplementation of these kind of substances can give a life- long environmental problem to soil ecosystem and human health. Endophyets An organism residing in plants can also produce plant growth promoting compounds which can be eco-friendly alternative to such toxic chemicals. Indian Gooseberry commonly known as "Amla" is scientifically known as *Phyllathus emblica* L. which is an angiosperm of family Phyllanthaceae and order Malpighiales. This plant has been reported with anti-diarrheal, antibacterial, antiviral, anti-dysenteric and resistance building properties. Amla plant has not been searched thoroughly for the presence of endophytes; current database reflects very few Amla endophytes till time. Treasure hunting of Amla plants for endophytes can lead to some potent bioactive compound producing isolates which can enhance plant growth with their efficient Plant Growth Promoting activity like nutrient availability and stress tolarence. In search of such endophytes, Amla plant parts like root, stem, leaves and fruits sample were analyzed; isolation of bacterial endophytes were carried out from surface sterilized parts and 8 bacterial isolates from roots, 7 bacterial isolates from stem, 3 isolates from fruits and 2 isolates from leaves were isolated .These isolates were further checked for their beneficial impact on plant growth enhancement and different PGPR characterization. Detailed results will be discussed at the time of presentation. Use of Such isolates as inoculums can offer a very environmental friendly and sustainable source in a field of agriculture and medicine.

Keywords: . Endophytes, amla, *Phyllathus emblica*

ABSTRACT CODE: OF16

A BIBLIOMETRIC ANALYSIS OF MICROBES FOR SUSTAINABLE DEVELOPMENT

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The present article does the bibliometric analysis of the scholarly publications on microbes for sustainable development. The data has been analysed from 2008 to 2021. Scopus has been utilized for the bibliometric analysis. The maximum number of publications in this area of research have been found to be published in India during the period of study.

Keywords: Bibliometric analysis

ABSTRACT CODE: OF17

METAGENOMICS IN THE PRODUCTION OF INDUSTRIALLY IMPORTANT CELLULASE

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Metagenomics, a study of collective microbial genomes isolated directly from environmental samples, is a rapidly growing field of research that aims at studying the microbiota of a particular habitat collectively to understand the true diversity of microbes, their functions, interactions and evolution. The present investigation was undertaken to explore the goat rumen digesta for cellulase production using metagenomic approach. Metagenomic DNA (mgDNA) was extracted from goat rumen digesta using five different methods. The optimum method for mgDNA extraction was developed in our laboratory and yielded 240.6 ± 8.1 µg/g goat rumen digesta, the highest DNA yield obtained among all the methods tested. The mgDNA isolated was partially digested with BamHI and the mgDNA fragments (0.5-2.0 kb) were ligated into BamHI digested pUC19 cloning vector for mgDNA library preparation. The mgDNA library was assessed by digesting the recombinant pUC19 plasmid DNA isolated from eleven randomly chosen recombinant bacterial colonies with KpnI. All the chosen recombinant clones showed a distinct restriction pattern confirming the presence of a DNA insert, each with a different size. The mgDNA library was screened for cellulase positive clones on carboxymethyl cellulose (CMC) agar plates. On screening the recombinant bacterial colonies, the cellulolytic clone was identified by the formation of yellow halos around the colony after 24-36 h of incubation at 37 ºC. The presence of ~1.5 kb DNA insert was observed with the restriction digestion of the recombinant pUC19 plasmid DNA followed by DNA sequencing. The sequencing of cellulolytic DNA insert (CelT3) revealed an ORF of 1,122 bp encoding the protein with 373 amino acids which showed 96% sequence homology with the cellulase of an uncultured bacterium. The purified protein exhibited a specific activity of 17.74 U/mg with 4.42 purification fold. Biochemical characterization of the CelT3 cellulase revealed maximum relative activity in the presence of CMC suggesting it to be endoglucanase in nature. The recombinant cellulase under study may prove beneficial in penetrating the resilient architecture of cellulosic biomass for its efficient deconstruction.

Keywords: Cellulase characterization, Clone library, Metagenomic DNA

ABSTRACT CODE: OF18

BIOREMEDIATION OF HEAVY METAL POLLUTANT LEAD BY MICROALGAE AND ITS IMPACT ON THEIR GROWTH AND CHLOROPHYLL-A CONTENT : A REVIEW

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One of the major pollutants of water are the heavy metals which affect various parameters in the water bodies. An increase in their concentration affects the water quality and can have drastic impact on organisms in these water bodies. Microalgae can be considered as an effective bioremediation tool for the removal of these heavy metals due to their capability to adapt to various changing environmental conditions, fast growth rate, simple methods of culturing and ecological sustainability. Lead is one of the toxic heavy metals which is known to show harmful impact on aquatic animals as well as human health. As this metal does not have any significant biological function, it tends to get accumulated in microalgal cells, subsequently getting transferred to other organisms through food chain. It is important to study the effects of Lead toxicity on various aspects related to microalgae which can affect the survival of these organisms. Though microalgae are an effective biosorbent, after a certain limit of Lead concentration, drastic decline in their growth rate and harmful effects on their photosynthetic pigments have been observed. This is an abstract for a review paper on bioremediation of heavy metal Lead using microalgae and also the impact of this process on growth and chlorophyll-a content of microalgae.

Keywords: Microalgae, Bioremediation, Heavy metal Lead, Ecological sustainability, Chlorophyll-a.

ABSTRACT CODE: OF19

CULTURE-INDEPENDENT EXPLORATION OF THE HYPERSALINE ECOSYSTEM INDICATES THE ENVIRONMENT-SPECIFIC MICROBIOME EVOLUTION

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A holistic assessment of the influence of the changing environment on life forms is very crucial in the current scenario to set goals for preservation of the diversified life forms. Exploration of the microbiome with a culture independent approach from the diverse habitat could unveil the environmental influence on microbiome maturation. Freshwater, saline, and alkaline water are diverse ecosystems and their inhabitants should have evolved differently to meet up environmental requirements. Influence of the environment could be easily deduced by exploring these ecosystems for its microbial inhabitants. Hereby, the current study explores diversified metagenomes to understand the environmental influence on microbiota structure, genetic makeover, and physiological functions.

Saline, freshwater, and alkaline water metagenomes (a total of 212) were considered for analysis and data was processed to decode rRNA and protein features to define respective taxonomic uniqueness and probable microbiome functions. Comparative taxonomic analysis with identified rRNA features from these metagenomic datasets indicated that each ecosystem harbors significantly different ($P< 0.001$) microbial inhabitants. Comparative metagenomics using protein features also decoded differential abundance of metabolic features among studied ecosystems. The osmotic stress, oxidative stress, and photosynthesis related protein features were significantly (($P< 0.001$) abundant in saline ecosystems, while resistance to antibiotic and phenolic compounds were significantly ($P< 0.001$) abundant in freshwater ecosystems. Identification of the unique microbiota composition and their physiological functions indicates environment-specific microbiome evolution.

ABSTRACT CODE: OF20

EXPLORING HERBAL EXTRACTS FOR BETTER MANAGEMENT OF VIRAL DISEASES

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Viral infections have caused wide-scale suffering and death globally throughout the history, very recent being the ongoing, deadly Covid-19 infection. It is well known that viral infections are mainly transmitted between individuals through the respiratory and oral tracts. Several alcohol and other chemicals based antiviral substances, like sanitisers and disinfectants are available to kill the virus and stop the transmission. But on the other hand, these on prolonged use have some serious side effects in humans e.g., making the skin rough and scaly, depletion of beneficial microflora, contributing to rise in antimicrobial resistance and developing other dermal complications in the patients, etc. The use of natural or herbal based antiviral substances, conversely, can address most of these drawbacks of the alcohol or chemical-based compounds. There are many scoring points of these natural/herbal sanitisers and disinfectants, *viz.* they are soft on the skin and maintain its normal texture without developing any dermal complications, the essential microflora on the surface of skin remains intact and there is also no contribution to antimicrobial resistance, even on prolong use. Moreover, it is also cost effective, as compared to chemical antiviral compounds. India has been traditionally known to possess a rich source of many medicinal plants and herbs with potent antiviral property, exhibited from different parts like leaf, stem, root and flowers. Some examples are garlic (*Allium sativum*), mint (Mentha), ginger (*Zingiber officinale*), malabar nut (*Justicia adhatoda*), bhringraj (*Eclipta prostrata*), amla (*Phyllanthus emblica*), cinnamon (*Cinnamomum verum*), and pomegranate (*Punica granatum*). With this background, the idea of the current research was to look for new and potent herbal antiviral extracts, which can be formulated into effective antiviral therapies, leading to better management of viral diseases.

ABSTRACT CODE: OF21

GREEN SYNTHESIS OF METAL NANOPARTICLES USING NEEM (*Azadirachta indica*) AND THEIR APPLICATIONS

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Green synthesis of metal nanoparticles using plant sources has advantages over chemical/ physical methods as well as other biological methods, which involves use of enzymes, fungus and microorganisms. Plant mediated green synthesis of nanomaterials is simple, reproducible, cost effective, eco-benign, energy efficient and has ease of scalability. Neem (*Azadirachta indica*) plant, primarily cultivated in southern parts of Asia and Africa, is well known for its medicinal properties. That's why it has been used in the biosynthesis of metal nanoparticles. Neem contains various phytochemicals (e.g., terpenoids, flavonoids etc.) which acts as reducing as well as capping / stabilising agent. There is a marked difference in the physical and chemical properties of metal nanoparticles and that of the bulk material.

One pot synthesis of metal nanoparticles using neem involves reduction of metal salt with neem extract in aqueous medium. Formation of metal nanoparticles is easily monitored visually, from the change in colour of the reaction mixture. Metal nanoparticles have been characterized by UV-visible spectroscopy, FT-IR spectroscopy, TEM, EDAX and many other physicochemical and morphological techniques. Recently, Neem has been reportedly used to synthesize Ag, Au, ZnO and many other metal nanoparticles (M NPs). These M NPs have been used waste-water treatment as well as has many biomedical applications i.e., as an antimicrobial agent, etc. Recent progress of applications of metal nanoparticles synthesized using neem extract has been reviewed. Synergistic effect of M NPs and neem extract has been observed and this has led to enhanced antibacterial activity.

Keywords: Eco-benign, Nanoparticles

ABSTRACT CODE: OF22

MITIGATION OF ANTIMICROBIAL RESISTANCE THROUGH BLENDED APPROACH

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The misuse and overuse of antibiotics can cause Antimicrobial Resistance (AMR) which according to WHO is one of the top 10 global public health threats facing humanity. The emergence of coronovirus disease 2019 (COVID 19) pandemic has posed serious challenge on the antimicrobial stewardship activities and drive antimicrobial resistance due to the shift of the focus of health care system of the world towards the treatment or management of the covid 19 disease. To mitigate the impact of coronavirus disease on AMR, there is an urgent need to train and educate general public about the practices to be followed to reduce the unnecessary and improper usage of antibiotics. Preliminary data collected by our lab indicated increasing drug resistant strains from fresh produce which could narrow down to the presence of these organisms in the manure and compost used in fields. Use of such manure and compost in fields could have direct relevance to increased resistance observed by us in fresh produce. Studies are underway to prove the transport of these organisms and resistant genes in plants. In an attempt to sensitize public, there is a need to share the scientific data generated for these societal drugs. Working in this direction, our students have been conducting workshops and online surveys for school and college students to understand their knowledge of these drugs and the associated problem. Further, through these initiatives, structured understanding of the laboratory results of the project are shared with the students. The present study envisages to create an awareness of the resistance bomb that has engulfed the society today with a hope for a corrective measure being suggested by young and budding scientists. Who knows one such idea would lead to an end of this critical problem!!

Keywords: Antibiotics, Antimicrobial Resistance, Antimicrobial resistance genes, blended learning

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ABSTRACT CODE: OF23

HERBICIDE REMOVAL BY WEEDS AND EPIPHYTIC ROOT BACTERIA

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Acorus calamus, *Typha latifolia* and *Phragmites karka*, the weeds, and their epiphytic root bacteria were subjected to various concentrations of herbicide atrazine individually and in plant–bacterium combination. It was observed that *A. calamus–Pseudomonas* sp. strain ACB combination showed 91% and 87% removal of 5 mg l^{-1} and 10 mg l^{-1} atrazine respectively. There was a significant rise in herbicide removal by plant–bacterium combination as compared to removal by either plant or bacterium alone indicative of a mutualistic action of the hydrophytes and bacteria. To the best of knowledge this is the first report on the capability of singular plant-bacterium pairs for atrazine remediation. The isolates showed enhanced growth in the presence of the weeds and were able to ameliorate atrazine stress in them. These strains also displayed plant growth promoting traits in vitro. Application of plant–bacterium mutualistic symbiosis for atrazine remediation is facile, easy and environmental-friendly technique, and this phytoremediation–rhizoremediation pairing is suggested to be used in large-scale applications to establish their potential for remediation of polluted sites.

ABSTRACT CODE: OF24

Covid-19 Vaccine's Effectiveness and Safety Profile on Vaccination Acceptance: A Prospective Demographic Post Vaccination Study

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BACKGROUND:
Since the World Health Organization (WHO) on March 11, 2020, has declared the novel coronavirus (COVID-19) outbreak a global pandemic, there was no doubt that vaccination is the ideal protocol to tackle it efficiently.
METHODS:
A cross-sectional study was conducted by distributing an online survey targeted toward a group of people who received any COVID-19 vaccines. Data were statistically analyzed and used to predict the after effects of post vaccination.
RESULTS:
25.2% of participants did not suffer with any of the post vaccination symptoms. While around 75% suffered from mild to moderate side effects. Tiredness (41%), myalgia (27%), fever (42%), headache (30%), chills (13%), pain at injection site (12%), joint pain (12%), nausea (7%), persistent stomach pain (1%) and diarrhea (0.7%) were the most prevalent symptoms. The frequency of symptoms was 75% (3rd decade or 20-29 years), 80% (4th decade or 30-39 years), 73% (5th decade), 62% (6th decade), 48% (7th decade) and 34% (8th decade or 70-79 years). Post-vaccination symptoms were more likely to be reported by women (86.1%) compared to men (44.2%). Among those who reported symptoms, 44.1% men and 50% women noticed them within the first 12 hours, 37.2% men and 35.6% women noticed symptoms within 12 to 24 hours and 18.6% men and 14.7% women noticed symptoms after 24 hours. In this study it was observed that the respondents who were vaccinated with single dose had only 5.5% chances of Covid infection and those who were vaccinated with both the dose were having only 4.8% chances of Covid infection.
CONCLUSIONS:
The present study confirmed that all the newly formulated COVID-19 vaccines are safe.

ABSTRACT CODE: OF25

SARS-COV-2 VACCINES: A GLIMMER OF HOPE

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SARS-CoV-2 or Severe Acute Respiratory Syndrome Coronavirus 2 is a zoonotic disease caused by novel coronavirus and has been declared as a pandemic by WHO. It has a high transmissibility rate with a basic reproduction number (Ro) of 1.4 to 5.5 making it a rapidly spreading disease with a mortality rate of 2-5% which is quite lethal. Till date about 22 crore people have got the disease and approximately 46 lakh have succumbed globally. More and more people all over the world are getting infected by the disease as there is no specific treatment and the mortality figure continues to surge. The case management is basically supportive and symptomatic right now. The disease is prevalent in 221 countries all over the globe and with the pandemic still spreading, most of us may get the disease at a certain period of time. Therefore, measures that minimise the infection risk and diminish the severity of clinical course are necessary and crucial amidst all public health measures. As a comprehensive management at all levels primary prevention by specific protection through vaccination is ideal and holds the key to decrease the infectivity, spread, severity and complications The vaccines which have been developed by the scientists in a short period of time fully backed by clinical trials have been shown to be highly efficacious (with efficacy up to 80%) and offer the only ray of hope of tackling the scourge efficiently. A large number of Covid-19 vaccines are being used all over the world using many technologies and platforms that include non-replicating viral vectored vaccine (Covishield, Sputnik), protein subunit, nucleic acid (DNA,RNA)(Pfizer and Moderna vaccines), live attenuated and inactivated vaccines (Covaxin) .The present study reviews the efficacy of various vaccines which are under trial globally.

Keywords: SARS COVID 2, Coronavirus, Covishield, Covaxin

ABSTRACT CODE: OF26

STRUCTURAL CHANGES IN TNAA, GADB AND TDC GENES OF HUMAN GUT BACTERIAL COMMUNITY LEAD TO VARIATIONS IN NEUROTRANSMITTER LEVELS DURING DEPRESSION

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A philharmonic orchestra between gut microbiota and neurotransmitters is the key to good physical and mental health. Disturbances in the gut microbial ecosystem can adversly impact the homeostasis of the host physiology. Depression has also been associated with gut dysbacteriosis in the past decade as a major cause. This is due to the bidirectional communication linking the gut microflora and the brain that forms the Gut-Brain Axis. The levels of neurotransmitters like Serotonin, Dopamine, and Gamma-Aminobutyric Acid (GABA) are known to decrease in case of depression. These neurotransmitters are majorly synthesized in the gut and changes in the gut microbiome or their metabolites can lead to decreased levels of these neurotransmitters which can further elevate or ameliorate depression. Metagenomics studies of the gut microbiome variability under various stress conditions or dysbiosis has so far focussed on the disparity in the alpha and beta diversity of microbes. Attempts have been made to identify variations in gene structures responsible for the biosynthesis of dissimilitude metabolites during depression. Three genes namely, tnaA, tdc, and gabB responsible for the synthesis of Indole, Tyramine, and GABA, respectively were selected. Present study indicate that the variations in these gene structures are responsible for diverting the biosynthetic pathways of neurotransmtters implicated in depression.

ABSTRACT CODE :OF27

GENOME-BASED RECLASSIFICATION OF *AMYCOLATOPSIS EURYTHERMA* AS A LATER HETEROTYPIC SYNONYM OF *AMYCOLATOPSIS THERMOFLAVA*

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The work carried out was focused on the clarification of taxonomic assignment of two closely related species of *Amycolatopsis* .For 48 type strains of *Amycolatopsis* genome sequences were available in public database at the time of analysis .It showed that *Amycolatopsis eurytherma* Kim et al ,2002 .and *Amycolatopsis thermoflava* Chun et al 1999 .were conspecific .This was confirmed by16 S rRNA gene sequence ,(98.85%) average nucleotide identity or ANI,(98.75%) average amino acid identity or AAI (98.63%) and digital DNA-DNA hybridization(87.8%) analysis .These values were high enough to indicate that they belong to same species .This resulted in reclassification of *Amycolatopsis eurytherma* Kim et al 2002 .as a later heterotypic synonym of *Amycolatopsis thermoflava* Chun et al.1999 .

Keywords :Amycolatopsis ,Reclassification ,Heterotypic synonym

ABSTRACT CODE: OF28

PLANT GROWTH PROMOTING ACTIVITY OF THERMOTOLERANT *PSEUDOMONAS EXTREMORIENTALIS* OBTAINED FROM TATTAPANI, HOT SPRING OF CHHATTISGARH, INDIA

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The present study was designed to analyse the profile of microbial community inhabiting hot water spring Tattapani, Chhattisgarh, India through culturable approach. The spring water was characterized and temperature was recorded as 85°C with slightly alkaline pH (7.5). Bacterial diversity from the spring was studied and found that 21 bacterial isolates at 30°C and 16 bacterial isolates at 60°C. Morphological characterization showed distinct colonies. Molecular characterization revealed *Pseudomonas* as abundant genera among Proteobacteria followed by *Bacillus, Anoxybacillus, Geobacillus* among firmicutes and *Chryseobacterium* in the phylum bacteroidetes on the basis of 16s rRNA gene sequence. Salinity and thermotolerance of cultivated genera was evaluated and found that bacterial isolates were tolerant in the range of 30°C to 70°C temperature and 0-10% NaCl concentration. All the isolates were screened for plant growth promoting traits. Bacterial strain *Pseudomonas extremorientalis* RPB 22 was selected on the basis of multifarious plant growth promoting traits possessed by them. Strain RPB22 showed solubilisation of inorganic tri-calcium phosphate (333 µg/mL). Similarly, inorganic potassium solubilisation was also showed as 10.5 mg/l. Other PGP traits such as zinc solubilisation, siderophore as well as IAA production was also recorded. HPLC analysis of phosphate solubilizing strain RPB22 showed presence of multiple organic acids, among them mallic acid followed by oxalic acid was found highest when supplemented with aluminium phosphate. Seed treatment with strain RPB22 on chickpea showed increased shoot and root parameters. Finding of the study suggest the role of multifarious plant growth promoting strains RPB22 in sustainable agriculture for biofertilizer production in the arid region and areas where temperature is high.

Keywords: Thermotolerant, Hot spring, Culturable, Diversity

ABSTRACT CODE: OF29

SIDE-EFFECTS AND BREAKTHROUGH INFECTIONS ASSOCIATED WITH COVID- 19 VACCINES AMONG INDIAN POPULATION

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Vaccines against Covid-19 provide immunity to deter severe morbidities associated with the infection. However, it does not prevent infection all together in all exposed individuals. Further, emerging variants of SARS-CoV-2 impose a threat concerning competency of the vaccines in combating the infection. This study aims to proofread the efficacy of vaccination against COVID-19 on Indian population, and to determine the variability in side effects and extent of breakthrough infections in various demographic groups. A retrospective study was conducted using pre-validated questionnaire encompassing social, demographic, general health, status of SARS-CoV-2 infection, vaccination, associated side- effects and breakthrough infections in Indian population. Informed consent and ethical approval were obtained as per Indian Council of Medical Research (ICMR) guidelines. Data has been compiled in Microsoft Excel and analysed for statistical differences using STATA 11. 2051 responses were collected from individuals above 18 years between May 2021 to August 2021. Amongst these 41.06% males respondents and 33.07% female respondents had suffered from SARS-CoV-2 infection. Notably among 876 vaccinated, 297 developed side effects with major fraction of younger participants, age 18-40years, getting affected (44.29%). Further, significantly more females (53.9%) of reproductive age developed side effects than males (35.58%). Breakthrough infections were observed in 11.91% vaccinated participants such that older age group, 41years and above (15%), and those with history of chronic disease were found to be at higher risk. This study motivates to conduct clinical research for determining sex and age based personalized dose of vaccine for individuals.

Abstract Code: OF30

UTILIZATION OF LIGNOCELLULOSIC AGRICULTURE WASTES FOR MUSHROOM CULTIVATION AND RECOVERY OF LIGNOCELLULOLYTIC ENZYMES

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A large amount of lignocellulosic wastes is produced worldwide in various agricultural sectors. Burning of these wastes create major global environmental problems. Lignocellulosic material mainly consists of cellulose, hemicellulose and lignin, which can serve as a suitable substrate for mushroom production through solid-state fermentation process. Mushrooms, typically belongs to order Agaricales in the phylum Basidiomycota, and produces extracellular lignocellulolytic enzymes which degrade the lignocellulosic substrates. Therefore, mushroom cultivation using variety of lignocellulosic waste can be a beneficial approach for bioconversion of such an agricultural menace. In the current study, the lignocellulosic waste chosen are rice straw (an environmental havoc in current scenario), wheat straw, sugarcane straw and small garden twigs. The waste is segregated on the basis of their levels of complexity and is used for cultivation of different mushroom species i.e., *Agaricus bisporus, Lentinula* spp., *Pleurotus* spp. We are also interested in isolation of extracellular lignocellulolitic enzymes from the spent substrate.

Keywords: lignocellulosic materials, lignocellulolytic enzymes, mushroom cultivation, solid state fermentation

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ABSTRACT CODE: OF31

A REPORT ON THE INDIAN LABOULBENIOMYCETES

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Fungi and arthropods have shared habitats for more than 300 million years. Due to this close proximity, parasitism evolved between them. Entomogenous fungi come from12 classes of fungi, most common being Laboulbeniales, Pyrenomycetes, Hyphomycetes, and Zygomycetes Our interest is in the Laboulbeniomycetes, obligate associates of arthropods as biotrophs or for dispersal. The class Laboulbeniomycetes has approximately 115 genera occurring on members of at least 11 insect orders, Coleoptera being the most common (80%), followed by Diptera (10%). Two orders of the Laboulbeniomycetes (Laboulbeniales and Herpomycetales) do not form hyphae, their entire life cycle occurs on an arthropod host, with ascospores dispersing to new arthropod hosts. All Laboulbeniales are biotrophic, requiring a living host for survival and propagation. Horizontal transmission through direct contact between adult hosts, is the common mode of perpetuation.

Fungal growth on the host can be seen as one or several thalli on various body parts. A thallus consists of several vegetative cells developing from the two-celled ascospore.The taxonomy and current classification of the group is based on the arrangement of cells of the thallus. Asexual reproduction is not known among Laboulbeniales. Roland Thaxter, the pioneer in this field, has given the most comprehensive record of the group in 5 monographs from1896-1931, including studies from India. Thereafter Batra described 15 species in 1963. Present Study reports 25 species belonging to 9 genera which are new records from India of which 2 were new to science. Life cycle studies on 16 species and SEM studies on 7 species of 3 genera were also carried out. There is a need of a new collaborative research environment including Insect mycology as a specialized discipline that joins mycology, entomology, invertebrate pathology.

ABSTRACT CODE : OS1

BIOCHEMICAL IDENTIFICATION OF DIFFERENT METABOLITES AND ANALYSIS OF MICROBIAL FERMENTATION DYNAMICS DURING THE NATURAL FERMENTATION OF PALM BEVERAGES OF EASTERN INDIA.

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Palm wine is an ethnic and indigenous alcoholic beverage produced from the natural fermentation of the sap obtained from various plants of Arecaceae (palm) family. It is known by different vernacular names in different parts of the world; in India, palm wine is mostly known as toddy, kallu or neera. Palm wine accommodates a complex microbiota and metabolic profile, which ultimately determine the quality and value of the product. In our study, a combinatorial approach of micro-environmental and metagenomic analysis on date palm (*Phoenix sylvestris* (L.)) wine of Eastern India were perfomed to check the effect of fermentation time on metabolite profile and microbial community structure. Physico-chemical analysis of different metabolic markers were performed on both the end-product samples and successional samples (0 h- 96 h); however, metagenomic analysis was performed only on successional samples till now. pH, sugar content (total sugar and reducing sugar), ˚BRIX value and ester content were found to be decreased with the progression of fermentation time. However, alcohol content, acidity, anti-oxidant potential, total phenolic and flavonoid contents were found to be increased in the later stages of fermentation or in the end-product samples. High-throughput metagenomic analysis revealed the dominance of Leuconostoc, Lactococcus and Hanseniaspora at the early stages of fermentation; however, later stages were found to be dominated by *Lactobacillus,* Gluconobacter and Saccharomyces. Other non-saccharomyces yeasts (*Torulaspora, Lachancea* and *Starmerella*) showed their uneven distribution throughout fermentation. Correlation and diversity (both alpha & beta) analysis of dominant microorganism were also performed. Computational analysis of toddy metagenome based on KEGG and MetaCyc databases showed different predictive functional profiles with enhanced bio-activity and nutritional properties, such as: biosynthesis of amino acids, vitamins, phenolic, flavonoids and organic acids, which prove toddy/palm wine as a functional drink.

Key words: High-throughput analysis, Successional changes, Natural fermentation, Predictive functionalities.

ABSTRACT CODE: OS2

POLY-GLUTAMIC ACID-PRODUCING BACTERIA ISOLATED FROM SOME NATURALLY FERMENTED SOYBEAN FOODS OF ARUNACHAL PRADESH, INDIA

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ABSTRACT

Polyglutamic acid (PGA) is a biodegradable anionic polyamide, naturally produced by *Bacillus* sp. in fermented soybean products. It is known to have various industrial uses. One of the well-known characteristic features of naturally fermented soybean (NFS) foods is the presence of stickiness which is mainly attributed to γ-PGA. North East India is a rich repository of production and consumption of fermented soybean with Arunachal Pradesh having maximum number of products. This study was intended to document the production of the fermented soybean products by some of the ethnic groups of Arunachal Pradesh. Four types of products- *peron namsing*, *peha*, *peruyann* and *grep chhurpi* were collected. Isolation of bacteria and screening for production of γ-PGA was carried out by measuring two main features- stickiness and viscosity. Bacterial strains with a stickiness measurement of more than or equal to 20 cm and a viscosity measurement of 10 cP (centipoise) were tentatively selected as good producers. Furthermore, the bacterial strains were then phenotypically and genotypically identified using 16S rRNA gene sequencing. A total of 1240 strains were isolated and 149 isolates were further selected based on the good stickiness measurement, which were further narrow down to 53 final representative strains based on the viscosity measurement. Using principal component analysis, a final two strains- *Bacillus subtilis* (MW680876) and *Bacillus tequilensis* (MW522577), were tentatively observed as the best producers of γ-PGA.

Keywords: Naturally fermented soybean foods, Arunachal Pradesh, γ-polyglutamic acid (PGA), *Bacillus*

ABSTRACT CODE: OS3

TECHNOLOGICAL PROPERTIES OF IDENTIFIED LACTIC ACID BACTERIA (LAB) ISOLATED FROM EXOTIC NATURALLY FERMENTED MILK (NFM) PRODUCTS- MAR, CHHURPI, AND CHURKAM OF ARUNACHAL PRADESH, INDIA

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Exotic NFM products of Arunachal Pradesh are rich sources of lactic acid bacteria, where both culture-dependent and culture-independent have already been explored. In this study, 76 identified LAB strains were screened for probiotic attributes using various standard in vitro tests. Using Principal component and heatmap analysis through groups formation and clustering patterns, two steps grouping were performed, firstly using standard probiotic evaluation tests that includes- acidification and coagulation, acid tolerance, bile tolerance, microbial attachment to hydrocarbons (MATH), auto-aggregation, co-aggregation, antimicrobial property, and bile salt hydrolysis. Secondly, with the same principal grouping method applied above, a secondary grouping was performed for extra experimental tests of interest which includes- beta galactosidase, exopolysaccharide production, cholesterol reduction, gamma amino butyric acid (GABA) production. In this study, several LAB strains were reported to have potential as probiotic candidates based on the experimental performed. From a total of 76 identified strains, 20 strains were selected from primary screening and further tested for the secondary experiments. Overall, strains Levilactobacillus brevis (AcCh91) and Lactococcus lactis subsp. cremoris (AyCk21) are the two most promising strains.

Keywords: Naturally fermented milk products, lactic acid bacteria, probiotics, principal component analysis (PCA).

ABSTRACT CODE: OS4

ALTERATIONS IN GUT MICROFLORA CAUSING ATHEROSCLEROTIC CARDIOVASCULAR DISEASE

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Atherosclerotic disorder (ACVD) is one among the leading causes of death worldwide. With the advent of a sedentary lifestyle, it is imperative to investigate the causes of such diseases and their prevention. Studies have shown the microbial community inhabiting the human gut are responsible for several conditions associated with ACVD. Gut microflora (microbiota) has been connected with ACVD and plays a vital role in its progression. Dysbiosis, along with altered amounts of some bioactive metabolites such as Trimethylamine -N- oxide (TMAO), short-chain fatty acids (SCFA), bile acids, methylamines, polyamines and lipopolysaccharide (LPS), can lead to atherosclerosis. Several factors are responsible for the dysbiosis of gut microflora including dietary fats. This review will summarize the role of gut microbiota in atherogenicity and their potential applications in its prevention. With an adequate understanding of the mechanisms of gut microbiota dysbiosis, scientists worldwide can develop potential therapeutics for ACVD.

Keywords: Atherosclerotic Cardiovascular Disease (ACVD), Gut microbiota, TMAO, SCFA

ABSTRACT CODE: OS5

A STUDY ON DYAMICS OF CILIATE COMMUNITY STRUCTURE TO MONITOR WATER QUALITY

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The present investigation studied the spatial and temporal variation of the physicochemical parameters and their correlation with the ciliate community structure. Samples were collected from three freshwater sites viz., Okhla Bird Sanctuary (OBS), Sanjay Lake (SL) and Raj Ghat (RJ) in alternate months for one year from September 2018 to August 2019. Physicochemical parameters studied were temperature, pH, dissolved oxygen (DO), total dissolved solids (TDS), water hardness (WH), chloride, sulphate, phosphate, nitrite, nitrate and ammonia. Ciliate diversity, structure and abundance were studied using various diversity indices. Multiple statistical methods such as Pearson correlation coefficients, principal component analysis (PCA) and non-metric multidimensional scaling (NMDS) were applied to analyze the data. Maximum ciliate diversity, richness and evenness was observed in the OBS site. Maximum ciliate diversity was observed from class Spirotrichea (47%), followed by Oligohymenophorea (20%), Prostomatea (16%), Phyllopharyngea (6%), Colpodea (5%), Heterotrichea (3%), Litostomatea (2%) and Karyorelictea (1%). Maximum diversity was observed during the monsoon and post monsoon seasons and lowest during the winter and summer seasons. The present study on the dynamics of the environment driven community assembly suggests that ciliates are good indicators for assessing community-level responses and can be useful in predicting the water quality as well as environmental degradation in future.

Keywords: Ciliates, diversity, freshwater, physicochemical, spirotrich.

ABSTRACT CODE: OS6

CONSERVATION PLAN FOR THE HINDON RIVER FROM MUZAFFARNAGAR TO GHAZIABAD

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Hindon River, a polluted tributary of the Yamuna, India, whose water quality is continuously deteriorated due to unaccounted wastewater sources, inadequate treatment capacity of sewerage infrastructure, and inefficient solid waste management plan in the catchment. Most studies focus only on the amount of pollution load generated and its characteristics to suggest a conservation strategy for a river. But it fails to address infrastructural and institutional shortcomings with comprehensive planning at the catchment level. This paper identifies the river›s pollution load from various point and non-point sources and existing gaps in the current treatment strategy to propose a conservation plan for the Hindon river for a stretch of 160 Km from Muzaffarnagar to Ghaziabad. Existing gaps in sewer coverage and untapped drains were identified to design adequate sewage infrastructure for collecting and treating municipal wastewater. After physiochemical and heavy metal analysis of the Hindon River for post and pre monsoon season, the quality of river water was assessed by NWQI and it was found that the water of Hindon is not suitable for any use. A total of 11 untapped drains were identified in the study stretch of 160 km of the river. Not all urban locations were covered under the sewerage network; therefore, they directly discharge their wastewater into the river. There is a gap of 68 MLD in treatment capacity in 2020, increasing to 293 MLD in 2050 (proposed design period). The current capacity of solid waste handling is 250 MT/day with a gap of 150 MT/day, which will increase 567 MT/day in 2035. Due to the complex nature of environmental issues, public participation and public awareness involving stakeholders and non-governmental organizations are necessary; therefore, such provisions are integrated into the plan. River conservation planning needs a catchment approach rather than a city or sector approach. It is a dynamic process that requires public participation and a proper infrastructural and institutional framework to deal with continuous population fluxes and the corresponding rise in pollution load from unaccounted sources, especially in a developing country like India. The overall cost of the Conversation plan of Hindon River for the study stretch is Rs 1362.35 crores.

Keywords: Hindon River, Yamuna, physiochemical

ABSTRACT CODE: OS7

ISOLATION OF LYTIC PHAGES VIRULENT TO *ENTEROBACTER CLOACAE*

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The emergence of drug resistant *Enterobacter cloacae* have posed a serious problem in clinical microbiology. This study was aimed to isolate lytic phage against drug resistant *Enterobacter cloacae*. To isolate the specific bacteriophages of *Enterobacter cloacae* from different water samples. A total 20 strains were collected from different samples of Clinical Bacteriology, Department of Microbiology, Institute of Medical Sciences, Banaras Hindu University, Varanasi. Water samples were collected from different site of Prayagraj and specific phages were isolated by using the double layer agar assay method. Bacteriophages were observed in the form of plaques on the bacterial lawn culture. The bacteriophage isolates have been characterized phenotypically and genotypically for future use. This experimentation concluded that antibiotic resistance to *E. cloacae* is over masked by another alternative method called Phage therapy.

ABSTRACT CODE: OS8

IN SILICO SCREENING OF PHYTOCOMPOUNDS TO CURE DENGUE

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Dengue virus, a member of the family Flaviviridae, has been the causative agent of one of the most recurring epidemic fevers in the history of humankind, Dengue Fever. Dengue infections have been known to occur since the late 17th century. Technological advancements have made it clear that there are four closely related serotypes, namely DENV-1, DENV-2, DENV-3, DENV4, which are responsible for the death of multitudes. Interestingly enough, recovering from the infection of one of the serotypes does give future immunity against that particular serotype but does not provide any from the rest. This leads us to question why our traditional treatments with the help of some phytocompounds seemingly work well against dengue infections regardless of the serotype causing it. Can the method of fighting the infection be replicated with the help of other phytochemicals? Do the phytochemicals need to work in groups, counteracting each other's side effects or do a few of them act as the catalyst to fight the infection? If this is the case, then can there be more such compounds which haven't been documented before? This research focuses on finding such phytocompounds and determining their effectiveness against the disease using in silico screening.

Keywords: Dengue, Flavivirus, DENV, Serotypes, Docking, Phytocompounds, In silico approach

ABSTRACT CODE: OS9

MAJOR RESPIRATORY DISEASE OUTBREAKS

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Respiratory diseases and infections are the major cause of health concerns throughout the world. These diseases are caused by a variety of factors, which maybe biotic or abiotic. It accounts for huge number of deaths worldwide. About 3 million people die from respiratory diseases each year. According to the World Health Organization, an epidemic outbreak is defined as the occurrence and rapid spread of cases of disease which is far greater than what would normally be expected in a particular community, geographical area or season whereas, a pandemic is a disease outbreak which spreads globally. Some of the diseases caused by biotic factors like bacteria, fungi, or viruses are H1N1 influenza A (1918-1920 and 2009-2010), H2N2 influenza (1957-1958), SARS (2003), COVID-19 (2019-still continued) and so on. Abiotic factors include smoking, allergens, air pollution and other occupational risks which cause various chronic obstructive pulmonary disease (COPD) such as emphysema and chronic bronchitis. Since the time immemorial, the world has gone through a significant number of respiratory disease outbreaks taking the lives of enormous number of people. According to the center for disease control & prevention (CDC), about 151,700-575,400 people worldwide died from (H1N1) pdm09 virus in 2009. It is estimated that about 1 million people died from H3N2 influenza A virus and 1.1 million people died from H2N2 virus. 774 people worldwide died during the SARS epidemic 2013 and about 47,62,089 people worldwide have been died due to COVID-19 pandemic. It is important to spread awareness among the people about various safety and preventive measures. Therefore, the main focus of the present study is on pulmonary disease outbreaks, their sources, treatment, prevention and containment so that people could become more alert for subsequent or similar outbreaks in future.

ABSTRACT CODE: OS10

MICROBIAL BIOREMEDIATION OF AGRICULTURAL SOILS POLLUTED WITH SULFONYLUREA HERBICIDES WITH RESPECT TO INDIA

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There is increase in the use of herbicides in agriculture to increase the crop production to satisfy world-wide demands. Sulfonylurea herbicides such as 'Metsulfuron' Methyl are widely used to control the broad-leaf weeds in wheat and various other crops. The excessive use of Sulfonylurea herbicides leads to contamination of agricultural soils, river system and nearby groundwater and causes hazardous effect to the environment. Among various technology Bioremediation is an eco-friendly, safe and cheapest process by which we can degrade the toxic chemicals from the agricultural soil using microorganism. In the present study the soil sample was collected from a wheat field previously treated with Metsulfuron herbicide, in district Pratapgarh (UP). Ten bacterial colonies were isolated using serial dilution technique followed by enrichment culture in mineral media with 50ppm Metsulfuron as only carbon source. The screening of the herbicide utilizing isolates was done by using spray plate technique for rapid selection. Among ten isolates, one isolate was found to be able to grow in herbicide. Identification of all the isolates were done by morphological and biochemical tests. Among the 10 isolates, one isolate was found to be able to grow in Metsulfuron. The selected isolate was also studied to find growth response under different concentration of Metsulfuron herbicide. Minimum and maximum growth response was found in 10 ppm and 50 ppm Metsulfuron concentration respectively. Isolate was not able to grow above concentration 100 ppm Metsulfuron. Finally, the isolate was able to grow at temperature 30^0 C, pH 7 and 50 ppm Metsulfuron concentration.

Keywords: Bioremediation, Sulfonylurea Herbicide, Spray Plate Technique, Bacterial isolates

ABSTRACT CODE: OS11

ARSENIC-TOLERANT AND PLANT-GROWTH PROMOTING RHIZOBACTERIA FROM AGRICULTURAL SOIL

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The carcinogenic effects associated with the metalloid arsenic are numerous and its contamination of agricultural soils in particular is of global concern. Rhizobacteria are known to have various functions in mobilising arsenic species in the soil thus preventing their uptake by plants. In this present study, soil from a paddy field of Manipur, India was estimated for arsenic content. Rhizobacteria were isolated and analysed for various biochemical tests and assayed for tolerance of concentrations of arsenite (As^{3+}) and arsenate (As^{5+}) followed by determination of MIC, MBC and MTC of the isolates. The isolates were further tested for their plant-growth promoting traits like indole, siderophore, ammonia, hydrogen cyanide production, phosphate solubilization and seed germination potential. After 16S rRNA gene sequencing and phylogenetic tree analysis, the isolates TNCR-17, TNR-14, TNB-16, TNCB-27, TNCB-55 and TNCR-102 were identified to be *Bacillus wiedmannii, Pseudomonas shirazica, Bacillus paramycoides, Bacillus altitudinis* and *Bacillus megaterium.*

Key words: Arsenic contamination, Arsenic tolerance, *Bacillus altitudinis, Bacillus megaterium, Bacillus paramycoides, Bacillus wiedmannii*, *Pseudomonas shirazica,* Plant Growth Promotion.

ABSTRACT CODE: OS12

CO-TRANSCRIPTIONAL ANALYSIS OF GENES INVOLVED IN METABOLIC PATHWAY OF CARBARYL DEGRADATION IN *PSEUDOMONAS* SP. C5PP

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Soil isolate, *Pseudomonas* sp. C5pp has been reported to degrade Carbaryl as the sole source of carbon and energy. The metabolic pathway responsible for degradation and the enzyme involved have already been elucidated. Carbon source dependent enzyme activity studies have suggested the degradation enzymes are inducible. The gene annotation and nucleotide sequence of super-contig revealed that genes involved in Carbaryl utilization are arranged in the form of three gene clusters (upper, middle and lower). In addition to that, the *in-silico* analysis using BPROM and SAPPHIRE has been used to predict probable promoters for genes involved in Carbaryl degradation. The co-transcriptional analysis was performed using gene specific primers and cDNA prepared from Carbaryl and salicylate grown cells. In the presence of Carbaryl all the genes encoding the enzymes for degradation are induced (genes from upper, middle and lower operon were co-transcribed as polycistronic-mRNA). While in the presence of salicylate, only genes of middle and lower pathway were transcribed as polycistronic-mRNA. Therefore, the co-transcriptional analysis study confirms the operonic arrangement of the genes from three pathways involved in the Carbaryl degradation by the strain *Pseudomonas* sp. C5pp.

Keywords: Carbaryl degradation, *Pseudomonas* sp. C5pp.

ABSTRACT CODE: OS13

PLANT GROWTH PROMOTION AND ANTAGONISTIC POTENTIAL OF BACTERIAL ENDOPHYTES FROM OCIMUM SANCTUM LINN. AGAINST ROOT ROT PATHOGEN FUSARIUM OXYSPORUM IN PISUM SATIVUM

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The present study demonstrated the bio-efficacy of consortium inoculant bio formulated with two antagonistic Ocimum sanctum leaves endophytes Pseudomonas aeruginosa OS_12 and Aneurinibacillus aneurinilyticus OS_25 on growth promotion and induction of systemic defensive response in pea plants challenged with root rot pathogen Fusarium oxysporum f.sp. pisi.

Both the isolates possessed multifunctional growth promoting traits as well as have potential to produce antifungal volatile organic compounds as analysed by GC-MS. Scanning electron micrographs exhibit distinct morphological changes in fungal hyphal structures in the presence of biocontrol strains as reflected in in vitro dual culture assay.

Through in planta trials in plastic pots significant changes in plants were remarkably found with respect to disease incidence, morphological and biochemical parameters of pea plants under normal as well as biotic stress conditions. Furthermore, the inoculation of pea plants with strains OS_12 and OS_25 led to significant ($P<0.05$) induction of systemic resistance in Fusarium challenged plants by enhancing the activity of antioxidants and defense related enzymes such as Phenylalanine ammonia lyase (PAL), peroxidase (PO), polyphenol oxidase (PPO), ascorbate oxidase (AO), catalase (CAT) and total phenolic content.

Thus, this works clearly demonstrated how synergistic interaction between the biocontrol bacterial isolates promote plant growth and induced defense response under fungus infected condition.

Keywords: bio-efficacy of consortium, in planta trials, Ocimum sanctum, Pseudomonas aeruginosa OS_12, Aneurinibacillus aneurinilyticus OS_25, Fusarium oxysporum f.sp. pisi.

ABSTRACT CODE: OS14

NOVEL BACILLUS ALTITUDINIS STRAIN KMS-6 AS POTENTIAL BIOCONTROL AGENT AGAINST ROOT-KNOT NEMATODE MELOIDOGYNE JAVANICA

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Root-knot nematodes, especially *Meloidogyne* species possess huge threats to major fruit and vegetable crops across the globe causing economic losses of millions of dollars every year. The use of synthetic nematicides against such pests have deleterious effects on environment and human health. The management of these phytopathogens via biological means is an emerging eco-friendly trend being opted nowadays. In this context, bacterial strain KMS-6 was isolated from nematodes infested soil belonging to research field of CCS HAU, Hisar and identified as *Bacillus altitudinis* based on 16S rRNA gene sequence analysis (accession no. MT626660). KMS-6 was tested against *M. javanica* eggs and second stage juveniles under *in vitro*, greenhouse and field conditions. Under *in vitro* conditions, KMS-6 treatment resulted in potential hatching inhibition and up to 86% J2s mortality. In greenhouse experiments on brinjal (in 2018) and tomato (in 2021), a significant reduction in number of eggs (76%), galls (80%), and final nematode population (92%) was seen compared to control, and carbofuran treatment. Similar results were obtained in field trials on brinjal and cucumber, in 2018 and 2019, respectively. In addition to this, KMS-6 significantly enhanced plant growth and yield. Based on this data, *B. altitudinis* KMS-6 could be used as a potent biocontrol agent against root-knot nematodes and an eco-friendly tool for sustainable agriculture.

Keywords: Root-knot nematodes, *Meloidogyne javanica*, *B. altitudinis*, biocontrol

ABSTRACT CODE: OS15

GREEN NANOTECHNOLOGY: SUSTAINABLE PRODUCTION OF BIOGAS AND METHANE BY USING ANAEROBIC DIGESTION OF LIVESTOCK WASTE

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It has been reported that nanoparticles (NPs) have the ability to enhance the anaerobic digestion process. These also accelerate the digestion of livestock waste, which enhances the biogas as well as methane potential. The effects of iron (Fe) NPs on biogas and methane production were investigated using a batch type anaerobic digestion system. For this purpose, Fe NPs was synthesised by using neem leaves extract (used as a reducing and capping agent) and implemented to study the effects of these Fe NPs with different concentrations on biogas and methane production. These NPs were characterized by UV-Vis spectroscopy, particle size analyser, zeta potential analyser and transmission electron microscopy. The best results of NPs additives were determined based on the statistical analysis (R-software), which were observed @18 mg/L Fe NPs ($p < 0.05$). These Fe NPs additives delivered the highest biogas (22.4 %) and methane (30.9%) yields in comparison with their other concentrations (9, 12, 15, 21 mg/L) and the control. After completion of digestion pH was found to be increased and Total Solids, Volatile Solids, Total Volatile Fatty Acids, organic carbon content and dehydrogenase activity decreased in all treatments with maximum degradation (43.1%) of total solids was observed with 18 mg/L Fe NPs.

Keywords: Anaerobic, biogas, dehydrogenase, nanoparticles, zeta potential

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ABSTRACT CODE: OS16

IN VITRO EVALUATION OF COMBINATION OF BIO AGENTS AGAINST WILT OF CUMIN CAUSED BY FUSARIUMOXYSPORUMF. SP. CUMIINI.

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Fusarium wilt is a widespread disease induced by *Fusarium oxysporu*m. It is an extreme condition which causes damping-off, root wilt and vascular wilt. Across all cumin-cultivar farms, it is causes considerable yield loss. Under suitable conditions, the disease might lead to a complete losses in productivity. Combinations of biological control that are compatible with each other are a viable approach to managing *Fusarium* wilt, according to the current study. The study was conducted to determine the beneficiary aspects of combining different species of *Trichoderma* spp., Pseudomonas spp. and Bacillus spp. i.e *Trichoderma viride* +T*richoderma harzianum*+*T.konngii, A.flavus*+*T.konngii,T.konngii* + *Trichoderma viride*, *A.flavus* +*Trichoderma viride, Pseudomonas putida*+ *Bacillus subtilis,Bacillus subtilis*+ *Pseudomonas fluorescens, Pseudomonas fluorescens*+ *Pseudomonas putida* to control the *Fusarium* wilt. The results showed that all treatments enhanced plant growth, yield, and seed quality in addition to plant growth. Under greenhouse conditions, the synergistic treatment of arbuscular mycorrhizal fungi and bacteria, Trichoderma harzianum, and Pseudomonas fluorescens offered the best growth and yield characteristics, resulting in an 80% reduction in disease severity compared to the control treatment. Based on their efficacy, this synergistic combination may be especially effective at reducing cumin wilt disease caused by *F. oxysporum,* as well as improving growth, productivity, and seed quality.

Keywords: *Fusarium* wilt, *Fusarium oxysporum,* biological control

ABSTRACT CODE: OS17

Azospirillum, A PLANT GROWTH PROMOTING RHIZOBACTERIA- A PROMISING INTERVENTION TO SUSTAINABLE AGRICULTURE: AN INDIAN PERSPECTIVE IN CONTEXT TO FINGER MILLET [*Eleusine coracana* (L.) Gaertn.]

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Crop growth and productivity has largely been vulnerable to various abiotic and biotic stresses that are intensified due to global climate change and the current progress in agricultural production does not really cater to the demand of the burgeoning human population. Therefore, developing improved varieties and designing newer approaches for crop improvement against stress tolerance have become a priority now-a-day. However, most of the crop improvement strategies are directed toward staple cereals such as rice, wheat, maize etc., whereas attention on minor cereals such as finger millet [*Eleusine coracana* (L.) Gaertn.] lags far behind. Finger millet is an important, nutritionally rich crop of semiarid and tropical regions, and its rhizospheric zone harbours a wide diversity of plant growth promoting rhizobacteria. Plant growth promoting rhizobacteria (PGPR) are root colonizing bacteria that establish symbiotic relationships with plants promoting plant growth. PGPR promotes plant growth either directly by promoting nutrient availability and acquisition or indirectly by reducing the proliferation of pathogens that hamper plant growth. One such PGPR is *Azospirillum.* Recent results have shown that *Azospirillum*-inoculated finger millet crops enhanced the growth and yield with a great supply of nitrogen under stress condition to the crop when applied by seed, seedling and soil application method. The present research talks about the phosphorus solubilization, production of phytohormones (IAA, Gibberellic acid, Cytokinin), increased photosynthetic pigments, restoration of vegetation in harsh environment, enhance seed quality, alleviate biotic and abiotic stresses, etc. by *Azospirillum* thus enhancing the growth and yield of the crop over untreated ones.

Keywords: Finger millet, crop improvement strategies, Plant growth promoting rhizobacteria

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ABSTRACT CODE: OS18

BIOFLOC TECHNOLOGY AS AN APPROACH TOWARDS SUSTAINABLE AQUACULTURE

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The aquaculture industry is contributing significantly to nourish the world population. Unfortunately, it is associated with some serious negative impacts on the environment such as consumption of excess amount of freshwater; deterioration of water quality of the culture water; excessive wastage of feed; and significant minimization of biodiversity. The main aim of aquaculture is to increase the food production in minimum time and with least resources; but this could prove to be advantageous only when it is done sustainably. One solution to this problem is the use of Biofloc Technology (BFT). It involves the use of microorganisms to improve the water quality by decreasing its nitrogen content accumulated in the form of ammonia and serve as protein-rich feed produced *in-situ*. Biofloc is the composite of several diverse microorganisms and organic matter in the culture water. The growth of biofloc is stimulated by increasing the C/N ratio by the addition of external carbon source which leads to the increased growth of heterotrophic bacteria which will now require nitrogen for their protein build-up. Then the nitrogen would be consumed by the bacteria in the form of faecal matter of fish or uneaten feed; thereby reducing the nitrogen content in the water. The biofloc now serve as a protein-rich diet to the fish and minimise the need for expensive external feed with the additional advantage of improving the water quality with zero or minimal exchange of water.

Keywords: Aquaculture, Biofloc technology, microorganisms, C/N ratio

ABSTRACT CODE: OS19

ETHANOL PRODUCTION FROM SUGARCANE MOLASSES BY YEAST ISOLATED FROM DISTILLED ALCOHOLIC BEVERAGE OF NORTHEAST INDIA AND COMPARISON OF FERMENTATIVE CAPACITY WITH COMMERCIAL YEAST STARTER

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Significant efforts have been made lately in conversion of biomass to ethanol fuel, which is widely regarded as the cleanest substitute to fossil fuels. This study is about the production of Ethanol from yeast which was isolated from Raksi- a distilled alcoholic beverage native to high-altitude regions of northern and north-eastern parts of India. This yeast showed high similarity with Saccharomyces cerevisiae based on 16s rDNA based molecular method. First grade molasses (56% total reducing sugar) was used as the feedstock in this study. The use of agricultural wastes for production of bioethanol had gained much interest, as they are cheaper, readily available and renewable. This study also compares the fermentative capacity of the yeast with commercial yeast starters. Real-time monitoring of fermentable sugars was done using Brix refractometer and the fermentation was stopped after 72 hours. High performance liquid chromatography (HPLC) results revealed that the yield of Ethanol increases gradually and reaches maximum at 72 hours. Residual sugar was also measured by HPLC at 8 hour intervals. It was found that ethanol yield is significantly dependent on the amount of fermentable sugar content of biomass being used for the production.

Keywords: Ethanol production, sugarcane molasse, alcoholic beverage, commercial yeast

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ABSTRACT CODE: OS20

PRODUCTION AND CHARACTERIZATION OF THERMOPHILIC BACTERIAL L-ASPARAGINASE

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L-asparaginase (L-asparagine amidohydrolase, ASNase (E.C. 3.5.1.1) exhibits huge industrial potential due to its anti-leukemic properties. As a medicine L-ASNase can be used in the treatment of acute lymphoblastic leukemia (ALL), acute myeloblastic leukemia (AML), and other lymphoid in malignancies along with other drugs. Besides L-ASNAse applications as an anti-leukemic therapeutic agent, this enzyme finds applications in food processing industries as an acrylamide degrading agent and as a biosensor for the observation of L-asparagine in physiological fluids at nano-levels.

At present, two L-asparaginases from *E. coli* and *Erwinia* are being highly used due to the absence of glutaminase activity. However, the problems associated with these L-Asparaginases such as toxicity, allergy and immune-suppression, and thermostability that suggest discovering more potential L-ASNase producing isolates. In the present investigation, we have isolated several bacterial samples which showed L-ASNase activity from various environmental samples viz., soil, compost soil, cow/blue bull dung, effluent, and sewage water. Modified Czapek-Dox (C-Dox) agar medium along with L-asparagine and phenol red (pH indicator) was used to L-asparaginase producing bacteria. Approximately thirty isolates were recovered having L-asparaginase activity, one potential isolate was further processed based on the characteristics of the L-asparaginase. Preliminary characterization of the extracellular L-asparaginase showed thermostability at 60-70 °C, therefore, it could be used in the food processing industry to avoid acrylamide accumulation in various food products. Biochemical characterization revealed that it is a member of Pseudomonadaceae. The species-level identification is being carried out using the 16S rRNA gene and this work is in progress. The production of L-asparaginase is being optimized by a ‘one variable at a time’ approach, where 3% (v/v) inoculum size enhanced the production under acidic pH (6.0) and mesophilic temperature of 37 °C. The other parameters for optimizing the production of thermophilic L-asparaginase are in progress.

Keywords: Thermophilic, L-asparaginase, acute lymphoblastic leukemia

ABSTRACT CODE: OS21

BIO-DESULFURIZATION OF DIBENZOTHIOPHENE AND THIOPHENE IN LIQUID FUELS USING AN ENVIRONMENTALLY ISOLATED BACTERIUM

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Liquid fuels such as petrol and diesel contain some amount of sulfur in inorganic and organic forms. On combustion of these fuels sulfur releases to the environment in the form of sulfur dioxide (SO_2). The released sulfur reacted to the environmental moisture and other environmental gases, results in the formation of complex acids such as sulfuric acid and hydrochloric acid. Several methods such as hydrodesulfurization (HDS), oxidative desulfurization (ODS), and adsorptive desulfurization (ADS), were already developed to overcome/remove the sulfur content from liquid fuels. These methods are efficient, however they required sophisticated physical and chemical parameters such as high temperature and pressure, various gasses and other chemicals. Bacterial desulfurization is an emerging option to make the process efficient and cost effective. Here we have isolated a bacterial strain from the effluent of a petroleum industry. The isolated bacterium was identified by Gram staining and 16S rRNA sequencing. The desulfurization tests were performed in the wide concentration range (50 to 300 ppm) of sufur compounds namely, dibenzothiophene (DBT) and thiophene (TH). The selected strain was capable for the efficient removal (up to approximately 90 %) of these compounds at 30 ^{O}C temperature and 1 atm pressure. The concentrations of sulfur compounds were determined using flame ionized gas chromatography analysis. The initial and final product of desulfurization (before and after desulfurization) was confirmed by gas chromatography – mass spectroscopic (GC-MS) analysis.

Keywords: dibenzothiophene, thiophene, desulfurization

ABSTRACT CODE: OS22

SCREENING OF FUNGI FOR SUBMERGED PRODUCTION OF LIGNOLYTIC ENZYMES FOR BETTER DELIGNIFICATION AND SACCHARIFICATION OF RICE STRAW

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Bio-pretreatment of lignocellulosic biomass for 2G bioethanol production is contracting attention of many industries which want to replace acid pretreatment to reduce maintenance cost of whole process. Lignin modifying enzymes (LMEs) used in bio-pretreatment are obtained from white rot fungi which are considered to be the major producers of LMEs. Screening of white rot fungi and submerged production of LMEs is important for the ease of application of same in delignification and saccharification. In this study we screened various fungi with the help of plate assay and full factorial designed (FFD). This screening led us to select two fungi *(Trametes versicolor and Pleurotus ostreatus)* which we evaluated further. Gel analysis (SDS and native) of broth from these fungi confirmed our findings. Proteomic analysis of one of the fungi revealed that rice straw is a good inducer for secretion of more lignin modifying enzymes like manganese peroxidase (MnP), versatile peroxidase (VP) apart from laccase. Further, to remove the negative effect of laccase after delignification, introduction of washing step before saccharification gave better efficiencies as compared to unwashed control. Hence, we recommend that washing step should be included between biomass pretreatment and saccharification to achieve significant cellulose to glucose conversion for commercial applications.

Keywords: Bio-pretreatment, Lignocellulose, Proteomic analysis

ABSTRACT CODE: OS23

A COMPARATIVE STUDY OF PHYSICO-CHEMICAL PARAMETERS AND CILIATE DIVERSITY OF LEACHATE CONTAMINATED SOIL FROM THE LANDFILL AND THE SOIL FROM HUMAN INHABITANT LAND

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Landfilling is considered to be a safe and economical approach for waste disposal but this is true only for engineered landfills. Engineered landfills are seldom found in developing countries like India. The generation of leachate from the landfilled municipal solid waste is a major concern nowadays. Leachate is the result of two main phenomena occurring in a landfill: infiltration of water in the deposited waste mass and mass transfer of substances from waste to infiltrating water. This leachate can cause severe environmental degradation and also pollute natural resources like soil and soil microbes. In the present study, the physico-chemical parameters and ciliate diversity of soil contaminated with leachate from a Okhla landfill and non-contaminated soil from human inhabitant site (ANDC) were compared. It was observed that the physico chemical parameters including water holding capacity, pH, electrical conductivity, calcium and magnesium, calcium carbonate, soil organic matter, nitrogen and cation exchange capacity of soil contaminated with leachate from Okhla landfill were found to be significantly different from the ANDC. The Shannon-Weiner diversity index was found to be significantly higher at ANDC. Results clearly suggest that the disposal of municipal solid waste significantly alters the physico-chemical parameters of leachate contaminated soil of Okhla landfill. This study might help in assessing changes the physico-chemical and biological properties of the soil. Also, it can be used to develop an improved strategy for better municipal solid waste disposal and management.

Keywords: Ciliate diversity index, Contaminated soil, Physico-chemical parameter

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ABSTRACT CODE: OS24

MICROBIAL XYLITOL PRODUCTION USING A NEWLY ISOLATED *CANDIDA TROPICALIS* K2

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The generation of valuable chemicals and fuels from lignocellulosic biomass or agricultural waste is the primary objective of a biorefinery in the present context of climate change and pollution. By reinforcing C5 and C6 sugars produced from agro-industrial waste, microbial cell factories may be used to produce commercially viable biochemicals on a long-term basis. Most of the microbial system lack pentose utilizing machinery because pentoses are the less preferable source of carbon for their growth and development. The efficient use of pentose and hexose sugars is critical for integrated biorefinery. Exploration of organic waste from various habitats (Sugar mill/ industrial waste/ vegetable waste/ sewage and forest) led to screening and isolation of xylitol producing yeast which was phylogenetically identified as *Candida tropicalis* K2. The newly isolated strain was explored, and fermentation parameters were optimized for xylitol production. Isolate K2 produced 90 g/L xylitol with a yield of 0.90 g/g and volumetric productivity of 1.5 g/L/h, when 100 g/L of xylose was used along with 20 g/L of glycerol as a co-substrate in batch fermentation. Therefore, the isolate *Candida tropicalis* K2 would be a good candidate for the xylitol production which can efficiently use pentose sugars present in lignocellulosic biomass.

Keywords: Biorefinery, *Candida tropicalis*, Pentose sugar, Xylitol

ABSTRACT CODE: OS25

ISOLATION AND SCREENING OF PIGMENT PRODUCING PLANTS FROM THE *BIXA ORELLANA* AND *BETA VULGARIS* SPP.

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Pigments are a type of coloring component which are utilized by humans to add colors in their lives. Using synthetic pigments for the purpose of coloring food, clothes, fruit juices, paints are accepted worldwide previously, but due to hazardous impact of sythetic colors on environment and also on human health made to go for alternative sources of the pigments which are safe to use. Isolation of natural pigment is an another preference that will increase the supply of pigment from natural sources while minimizing environmental and health risks. Thus, there is a growing necessity for biocolor derived from natural sources that can substitute synthetic colors. Natural colorants are commonly found from plants, animals and microorganisms. Plant pigments have several benefits, so it seems much of prominence for pigment production. *Bixa orellana* and *Beta vulgaris* were isolated for yellow, orange and red color pigments from natural ecological source. Pigment isolation from plants requires extract preparation and then isolation of pigments using different solvents. Extracted pigments were analysed by preliminary screening techniques such as phytochemical assay and various confirmation tests.

Keywords: Pigment production, *Bixa Orellana*, *Beta vulgaris*

ABSTRACT CODE: OS26

BIOPROSPECTION OF HYDROLYTIC ENZYMES FROM SOIL BACTERIA OF THATTEKAD BIRD SANCTUARY IN THE WESTERN GHATS

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Thattekad bird sanctuary, located in the Western Ghats of Kerala, consisting of an unexplored microbial community, is selected as the study area for the present investigation. This biogeographic zone falls in a transition area between the moist deciduous forests and the montane rain forests of the South Western Ghats. Thattekad is a hotspot of endemism that is famed for its bird diversity and this area has never been inquired for microbial biodiversity. The forest soil usually is rich source of such exoenzyme producing microbes due to the presence of organic matter. The high demand for microbial enzymes in the industry directed the focus of this study to exoenzyme profiling of relevant bacterial isolates from forest soil. Thirty-four promising multi enzyme producing bacterial isolates exhibited high enzymatic indices for nine enzymes studied: namely amylase, cellulase, pectinase, caseinase, gelatinase, lipase, esterase, ligninase, and xylanase. These isolates were further characterized using polyphasic identification techniques and submitted to Gen Bank after 16S rRNA gene sequencing. Phylogenetic tree construction was done using MEGA X software. Based on the taxonomic classification, the identified strains come under two different categories of phylum; *firmicutes* and *proteobacteria*. In our study, the bacteria belonging to the phylum *firmicutes* from this area secreted more exoenzymes than that of bacteria from phylum *proteobacteria*. To explore the biotechnological potential of the isolates the best enzyme producer was used for the bioconversion of biomass for bioethanol production. Pre-treatment of banana peels with the exoenzymes, amylase, cellulase and xylanase produced by the strain *Brevibacillus parabrevis strain TBS028* enhanced the production of bioethanol. Quantitative analysis showed that the bioethanol production of enzyme treated banana peel hydrolysate was 76% when compared to untreated control substrate, which was 28%. This is a promising indication of the presence of active metabolites producing microbes from forest soil that can be harnessed for various industrial purposes.

Key words: Western Ghat, Soil Bacteria, Multienzyme, Bioprospection

ABSTRACT CODE: OS27

EFFECT OF *FUSARIUM OXYSPORUM* ON CUMIN PRODUCTION AND NATURAL WAY TO INHIBIT PLANT PATHOGENIC FUNGI FOR CONSERVATION OF CUMIN

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Cumin (*Cuminum cyminum L.*) is one of the most seasoned seed spices and the significant creation. Limitation is wither brought about by *Fusarium oxysporum f. sp. cumini* (Foc) and harvest misfortunes could be up to 60%. *Fusarium oxysporum f. sp* is a significant infection that causes shrivel sickness cumin crop world over. Management through chemical fungicides cause genuine natural issues and are poisonous to non-target living beings also. Plant metabolites and plant based pesticides have all the earmarks of being one of the better choices as they are known to have insignificant ecological effect and risk to shoppers rather than manufactured pesticides. In an approach towards the improvement of eco-accommodating administration, in vitro antifungal test was led against *Fusarium oxysporum f. sp.* utilizing plant concentrates of two plants. Plant extract were prepared by six different solvent system for extraction of polar and non polar compound. The poison food strategy was utilized for the assessment of antifungal movement of the concentrates at four distinct focuses (4%, 6%, 8% ,10%and 12%) on mycelial development of FOc. The result showed significant antifungal activity of selected plant against pathogenic fungi. This work shows that the plant extract could be a decent option in fostering a powerful plant based fungicides which can be utilized in natural cultivating for the administration of *Fusarium oxysporum*.

Keywords: *Fusarium oxysporum f. sp. Cumini,* chemical fungicides, natural fungicides, poison food strategy

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ABSTRACT CODE: OS28

BIODEGRADATION OF DIFFERENT GRADES OF PLASTIC USING BACTERIAL STRAINS AND ISOLATION OF OTHERS FROM GARBAGE SOIL

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Increasing polymer saturation and its rate of degradation is a serious global problem which can be tackled by using biological agents. This study was undertaken to isolate bacteria from garbage soil and compare their degradation activity with reference strains on different plastic grades. *Bacillus subtilis, Pseudomonas aeruginosa*, were inoculated in a carbon-free mineral medium containing pre-weighed pieces of LDPE and HDPE and were incubated for a period of 26 months. Simultaneously, soil samples and plastic were collected from dump yards and were inoculated into another carbon-free medium containing pre-weighed LDPE. 9 bacterial strains were isolated from soil samples of which 4 were incubated with preweighed LDPE in carbon free medium. Growth was observed in all the flasks, which indicate the utilization of plastic as carbon source by bacteria. The changes in weights of plastic observed periodically for 26 months showed that LDPE plastics showed a greater decline in weight when compared to HDPE. Furthermore, on comparing the values of *Bacillus* and *Pseudomonas*, the weight decrease was more in the case of *Bacillus*. Whereas, in *Pseudomonas*, an increase in weight was observed in some cases due to formation of biofilms. The isolates from garbage soil also showed presence of biofilms, indicating growth. *Bacillus* and *Pseudomonas* are capable of plastic degradation. The results also show that LDPE has more degradation than HDPE. Furthermore, the isolates obtained from garbage soil, Gram positive cocci, Gram positive rods, and Gram negative rods etc. showed growth in mineral medium thus suggesting they are plastic degraders.

ABSTRACT CODE: OS29

UPTAKE AND METABOLISATION of HCH ISOMERS IN TREES EXAMINED OVER AN ANNUAL GROWTH PERIOD BY COMPOUND SEPCIFIC ISOTOPE ANALYSIS AND ENANTIOMER FRACTIONATION

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To understand the role of plants for natural attenuation, a field study was conducted to characterize the fate of HCH in tress over an annual growth period using compound-specific isotope analysis (CSIA) and enantiomer fraction. Stable and slightly higher $\delta^{13}C$ and $\delta^{37}Cl$ values of HCH of host soil samples compared to the muck (consisting nearly exclusively of HCH) revealed that no or only minor HCH transformation takes place in soil which is most likely caused by a low HCH bioavailibity. In contrast, an increase of $\delta^{13}C$ and $\delta^{37}Cl$ values in trees indicated the transformation of HCH. A large variability of $\delta^{13}C$ and $\delta^{37}Cl$ values in tree over the growth period was observed, representing different transformation extents among different seasons which is further supported by the shift of the enantiomer fraction (-) indicating the preferential transformation of enantiomers also varied over the different growth periods. Based on dual element isotope analysis, different predominant transformation mechanisms were observed during the growing seasons. Our observation implies that plants are acting as biological pumps driving a cycle of uptake and metabolisation and refeed during littering to soil catalyzing transformation. The finding of changes of transformation mechanism in different seasons has implications for phytoscreening and shed new light on phytoremediation of HCH at field sites.

ABSTRACT CODE: OS30

IN-SILICO CHARACTERIZATION AND MOLECULAR RESPONSE OF STRESS-RESPONSIVE GENES UNDER HEAVY METAL STRESS IN FRESHWATER CILIATES

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Due to various anthropogenic activities, the heavy metal concentration is exponentially increasing in the environment. Prolonged metal exposure beyond certain threshold level causes deleterious effects on the living organisms. To tolerate such adverse conditions, microorganisms exhibit wide range of molecular mechanisms for the metal detoxification that include increased expression of stress-inducible genes. Among microorganisms, ciliates, which are single-celled eukaryotic protists, are highly sensitive to any kind of environmental changes, which make them promising model systems for conducting ecotoxicological studies. In this study, effects of heavy metals namely cadmium (Cd) and copper (Cu) on the expression of stress responsive genes like cytosolic heat-shock protein 70 (*hsp70*), manganese-superoxide dismutase (*Mn-sod*), and catalase (*cat*) in the freshwater ciliates (*Tetmemena saprai* and *Euplotes aediculatus*), was studied. Also, the activity of antioxidant enzymes (superoxide dismutase, catalase, and glutathione peroxidase) in these ciliates under metal stress, was determined. Increased enzyme activity and expression of these genes was noticed with an increase in metal concentration and duration of metal exposure. The cytosolic *hsp70*, *Mn-sod*, and *cat* genes of theses ciliates were also sequenced and characterized using bioinformatics tools. Besides, systematic bioinformatics approach was employed to identify and characterize metalloproteins (Cd, Cu, and cysteine-rich) involved in cell defence mechanisms from the whole genome data of *Tetmemena* sp. SeJ-2015 (GenBank accession number LASU02000000). Heat-shock proteins and antioxidant enzymes detected from the predicted metalloproteins of *Tetmemena* sp. SeJ-2015 was compared with *T. saprai.* Similarly, the structure and functions of the stress-response genes in *E. aediculatus* determined in this study was compared with the other reported and closely related ciliates. Also, the catalytic sites of these genes were elucidated using molecular docking techniques. This study will help in understanding the role of these stress-responsive genes in metal detoxification in ciliates.

ABSTRACT CODE : OS31

EVIDENCE OF RESISTANCE TO 3RD GENERATION CEPHALOSPORIN IN BACTERIA ISOLATED FROM SOIL OF INDIAN HIMALAYAN REGION

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The class of 3rd generation cephalosporin is most commonly prescribed for treatment of several bacterial infections such as community-acquired pneumonia, meningitis and urinary tract infections. Bacterial resistance towards this class of drugs is increasing and so is the distribution of cephalosporin-resistant bacteria. Hence, it is vital to screen for the presence of antimicrobial resistance (AMR) in ecological niches that are previously unexplored. In this study, bacteria were isolated from soil sampled from different depths of Lam Pokhari Lake Basin located in Eastern Himalayas, Sikkim, India. Agar-well diffusion assay was used to track AMR in four bacterial isolates against the antibiotic- Monocef (Ceftriaxone) which belongs to the class of 3rd generation Cephalosporin, spanning a range of concentration from 0.06 µg/ml to 64 µg/ml. The study revealed that one isolate was resistant to Monocef. Minimal bactericidal concentration (MBC) of this isolate was determined by further testing with Monocef concentration up to 384 µg/ml. In addition, MIC was determined using Resazurin-based 96-well plate microdilution method with Monocef concentration ranging from 0.03 µg/ml to 384 µg/ml of. This isolate was identified as *Staphylococcus sp.* based on 16s rDNA based molecular method. This bacterium has never been exposed to this class of drug given that it is obtained from low depth of the soil. Thus it is pertinent to look at the resistance phenotype of this particular bacterium and get an in-depth understanding of the resistance genes harbored by performing genotypic characterization.

ABSTRACT CODE: OS32

COVID-19 INDUCED COAGULOPATHY (CIC): THROMBOTIC MANIFESTATIONS OF VIRAL INFECTION

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Coronavirus disease 2019 (COVID-19) is caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and may result in an overactive coagulative system, thereby resulting in serious cardiovascular consequences in critically affected patients. The respiratory tract is a primary target for COVID-19 infection, which is manifested as acute lung injury in the most severe form of the viral infection, leading to respiratory failure. A proportion of infected patients may progress to serious systemic disease including dysfunction of multiple organs, acute respiratory distress syndrome (ARDS), and coagulation abnormalities, all of which are associated with increased mortality, additionally depending on age and compromised immunity. Coagulation abnormalities associated with COVID-19 mimic other systemic coagulopathies otherwise involved in other severe infections, such as disseminated intravascular coagulation (DIC) and may be termed COVID-19 induced coagulopathy (CIC). There is substantial evidence that patients with severe COVID-19 exhibiting CIC can develop venous and arterial thromboembolic complications. In the initial stages of CIC, significant elevation of D-dimer and fibrin/fibrinogen degradation products is observed. Alteration in prothrombin time, activated partial thromboplastin time, and platelet counts are less common in the early phase of the disease. In patients admitted to intensive care units (ICUs), coagulation test screening involving the measurement of D-dimer and fibrinogen levels, has been recommended. Prior established protocols for thromboembolic prophylaxis are also followed for CIC, including the use of heparin and other standard supportive care measures. In the present review, we summarize the characteristics of CIC and its implications for thrombosis, clinical findings of coagulation parameters in SARS-CoV-2 infected patients with incidences of thromboembolic events and plausible therapeutic measures.

ABSTRACT CODE: OS33

CHALLENGES AND OPPORTUNITIES IN THE DEVELOPMENT OF COVID-19 VACCINES

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The COVID-19 pandemic has caused great upheaval and devastation across the globe, responsible for damage to all facets of life including physical and mental health as well as the economy. This has led to extensive and concerted efforts being made by researchers and medical professionals the world over with the goal of attaining ascendency over this pandemic. The development of vaccines including both traditional and recently developed vaccine platforms have made tremendous advancements following the onslaught of the pandemic. The goal of vaccinating an individual is to produce a suitable immune response, leading to the establishment of immunological memory against a specific pathogen. The eventual goal of vaccination is to achieve herd immunity. In order to achieve herd immunity majority of the population must be vaccinated. Various vaccination platforms have been employed in the development of suitable prophylactic option against SARS-CoV-2 including more traditional techniques namely live attenuated vaccines, inactivated vaccines, vector vaccine and protein subunit vaccines as well as more contemporary approaches namely nucleic acid vaccines including mRNA based and DNA based, and recombinant protein subunit vaccines. Plant based vaccines using virus like particles, agrobacterium induced nucleus transformation, and bioinformatics supported vaccine designing have also been applied towards vaccine development for COVID-19. Discussion about the various vaccination platforms available for use and in the pipeline is vital for not only a better understanding of the various options available currently, it also helps ensure that future research in this field attains the development of better and more effective therapeutic and prophylactic options.

ABSTRACT CODE: OS34

THE REQUIRED SYNERGY OF BIOACOUSTICS AND CONSERVATION TACTICS FOR AMPHIBIANS IN SEMI-URBAN AND URBAN SETTINGS.

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Amphibians, particularly anurans offer a vast diversity of vocalization and showcase varied acoustic behaviour. This enables the determination and quantification of their vocal attributes. It allows analysis and visualization of calls to study and distinguish between various properties pertaining to different species, driving the postulation of necessary conclusions. It enables a comprehensive study of cohabitation amongst diverse species, their spatial and acoustic partitioning. This allows the exploration of integrated systems governing interactions in their existential ecosystem. The data collected also serves as the basis of exploring evolutionary relations between species and their development over years, comparing different call properties between related and unrelated species and determining their ancestral connectivity. It enables population monitoring and adds to the taxonomic database for further utilization in multidisciplinary research avenues. Amphibians face multiple anthropogenic threats (road kills, declining and degrading habitat, urban pollution, etc. being amongst the top impactors) in the urban vicinity, the utilization and implementation of acoustic analysis is crucial for the system maintenance. It would ensure the regulation and monitoring of amphibian species declining or disappearing in the niche. Due to lack of significant data recorded in the multiple taxonomic databases, many species go extinct unrecognized. Recognizing the need of amphibian species conservation in the urban set up, bioacoustics, thus serves as the keystone to understanding the governing mechanisms of amphibian behaviour, recognition and protection.

Keywords: Bioacoustics, Amphibians, Delhi-NCR

ABSTRACT CODE: OS35

ENHANCED ANTIMICROBIAL ACTIVITY OF BERBERINE LOADED BIPOLYMERIC (ACACIA/GELLAN GUM) NANOCARRIER

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Berberine is a natural plant alkaloid and has been reported to possess antimicrobial activity. However, its clinical application has been hampered due to its poor bioavailability, low solubility and lesser absorption. Nanoencapsulation of berberine using a suitable carrier solves this problem. In the present study, berberine nanocomplexes were synthesized with biodegradable polyanionic gums, which in addition to berberine's bioavailability and efficacy; also promotes its biological activities. Novel berberine nanocomplexes were prepared with acacia and gellan gum by ionic complexation method using tween 20 as a surfactant and glutaraldehyde as a cross-linking agent. The effects of concentration of tween-20, gum acacia and gellan gum on particle size and % encapsulation were studied with the help of 3-level central composite experimental design. These nanocomplexes were characterized by Fourier transform infrared spectroscopy (FTIR) and Transmission electron microscopy (TEM). Particle size and encapsulation efficiency of optimized formulation were 254.3 nm and 93.3 %, respectively. Berberine nanocomplexes were observed in transmission electron microscopy to be spherical in shape and 207.2 nm in size. Well diffusion method was used to investigate the antibacterial activity of berberine nanocomplexes against four bacterial strains and two fungal strains. In conclusion, antimicrobial activity of berberine nanocomplexes was improved upon encapsulation in gum nanocomplexes as compared to berberine alone.

Keywords: Antimicrobial, Encapsulation

ABSTRACT CODE: OS36

INCLUSIVE APPROACH OF INNOVATIVE RESEARCH WITH BIOPOLYMERS AS REMEDIATING AGENTS IN WASTE WATER TREATMENT

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In the pursuit of co-creating the academic environment and community empowerment, the inclusive approach of innovative research and the productive outcomes has emerged as a key methodology for advancing knowledge. Given study presents the creation of a readily separable, Fe_3O_4-loaded chitin nanomaterial (MCH NM) as a potential adsorbent for the removal of Reactive Blue 13 (RB13) dye from aqueous solution under visible light (420 nm) using a simple Co-precipitation process. This nanomaterial was studied using a variety of physicochemical approaches; MCH NM has a band gap energy of 2.257 eV, as determined using Tauc's plot with UV–visible spectroscopy. The tendency of the polymer chains to achieve extended configurations at equilibrium, beyond which an elastic retractive force prohibits further expansion, gives MCH NM outstanding swelling properties. The interaction between dye and adsorbent is described using zero-point charge and zeta potential approaches. Batch adsorption tests on MCH NM indicate outstanding adsorption activity towards RB13 dye, with a maximum value of 199.02 mg/g in 22 minutes, the highest value ever reported for any reactive dye. The Langmuir isotherm model and pseudo second order model were well suited to the equilibrium adsorption data and adsorption kinetics, indicating chemically rate regulated monolayer adsorption. Thermodynamic investigations show that the adsorption process is exothermic and spontaneous. These exploratory studies and research findings results to knowledge integration and desired learning outcomes.

ABSTRACT CODE: OS37

GUAR GUM BASED NANOCOMPOSITES AS EFFICIENT ADSORBENTS FOR DYES AND METAL IONS FROM WASTE WATER

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One of the key techniques toward academic empowerment and knowledge enrichment is through synergistic constructive innovative research. The abstract illustrates one of the innovative ways of eradication of hazardous pollutants from waste water. Synthetic dyes and heavy metal ions are especially known, since long time back, for their high toxicity, carcinogenicity and non-biodegradability thereby posing serious threat to various life forms on earth. Researchers nowadays are relentlessly on a race exploring sustainable materials and techniques for the mitigation these toxic contaminants from water bodies. Biopolymers such as guar gum, owing to it high abundance, low cost and non-toxicity prove to be potential candidates in this field. Plenty of hydroxyl groups in the polymer backbone enable guar gum to be functionalised or grafted in a versatile manner proving itself as an excellent starting substance for fabricating upgraded materials. Guar gum or its derivatives when grafted with other materials (natural or synthetic) gives rise to unique 3-D upgraded nano materials which still reserve the inherent beneficial properties of natural guar gum simultaneously doing away with the deficiencies which may restrict their applications in certain fields. Hence, guar gum-based nanocomposites act as superior adsorbents for a wide range of water pollutants including dyes and heavy metal ions thereby contributing a significant role in waste water remediation. The quality of the adsorbents is assessed through their adsorption capacity and percentage removal efficiency. The behaviour of the adsorption phenomenon on the adsorbents are investigated through isotherm and kinetics models, their recyclability and evaluation of thermodynamic parameters. A comprehensive analysis with convincing results suggests a good future perspective of commercialisation of guar gum based nano materials on a large scale for real life applications in water purification.

Keywords: Guar gum, isotherm, kinetics, Adsorption Capacity, Kinetics

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ABSTRACT CODE: OS38

SCIENTIFIC CORRELATION BETWEEN GUT MICROBIOME AND COVID-19, A SYSTEMATIC STUDY

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Covid-19 caused by SARS-CoV-2 has challenged prior understanding of infectious diseases and triggered a pressing need to explore options beyond conventional approach. Prima facie, SARS-Cov-2 causes lung infection through binding of ACE2 receptors present on the alveolar epithelial cells, however, as per various studies SARS-CoV-2 RNA was found in faeces as well. Since enterocytes of the small intestine also express ACE2 receptors which are proposed to increase their expression with age this may impact their tendency to develop gastrointestinal symptoms in COVID-19 . In addition to there is a considerable change in gut microbiota with ageing. lifestyle and diet in fact are found to be influencing Human healthy aging, and thus, longevity by targeting at least in part the gut microbiome which is essentially a collection of commensal microorganisms (microbiota). Diet, environmental factors and epigenetics play crucial role in shaping gut microbiota which can then influence immunity. Studies has identified that Covid-19 has been fatal in elderly patients wherein Gut microbiota diversity is decreased with ageing. Scientific analyses identified the role of gut microbiome in an array of excessive immune reactions during and post COVID-19 infection. Fecal micro flora exibited depletion of symbionts, Bacteroidetes, decreased levels of probiotic bacteria (e.g. *Lactobacillus* and *Bifidobacterium*) and enrichment of opportunistic pathogens composition which was found to be associated with COVID-19 severity. Improving gut microbiota can be leveraged to improve immunity in a prophylactic way for old people and immune-compromised patients. As per Human Gut microbiome project, microbes help the host by regulating physiological functions and impart protective immunity against pathogens. Studies also indicate strategies to alter the gut microbiome will modulate the immune responses of neutrophils, T-cell subsets, inflammatory cytokines, and Toll-like receptors thereby influencing pulmonary dysfunction. Examples are replete in which diet, nutrients and prebiotics exhibited significant reduction in the severity of COVID-19 infection by enrichment of “good bacteria” to change in the equilibrium between Th1/Th2 cells and thereby reducing the cytokine storm and hence the severity of COVID-19. Gut microbiota, cytokines and inflammatory markers perhaps play a role in magnitude of COVID-19 severity possibly via modulating host immune responses. Dietary intervention and lifestyle changes thus can rejuvenate gut microbiota and eradicate Gut Dysbiosis and related comorbidities reduce Covid severity significantly. This is therefore a sytematic study to review the role of Gut dysbiosis with COVID-19.

Abstract Code: OS39

Comprehensive Bioacoustical analysis of three anurans of Delhi-NCR

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Acoustic communication plays a key role in shaping the world of anurans. Most frogs and toads use acoustic signaling as a mechanism for breeding purposes. Among anurans, mostly males vocalize to attract a potential mate for reproduction. These vocalizations combined with a biological perspective give rise to bioacoustics, which has received much attention in behavioral ecology and physiology. It helps in generating objective data, which can further act as a non-invasive tool for population census and behavior monitoring of anurans from a group level to an individual level. Further, it effectively contributes towards the documentation and identification of these species. Our study aims to provide a bioacoustical diagnosis of three local anurans found in Delhi-NCR; Sphaerotheca breviceps, Duttaphrynus stomaticus, and Minervarya pierrei. Advertisement calls of these three species were recorded during their respective breeding seasons. A total of 29 call properties (temporal and spectral) properties were analyzed for our study which included call duration, call rise and fall time, pulse rate, dominant frequencies, pulse period, pulse duration, pulse rise, and fall time. A comparative study post-analysis laid down the distinct vocal features of the three studied species. Our study also helped in understanding the ecological requirements, co-existence of sympatric anurans, and also the length of the breeding season of anuran species. As local anurans of Delhi- NCR have seen a rapid decline in the last few decades our current study can significantly aid in the conservation and monitoring of these locally threatened anurans.

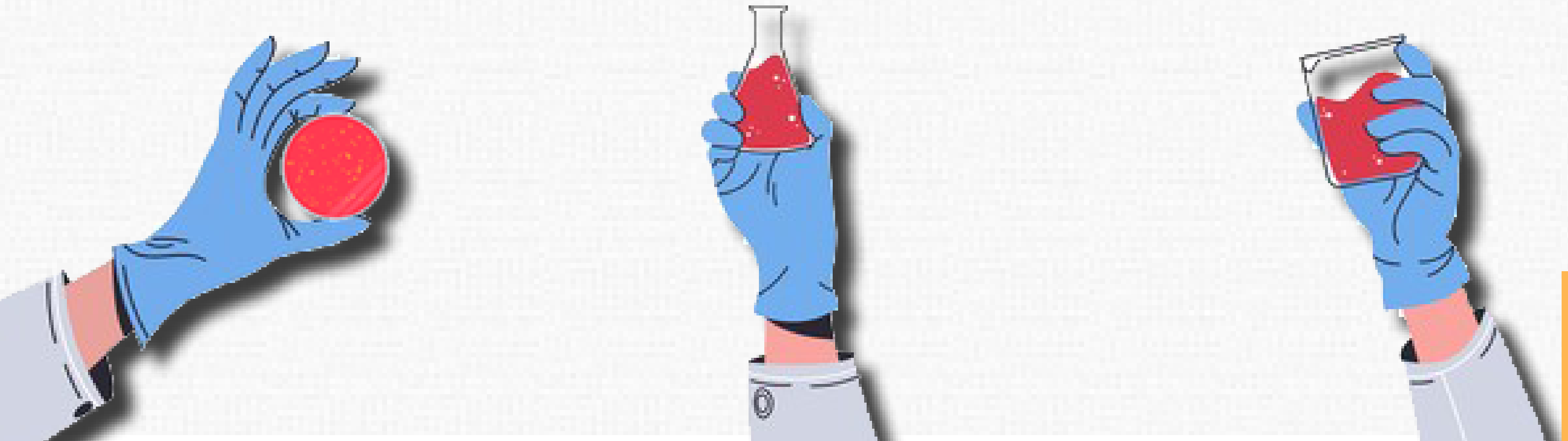
Messieurs, c'est les microbes qui auront le dernier mot."

Gentlemen, it is the microbes who will have the last word.

---------Louis Pasteur -------

Credit: Ted Horowitz Getty Images

POSTER
ABSTRACT



ABSTRACT CODE: PP1

IN SILICO CHARACTERIZATION OF GUT MICROBIOME PROTEINS INVOLVED IN THE BIOSYNTHESIS OF NEUROTRANSMITTERS IMPLICATED IN DEPRESSION

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With the changing lifestyle, 5% of adults suffer from depression which is becoming a major issue as projected by WHO 2021 reports. The role of the human gut microbiome is well evident in the etiology of depression through Gut-Brain Axis (GBA). The bacterial metabolites can induce or ameliorate depression. Tryptophan is an essential amino acid that helps in the synthesis of serotonin, a happy hormone. Tryptophan follows an alternative pathway to synthesize indole, catalysed by tryptophanase which is encoded by tnaA gene, in depression. Tyrosine, which is responsible for the synthesis of dopamine (contributes to mental and physical well-being) can be alternatively converted into tyramine in case of depression by tyrosine decarboxylase, encoded by tdc gene. Contrary to these, Gamma-Aminobutyric acid (GABA) is a neurotransmitter synthesized by the gut microbiome and is known to have antidepressant effects. It is synthesized from glutamate in the presence of glutamate decarboxylase encoded by gadB. The relative abundance of gut bacteria like *Bacteroides thetaiotaomicron and Enterococcus faecium* increases in depression whereas that of *Bacteroides cellulosilyticus* decreases. However, structures of these enzymes have not been characterized in these bacteria. Because of their crucial role in depression, it is important to characterize these enzymes structurally in depth. The present study aims to develop a protocol for in silico structural analysis of gut microbiome proteins. In this study, physicochemical properties were studied using the ProtParam tool and the secondary structure was formed with the help of PredictProtein. To understand the function of the proteins, their 3-D structures are derived using Homology Modeling and validated using Ramchandra plot analysis. The protein-protein interactions have been studied using STRING.

Keywords: depression, glutamate decarboxylase, gut microbiome, *in silico* analysis, tryptophanase, tyrosine decarboxylase

ABSTRACT CODE: PP2

HUMAN GUT BACTERIOCINS IN REGULATING PLASTICITY OF ADIPOCYTES AND THEIR ROLE IN OBESITY: AN IN-SILICO STUDY

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Obesity is an issue of concern that is transforming into an epidemic in both developed as well as developing countries. It has impacted one-third of the world population and is characterized by accumulation of excess body fat. The direct correlation of obesity has been established with increased risk of diabetes, cardiovascular disease, non-alcoholic fatty liver disease (NAFLD) and even colorectal cancer. In addition to high calorific diet and sedentary lifestyle, obesity has been directly related with the dysbiosis in the gut microbiota. The gut microflora undertakes various roles in the host organism to modulate fat storage and adiposity, including the ability to regulate the metabolic status and host weight, thus acting as a probiotic. Studies have previously suggested the role of bacteriocins, ribosomally produced multifunctional proteinaceous biomolecules, in adipocyte differentiation and development. Based on this, we conducted in-silico analysis to investigate the relationship between these peptides. Potential bacteriocin clusters were identified from the gastrointestinal tract in obese population using the Human Microbiome Project's reference genome database and genome-mining tool BAGEL. Predictions of protein function and structure from sequence by homology modelling of these peptides was carried out. Molecular docking approach was used to decipher the potential interactions between these bacteriocins, and the obesity associated factors. The preliminary results from this study will be presented in the poster.

Keywords: obesity, bacteriocin, in-silico analysis, molecular docking

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ABSTRACT CODE: PP3

STUDY OF ANTI-INFLAMMATORY EFFECTS OF GUT MICROBE *Faecalibacterium prausnitzii* IN IBD USING BIOINFORMATICS TOOLS

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Inflammatory Bowel Disease (IBD) is a chronic disease of the gastrointestinal tract causing intestinal inflammation. It is well established that the dysbiosis of gut flora results in loss of intestinal homeostasis and may trigger IBD. However, the pathogenesis of IBD is a complex process and remains largely unknown. In the recent studies it has been found that the gut bacterium *Faecalibacterium prausnitzii* is known to exhibit anti-inflammatory effect and its lower abundance was reported in IBD. In order to find Differentially Expressed Genes (DEGs) in the IBD samples (SN and BHI mediums), a GEOSET-GSE72048 was retrieved from Gene Expression Omnibus (GEO) and analyzed through GEO2R. Further Gene Ontology and pathway enrichment analysis of DEGs from different treatments were executed using Database for Annotation, Visualization and Integrated Discovery (DAVID). Protein-protein interaction analysis for DEGs was conducted using Search Tool for the Retrieval of Interacting Genes (STRING) visualizing via Cytoscape succeeded by hub gene identification and pathway enrichment analysis of the module selected from the interaction analysis. In this study, we identified DEGs. A significant interaction was detected for FCER1G, TFF3, SPHIK, LMO2, KLF11 etc. which are mainly involved in the T-cells differentiation, regulation of immune responses, cytokines signalling and cAMP-gene regulation. A detailed study of these genes under the effect of *Faecalibacterium prausnitzii* may lead to comprehensive understanding of this bacterium in IBD treatment as a probiotic.

Keywords - Cytokines signalling, gut flora, IBD

ABSTRACT CODE: PP4

PLANT–MICROBIOTA INTERACTIONS: PERSPECTIVES AND APPLICATIONS

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Plants are associated with microbiota through different interactions: competition, commensalism, mutualism and parasitism. Such interactions play an important role in plant growth promotion, biocontrol, production of pharmaceuticals and industrially important compounds, remediation and carbon sequestration. Plant-microbe interactions induce defense responses in plants preventing further infection through Systemic Acquired Resistance or Induced Systemic Resistance pathways. These interactions also impact microbiome structure and diversity. Nitrogen fixing microbial associations are well characterized in legumes. Bacteria like *Rhizobium* or Actinomycetes like *Frankia* provide nitrogen to legumes and actinorhizal plants while endophytic diazotrophs provide reduced nitrogen to non leguminous plants like sugarcane, wheat, rice. Understanding the mechanisms of plant-microbe interactions help in the development of microbe-based fertilizers for sustainable agricultural practices. Plant mycorrhizal interactions through endo or ectomycorrhizal associations, provide nutrients to the host plants. Molecular and genetic tools have facilitated the genome and transcriptome analysis of many symbionts. Signaling molecules between the plant and fungi and membrane based selective transporters of phosphorous and nitrogen have been identified. Interactions in the rhizosphere-plant microbiome interactions, root-root interactions and microbiome-plant interactions, have been studied. Role of AHL, quorum sensing molecules, volatile organic compounds, iron, zinc and cadmium in these interactions and the action of phytohormones in inducing defense responses in plants is known. Sophisticated techniques like amplicon sequencing and metagenomics are used to study microbiomes. Recent studies suggest that that there is a difference in the microbial associations of wild and domesticated plants. Crop plants are subject to both artificial and natural selection resulting in an altered microbiome composition. Genetically modified plants also impact rhizobacteria diversity. In our poster we will outline the processes involved in plant –microbe interactions and their role in sustainable growth.

ABSTRACT CODE: PP5

ANTIBIOTIC RESISTANT BACTERIA EMERGING FROM THE PHARMACEUTICAL INDUSTRIAL WASTEWATER

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Antibiotic resistance is a major problem in global health. Antibiotic-resistant occurs naturally but misuse and overuse of the antibiotics become more resistant to the antibiotic to treat the infection. Pharmaceutical products are the prescription drugs for the human and animal diseases and personal care drugs use in daily life basis. Pharmaceutical industries growing in India in a large scale. Pharmaceuticals industries manufacturing the many products like human and veterinary drugs use and release of active pharmaceutical substances into the soil and water through pharmaceutical plant. Industrial Treated and untreated wastewaters have been discharged into rivers and streams, leading to possible waterborne infection outbreaks which may represent a significant dissemination mechanism of antibiotic resistance genes among pathogenic bacterial populations. About 70% of resistant genes spread out in pathogenic and environmental microbes. A global approach to fight against antibiotic resistance, Antibiotic resistant bacteria are pathogenic and toxic to the environment. Antibiotic primarily induces gram-positive and negative bacteria, however the highest rank in gram-positive bacteria such as vancomycin-resistant *Enterococcus faecium* and methicillin-resistant *Staphylococcus aureus* (MRSA). The present study aims to determine the antibiotic resistance patterns of isolated bacterial strains in a pharmaceutical wastewater effluent in pharmaceuticals industries of Uttarakhand India. Sixteen isolates were obtained of multidrug resistant for further identification. Resistance pattern were determined using the standard Kirby-Bauer disk diffusion method following the Clinical and Laboratory Standards Institute (CSLI) guideline of these isolates were studied toward used the 9 antibiotics. The potential of the examined pharmaceutical wastewater effluent in spreading multi-drug resistance and the associated public health impact.

Keywords- Antibiotic resistance, pathogenic, vancomycin-resistance Enterococcus, superbugs, MRSA.

ABSTRACT CODE: PP6

IDENTIFYING BACTERIAL DIVERSITY OF INDIGENOUS SMOKELESS TOBACCO PRODUCTS

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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 Uttar Pradesh. Enumeration of bacteria revealed that SLT products harbor 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. As several Gram-negative bacteria contribute to their role in pathogenesis, the abundance of such bacteria in SLT products alarm prior to their use in chewing. 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 the QIIME2 pipeline.

ABSTRACT CODE :PP7

COMPUTATIONAL STUDY OF THE RELEVANCE OF GASTRIC-CANCER CELL LINE FOR GASTRIC TUMOR ANALYSIS INSINUATED BY *Helicobacter pylori* INFECTION

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Helicobacter pylori is a commensal gut bacterium and an opportunistic pathogen infecting approximately 50% of the world's population .It is attributed as a causative agent for gastric tumor development owing to the bacterial virulence genes -cagA and vacA .These genes affect the Epithelial Mesenchymal Transition) EMT (in gastric carcinoma ,inducing accelerated metastasis .To analyze the efficacy of targeted drugs ,gastric carcinoma cell lines prepared using plasmid vectors are used ,but oftentimes ,the results corresponding to the cell line experimentation differ from the results obtained upon analysis on the actual tumor samples .The aim of our study was to identify the relevance of gastric cancer cell line in conducting gastric tumor studies and to find potentially actionable genes and miRNAs involved in Epithelial Mesenchymal Transition) EMT (using various bioinformatics tools .After extensive literature survey ,a reliable gastric cancer cell line data and three tumor v/s normal GEO datasets with accession numbers :GSE54129 ,GSE81948 and GSE33651 were procured through GEO2R database .The three datasets were compared to identify 29 common DEGs with p-value10^{-5}> which were subsequently compared with the DEGs in cell line .This led to the identification of two potentially actionable genes -ACTN1 and COL1A1 .Further ,pathway enrichment analysis of the two genes was performed using KEGG .Survival analysis of both the genes showed a regressed survival rate in GC patients owing to overexpression of COL1A1 and ACTN1 .Upregulation and downregulation of various miRNAs relevant to the key genes was also studied upon thorough literature review .The genes identified in this study were found to be upregulated in both ,the cell line data and tumor data and may be used to study the underlying EMT pathway involved in progression and development of gastric cancer insinuated by *Helicobacter pylori* in the commensal host.

ABSTRACT CODE: PP8

VANILLIN CATABOLIC MACHINERY OF THE HUMAN GUT MICROBES EXPLAINS FOOD-DERIVED MICROBIOME EVOLUTION

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The human gut microbiome is a diverse array of microbes with a hundred times higher protein-coding capacity than the host. The presence of these enormous metabolic features potentiates human gut microbes to perform diversified metabolic and physiological functions that are otherwise impossible in the host. The human gut microbiome has been identified to play a vital role in the metabolism of carbohydrates, proteins, lipids, nucleic acids, drugs, etc. Despite it, the role of human gut microbes in the metabolism of commonly used food preservatives like sodium benzoate remains elusive. The current study was planned to explore the human gut microbiome for its structure, its genetic makeover, as well as its metabolic machinery involved in benzoate catabolism.

Objectives:

To rationalize the role of human gut microbes in vanillin catabolism
To assess the diet-derived human gut microbiome evolution hypothesis

Methods: Human gut microbiome composition was assessed by SSU rRNA gene sequence. Metabolic features involved in vanillin metabolism were identified with metagenomic and metabolomic data analysis.

Results: SSU rRNA indicates the dominance of Bacteroidetes followed by Firmicutes, Actinobacteria, and Proteobacteria. Metagenomic and metabolomic exploration identifies genetic and functional features of the protocatechuate and catechol-mediated pathway in vanillin catabolism among human gut microbes.

Discussion: The present study uses a multi-omic approach to rationalize the role of human gut microbes in benzoate metabolism. SSU rRNA and RNA features analysis synchronously indicates the dominance of Bacteroidetes followed by Firmicutes, Actinobacteria, and Proteobacteria. Metabolic feature extraction decodes the gene clusters for anaerobic and aerobic pathways of benzoate metabolism. Metabolomic analysis indicates the functional role of protocatechuate branch of the beta-ketoadipate pathway of the benzoate metabolism. Human gut microbes have metabolic machinery to catabolize sodium benzoate catabolism to counter its antimicrobial activity. Additionally, the outcome of the present study enriches our understanding of the evolutionary maturation of the human gut microbiome towards changes in dietary habits and the environmental requirement for successful sustenance in the variable gut environment.

Conclusion: Multi-omic approach catalogued human gut microbial gene clusters and the protein features involved in vanillin catabolism. This study strengthens the hypothesis of gut microbiome evolution with respect to dietary composition.

Key message: Human gut microbes have metabolic machinery to catabolize vanillin to counter its antimicrobial activity. Additionally, the human gut microbes show evolutionary maturation towards changes in dietary habits for successful sustenance in the variable gut environment.

Reference: Yadav M, Pandey R, Chauhan NS (2020) Catabolic Machinery of the Human Gut Microbes Bestow Resilience Against Vanillin Antimicrobial Nature. Front Microbiol 11:588545. doi:10.3389/fmicb.2020.588545

Keywords: Human microbiome, Antimicrobials, Food additives

ABSTRACT CODE: PP10

COMPARATIVE PHYLOGENOMIC ASSESSMENTOF CAMPYLOBACTER SPP. TO ELUCIDATE RELATEDNESS TO PATHOGENIC MEMBERS OF THE GENUS

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Campylobacter is a gram negative bacterial genus. Members of this genus are known to cause Campylobacteriosis, a diarrhoeal disease in humans. Some species of *Campylobacter,* like *C. fetus* and *C. jejuni* are also known to cause extra intestinal infections. Apart from this, *C. jejuni* has been implicated to contribute to cancer development due to the production of a genotoxic substance known as cytolethal distending toxin (CDT). Previous studies reveal that infectious diseases impute 20% of global cancer burden. In this turn, *C. jejuni* promotes colorectal cancer and also influences alteration in microbial community composition as well as function in the gut. In this study, Phylogenomic analysis of 40 species of *Campylobacter* was performed on the basis of 16s rRNA gene sequences; average nucleotide identity (ANI), tetranucleotide frequency, general genome distance calculation (GGDC) and 31 conserved bacterial marker genes to elucidate their Phylogenomic position. These analyses revealed that *C. coli and C. jejuni* form a monophyletic clade. Apart from this, *C. fetus and C. iguaniorum* also form a monophyletic clade. In addition, *C. vulpis* and *C. upsaliensis, C. troglodyt*is and *C. avium*, *C. showae* and *C. rectus* show closed relationship between them. *C. canadensis* was found to have a more distinct phylogenomic relation to the other thirty-nine species of *Campylobacter.* Two-way ANI scores revealed that *C. fetus*, *C. hyointestinalis* and *C. iguaniorum* fall in a single clade, as do *C. jejuni* and *C. coli* on the dendrogram. Further analysis is being carried out, including identification of genomic signatures involved in host pathogen interactions and functional profiling at gene, protein, and pathway level as well as pan genome analysis to reveal the core genome of this genus along with the flexible pan genome.

ABSTRACT CODE: PP11

COVID -19 THERAPEUTIC AGENTS AND THE MODULATION OF THE HUMAN MICROBIOME

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The sudden worldwide spread of Severe Acute Respiratory Syndrome Coronavirus (SARS-Cov2) resulted in the pandemic COVID-19 that impacted all aspects of human life. COVID-19 is characterized by a variety of symptoms, ranging from asymptomatic to acute respiratory distress syndrome. A variety of microbial species residing in different organs of the body can enhance immunity by displaying protective effect against pathogens. Interaction between microbial communities of different organs, for example gut and lung, has been established to play an important role in homeostasis. COVID-19 has been shown to disrupt this homeostasis by causing changes in the microbial constitution particularly in patients with abundance of opportunistic pathogens, however, further research is carried out to establish association between COVID-19 severity and alteration of the human microbiome. Treatment of COVID-19 included use of antibacterial, antiviral, corticosteroids and non-steroidal anti-inflammatory drugs, convalescent serum or plasma, monoclonal antibodies as well as ventilation for oxygen supply. Further, cell-based therapy, antithrombic therapy, certain immunomodulators, traditional medicines and other therapeutic agents are evaluated for the treatment of COVID-19. Many of these agents have been implicated in altering the resident microbial communities and thus, their role in modulating the human microbiome must be considered for effective treatment of COVID-19. Inadvertent alterations of the microbiota can lead to opportunistic infections and aggravating of symptoms with a disastrous consequence for the COVID-19 infected individuals. Use of probiotics, not only for the prevention of COVID-19 but also during and post-treatment is recommended to restore some of the original microbial constitution which gets altered by COVID-19 therapeutic agents.

Keywords: SARS-CoV2, COVID-19, human microbiome, therapeutic agents, probiotics

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ABSTRACT CODE: PP12

Exploring the River Ganga for Bacterial Diversity and Antibiotic Resistance Genes

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The Ganga River is considered as a symbol of purity and is also a vital source for the survival of human as well as other organisms thriving upon it. During its course from Gangotri to the urban areas, it is affected by increased anthropogenic activities and discharge of various effluent from industries etc which eventually results in increase organic load, heavy metals, chemicals compounds and pollutants, antibiotic resistant microbes and their genes in the river ecosystem. Of the many rivers, the Ganga river is the third largest river in the world by total amount of water discharged and largest river in India that receives 6087 MLD sewage water (76% of pollution load) from 138 drains. However, we have limited information on the bacterial diversity of this river as the majority of the studies on this river rely on traditional cultivation approaches. Therefore, there is an exigency to study and gain more detailed information of this river microbial community thriving inside and their role in the river ecosystem.We have isolated several bacteria from the river water and sediment samples on various media Where, the CFU and MPN count of these samples were in the range of 10-550 CFU/ml and 280-580 MPN/ml in the upstream region of the Ganga river however >1600 MPN/ml was observed in the downstream region respectively. On the basis of morphological and biochemical approaches, approximately seventy distinct isolates were segregated. The preliminary analysis revealed that the majority of the bacteria belong to the phyla Proteobacteria, Acidobacteria and Chloroflexi. Identification and characterization are still under process. We obtained significant number of bacteria belong to Enterobacteriaceae, however, the count of E. coli was non-significant. The 16S rRNA analysis of these isolates are under process. Alarmingly, the majority of the bacteria showed antibiotic resistance on various antibiotics. Each strain was observed for different antibiotics like chloramphenicol, tetracycline, Rifampicin, erythromycin, gentamycin, and bacitracin) by disc diffusion method. Besides, the minimum inhibitory concentration (MIC) of ampicillin was observed to be very high (8 mg) followed by Vancomycin (6 mg), chloramphenicol (4 mg), Rifampicin (90 µg), sulphonamide (120 µg). The outcome of this analysis will assist to understand the microbial diversity and their associated antibiotic resistance profile prevailing in the Ganga River.

ABSTRACT CODE: PP14

IMPORTANCE OF ZEOLITE IN SUSTAINABLE AGRICULTURE

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Zeolites are a part of agriculture, due to the usefulness of this rare micro porous structure to perform as a soil amendment and their district cation exchange capacity and adsorption. They are characterized by an ability to lose and gain water reversibly and to exchange some of their component elements without major changes of structure. Zeolite have good water holding capacity and soil drainage. It is extensively used in water treatment, gas adsorption, industrial gas separation, aquaculture, animal husbandry, ion exchange and also for order control. Zeolite can absorb upto 50% water, later this water is used by the plants for their metabolic activities. It is not only enable inorganic fertilizer but also it enables organic fertilizers to slowly release their nutrients. Zeolite can be used as a stabilizer, as a chelator and as a fertilizer. The most common natural zeolite clinoptilolite improves nitrogen fertilization efficiencies but reduces nitrate leaching. The use of zeolite in soil reclamation is another important use if this nano particle in agriculture. Zeolite improve the lateral spread of water into the root zone during irrigation and in drought stress condition water saved in the polymer is gradually adopted and limit need for re irrigation. The changes in soil physical properties carried out by addition of zeolite in the large scale lead to increase in the soil water retention capacity and also decrease the percolation. Zeolite could effectively ameliorate salinity stress and improve the nutrient balance in soil. It can enhance the efficiency of nutrient use by increasing the accessibility of phosphorus from phosphate rock, reduces loss by leaching of nutrients and also act as slow release of fertilizer without harming the environment. It also promote the formation of soil aggregate that increase the porosity of soil.

Keywords: Zeolite, Sustainability, Soil quality and Soil health

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ABSTRACT CODE: PP15

BIOREMEDIATION: FUTURE ASPECT FOR THE CLEANING OF AGRICULTURAL SOIL CONTAMINATED WITH CHLORINATED PESTICIDES

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Chlorinated pesticides such as Lindane is used in agricultural for crop protection in order to meet the demand of growing world population. Excessive application causes bioaccumulation which eventually give rise to significant threat i.e. carcinogenic to human health. These pesticides leached into the soil and into the groundwater of the earth. Conventional techniques of degrading these chemicals are fruitful but are energy intensive. Today is the requirement of worldwide concern to boost the sustainable development with low environmental impact. Bioremediation is considered as safe, less expensive and eco-friendly method for eliminating toxic chemicals from the pesticides contaminated soil. It is a process in which we can remove toxic chemicals into nontoxic chemicals by living organisms.

In the present study bacterial isolates were isolated from the Lindane contaminated soil and they were also evaluated for their Lindane utilizing potential as a carbon source. Ten bacterial colonies were isolated from the agricultural field of the Phaphamau, Prayagraj by enrichment culture method. Isolates were enriched in mineral media with 100 mg/l HCH as the only carbon source. The screening of the Lindane utilizing isolates was done using the spray plate technique for rapid selection. Identification of all the isolates were done by Morphological and biochemical tests. Among the 10 isolates, one isolate was found to be able to grow in Lindane. The selected isolate was also studied to find growth response under different concentration of Lindane pesticide. Minimum and maximum growth response was found in 10 mg/l and 100 mg/l Lindane concentration respectively. Isolate was not able to grow above concentration 150 mg/l Lindane. Finally the isolate was able to grow at temperature 30^0 C, pH 7 and 100 mg/l Lindane concentration.

Key Words: Bioremediation, Bacterial isolates, gamma-HCH, Spread plate technique.

ABSTRACT CODE: PP16

SKIN MICROBIOTA – HOST INTERACTIONS

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Microbiota is a term referred for collection of species of bacteria present within human and other mammalian hosts. Microbiota has intense effect on both innate and adaptive immunity. Health is connected with diverse microbiota that maintains the function of balance between T-effector and T- regulatory cells. The main focus of this abstract is on the skin microbiota host interactions. Skin is a network of dynamic ecosystem that is occupied by bacteria, archaea, fungi and viruses. These microbes are known as skin microbiota which are involved with cutaneous health and disease. The process of skin microbiota begins during the birth and primarily shifts to the other sites of body over the time. The microbiota moves particularly during puberty, with mainly increase of *Corynebacterium* and *Cutibacterium* all over the body mainly in moist sites. In adulthood, skin has continuous exposure with environment and surprisingly the microbial composition remain stable over the time. This stability shows that there is a mutual beneficial interaction that exists between microbes and host. The skin – resident microbes play an important role in maturation and homeostasis of immunity. Skin microbiota expresses various innate factors like interlukin 1a and antimicrobial peptides (AMPs). Therefore, it is important to understand the skin microbiota and host cell interactions so that host – microbiota specific treatments can be made to cure and prevent various skin infections.

ABSTRACT CODE:PP17

AGRICULTURAL MANAGEMENT OF COW DUNG

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Cow dung contains lignin, cellulose and hemicellulose, as it is a mixture of faeces and urine. It also contains different minerals like N, K along with trance amount of S, Fe, C, Mn. Cow dung harbours a rich microbial diversity containing different species of bacteria, protozoa and fungi. Cow dung is also used as a co-product in agriculture such as manure, biofertilizers, bio-pesticides and as a source of energy. It can also act as a purifier of all the wastes in the nature. It is the major source of biogas production in India. Addition of cow dung improves physical and chemical properties including nutritional composition of compost. Cow dung can be used as a soil conditioner as well as a substitute for chemical fertilizers because it contains organic matter. Integrated soil fertility management which include incorporation of cow dung along with other sources of nutrients resulting in greater yield response and better nutrient storage. This combination also improves soil organic matter, phosphate availability, exchangeable ions, effective cation exchange capacity and pH. Many biodynamic preparation obtained from cow dung have shown antagonistic effect against plant pathogen. Cow gung contains diverse group of microorganism which make them suitable for microbial degradation of pollutants. The natural ability of cow dung micro flora to degrade hydro carbons in soil contaminated with diesel oil is recently being investigated. The use of cow dung in a concentration that is appropriate for biodegradation of water contaminated with motor oil could be very effective. It can be utilized for the bio remediation of pesticides and these pesticides are degraded into some intermediate or less harmful compounds. For the removal of chromium from aqueous solution, dry cow dung powder has recently been used as an adsorption source. It may also serve as good substrate for enzyme production.

Keyword: Cow dung, Soil properties, Management, Sustainability

ABSTRACT CODE: PP18

INVESTIGATION OF BENZO(A)PYRENE DEGRADING BACTERIAL STRAINS FROM HYDROCARBONS CONTAMINATED SITES.

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PAH (Polycyclic aromatic hydrocarbons) are environmental pollutants that are mutagenic, carcinogenic and toxic to living organism and also remediation has received considerable attention due to their significant health concern and environmental pollution.PAH contaminated sites also contain indigenous microbes that can potentially degrade benzo(a)pyrene. A benzo(a) pyrene degrading bacterial strains isolated and for enrichment of benzo(a)pyrene degrading bacterial strains of collected oil contaminated soil. Soil sample treated with benzo(a)pyrene as a carbon source in MSM media.1 gram sample inoculated in 50ml MSM broth and incubated at 37 degree centigrade for 7 days at 140rpm orbital shaker. Strains grown in 20ppm-1000ppm benzo(a)pyrene on MSM agar plate incubated at 35 degree centigrade for 3 days and taken OD at 600nm by spectrophotometry , screened 4 highest OD strains and further analysis for benzo(a)pyrene degrading strains by dehyrogenase activity assay and sprinkle method also done .Strains to be able to degrade High Molecular weight PAH under aerobic, anaerobic and facultative condition. Strains could significantly degrade benzo(a)pyrene under iron –reducing anaerobic. The strains identified by gram staining, strain was gram -ve bacillus and rod shaped.Catalase test also done , result was +ve with bubble formation and further deoxygenase test ongoing. The future studies on the aerobic and anaerobic degradation of benzo(a)pyrene would be a great initiative to understand, identified the degradation pathway and characterization of catabolic genes of benzo(a)pyrene degrading strains ,these make them potential tool in oil prospecting and cleaning up of hydrocarbon contaminated sites.

Keywords- PAH, Environment, Degradation, Carcinogenic,Mutagenic

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ABSTRACT CODE :PP19

ROLE OF MICROBIAL BIODEGRADATION IN SUSTAINABLE WASTE MANAGEMENT

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India is facing major environmental challenges associated with waste generation and inadequate waste treatment and disposal .Rapid urbanisation and industrialization have put tremendous pressure on natural resources and the environment .The management and proper disposal of the voluminous waste that humans generate is a formidable task for the government and environmental agencies which are continuously seeking better ways of addressing these issues. Environment protection and sustainability are the major concerns in present scenario .This review paper gives an insight about the effective use of microorganisms in waste management and sustaining our environment in a greener way.

Microbial biodegradation is an important way of successfully combating this menace through the use of microorganisms ,which play an essential role in the natural recycling of living materials .Biodegradation is a biological way of degradation of chemical compounds .In this process a huge diversity of microbial population mainly bacteria ,yeast and fungi are used to degrade organic substances into smaller compounds .Microorganisms play important role in various waste treatment processes such as in sewage and soil treatment ,composting ,vermicomposting ,energy generation ,oil spillage ,treatment of xenobiotic compounds plastic waste and the list is endless .Microbiological methods of waste management can be utilized not only for environment clean-up but also for the value- added benefits of such methods.

Microbial biodegradation utilizes the natural ability of microorganisms to degrade ,transform or accumulate environmental pollutants ,hydrocarbons ,polychlorinated biphenyls ,polycyclic aromatic hydrocarbons ,heterocyclic compounds ,heavy metals ,pesticides etc .Use of microorganisms along with different biotechnological tools is the most effective method to treat a wide variety of wastes and toxicants .These methods include Bioremediation ,Biotransformation ,Biostimulation and Bioaugmentation which are being used to degrade huge range of contaminants .Now ,a ,days microorganisms have also been effectively used together with nanotechnology termed as nano-bioremediation for the clean-up of radioactive wastes .Use of genetically modified microorganisms in combating pollution even in extreme polluted conditions makes the microorganisms a boon to human welfare.

Microorganisms have proved invaluable in finding solutions for several problems mankind has encountered in maintaining the quality of the environment.

ABSTRACT CODE: PP20

Biological Importance of Heterocyclic Compounds

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Heterocyclic compounds are versatile pharmacophore class of compounds in organic chemistry. They are major constituents of pharmaceutically active compounds and play vital role in medicinal fields. From wide range of heterocyclic compounds, 60 heterocyclic compounds have minimal structural composition as at least one N, O or S along with carbon. Most of these compounds are nitrogen-containing (36.66%), followed by oxygen (16.66%) and sulfur (8.33%). Few of them contain more than one hetero atom in their ring such as N and O (18.33%),N and S (8.33%),S and O(1.66%) These compounds show numerous biological activities including anticancer (33.33%), antimicrobial (18.33%), antiviral (16.67%), antifungal (13.33%), antibacterial (11.66%) and anti-inflammatory activity (3.33%). Other activities include their role as analgesics, antibiotics and in treatment of mountain sickness. Right now, there are nearly thousands of heterocyclic compounds known and this number is rapidly increasing due to enormous advanced synthetic research activities.Therefore, it is of utmost importance to elucidate the role of heterocyclic compounds in various biological activities.

A Review Presentation for INSCR 2021, New Delhi

PLANT GROWTH PROMOTING BACTERIA (PGPB)

***AZOSPIRILLUM* Spp.**

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ABSTRACT

The old genus Azospirillum as a plant associated bacteria and its definition as a plant growth promoting bacteria (PGPB), two main characteristics defined the genus, as it fixes atmospheric N_2 and production of Phyotohormones.

CORE VALUES

- *Azosprillum* spp. plant interaction has multiple proposals were suggested for mechanism of action as PGPB enhances plant growth.
- The proposals include a single phytohormone activity, multiple phytohormones, N_2 fixation, assortments of small size molecules, enzymes, enhanced membrane activity, proliferation of root systems, enhanced water mineral uptake by xylem, mobilization of minerals, mitigation of environmental stresses (drought, toxic compound, salinity) and direct and indirect biological control of numerous pathogenic microflora.
- After analyzing all these mechanisms, it was concluded that this versatile genus Azospirillum possesses large potential mechanism by which it can effect crop growth. Consequently, this review study proposes or proves "Multiple Mechanism Theory".

METHODOLOGY & RESULTS

Inoculation of *Azospirillum brasilence* significantly induced root cell membranes to release protons (proteins), and also changed Phospholipid content in plant membrane. Azospirillum produces lactins which helps in growing cell mitosis. Most Azospirillum strains produce IAA *in vitro* form.

Inoculation of *Azospirillum* spp. Inhibits foliar bacterial diseases and soil borne fungal pathogens. Inoculations GAs deficient mutant dwarf rice with Azospirillum Gas producer reversed drawfism. Insertion gene of ACC deaminase in Azospirillum improved crop growth.

METHODOLOGY & RESULTS

Limited experimental data shows several strains of Azospirillum can solubilize, non soluble P and minerals from rocks and stones. Inoculation of *Azospirillum lipoferum* and *Azospirillum brasilense* in paddy crop showed that N_2 derived from atmosphere where 20% (*A. lipoferum*) 19.9% (*A. brasilense*) in Basmati rice and 58.9% (*A. lipoferum*) and 47.1% (*A. brasilense*) in super basmati rice. *Azospirillum halopraferans* inoculation under saline stress conditions saline tolerating over 3% NACL seawater. Inoculation of Azospirillum on wheat plants alleviated water stress under drought hit, rain failure and increased holding of moisture in soil-media. Azospirillum biofertiliser even stored for 31 weeks the organisms viability was not hindered.

Fig. 1 : TEM and SEM Images of Azospirillum

PRODUCTION OF PHYTOHARMONES

It is major property of many microorganisms and PGPB in general and specifically spp. of Azospirillum that stimulate and facilitate plant (crop) growth. *Azospirillum* spp. are known to produce phytohormones such as gibberlins (GAs), IAA (Indol 3 acetic acid), Polyamines, Cytokinis and Ethylene. So all these phytohormones were known to produce in culture media. GAs, Abscisic acid and *Azospirillum brasilnese* known to enhance seed generation of soyabean and wheat seeds.

Cytokinins: Combination of Azospirillum and Bradyrhizobium inoculations to soyabean showed essential formation of nods.

Polyamines: *Azospirillum brasilense* strain AZ39 widely used in wheat and maize as inoculants, known to produce polyamines such as Supermidine and Supermine in culture media.

N_2 Fixation: Most common mechanism is fixation of N_2 by *Azospirillum* spp. Significant increase in total N_2 in food grain of inoculated plants. Contribution of N_2 increase in plants and green house and field experiment studies indicated that N_2 fixation in plants and enhanced Nitrogenase (enzyme) activity in inoculated host plants.

CONCLUSION

Review studies (in specific) of "Multiple mechanism Theory" of versatile genus Azospirillum concludes that ecological viability (eco-friendly) and biologically feasible (in general). Adoption of genetic engineering (transgenics) and organic farming in agriculture system will lead to sustained good and quality food production.

REFERENCES ACKNOWLEDGEMENT

1. Yoav Bashan and Luz E.de-Bashan.
2. Achard P. Cheng. Alen Kina, S.A. Payusova, Alrarez M.I., Antonyuk L.P.

ACKNOWLEDGEMENT

My sincere gratitude to Dr. Raghavendra S. Kulkarni, Emirates Fellow, Indian Science Congress, Retd., Zoology Department, Gulbarga University, Kalaburagi.

Keywords: N_2 fixation, Phytohormones, Multiple mechanisms

ABSTRACT CODE: PP22

ENVIRONMENT AS A SOURCE OF PHAGES AGAINST MULTIDRUG-RESISTANT *KLEBSIELLA PNEUMONIA*

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Infections caused by multidrug-resistant *Klebsiella pneumoniae* (MDR-KP) have become a major global problem. The uncontrolled use of broad-spectrum antibiotics has resulted in the evolution of multidrug resistant bacteria, which is a serious hazard. Alternative feasible strategies to tackle bacterial infections, such as the use of bacteriophages, are thus urgently required. Phage isolation was performed by the double agar overlay method using MDR-KP as baiting hosts. Two phages (were isolated from 15 each of soil and water samples that were screened. Phages were purified by three rounds of single plaque purification, followed by phage enrichment to a high titre. Simultaneously, *K. pneumoniae* were isolated from these environmental samples. Typical colonies obtained on MacConkey agar were identified by biochemical tests and genotyping by PCR. A total of 15 isolates were obtained. Antibiotic susceptibility to six different antibiotics (i.e. Amikacin, Imipenem, Ceftazidime, Nalidixic acid, Ciprofloxacin, Tigecycline) by Kirby Bauer disc diffusion method was performed and all isolates were susceptible to all the antibiotics tested. The host range of phages was studied by spot assay on the lawns of a panel of environmental (n=15) and clinical isolates (n=15) of *K. pneumoniae*. Phages showed good lytic activity against their respective MDR hosts but were not active on any of the environmental isolates. Viable cell reduction and antibiofilm activity of the phages were also determined. The results of this study suggest the potential of phages to lyse and inactivate MDR -KP associated with infections in the healthcare environment. Further study is necessary to characterise these phages at genomic level.

ABSTRACT CODE: PP23

FISHING THROUGH THE INNATE DEFENSE SYSTEM: EXPLORING TLR22 FUNCTIONING IN *AEROMONAS HYDROPHILA*-INDUCED PATHOGENESIS

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Toll-like receptors (TLRs) are key flag-bearers of innate immune system that recognize pathogen associated molecular patterns (PAMPs) and damage associated molecular patterns (DAMPs). TLR22 is a unique TLR which is specific to aquatic life forms (fish and amphibians). To date, the precise role of TLR22 in fish-immunity remains elusive. In this study, we used headkidney macrophages (HKM) of fish to investigate the involvement of TLR22 in fish-immunity. Head-kidney, a major immunocompetent organ, was observed to be having highest *tlr22* expression; however, its expression in non-immune organs points to its possible alternative functions. We found that *A. hydrophila* infection upregulates *tlr22* expression in HKM. siRNA mediated silencing suggested TLR22 restricts intracellular *A. hydrophila* load in HKM. In addition, RNAi and inhibitor studies implicated TLR22 directs surge in proinflammatory cytokines, TNF-α and IL-1β. Furthermore, we observed significant increase in caspase-1 activity which is an important inflammatory caspase involved in maturation of IL-1β. Our results suggest the role of TLR22 in activating TNF-α/caspase-1/IL-1β proinflammatory cascade leading to caspase-3 mediated apoptosis of *A. hydrophila*-infected HKM. We conclude that TLR22 plays critical role in immune-surveillance and triggers proinflammatory cytokine surge leading to caspase-mediated HKM apoptosis and pathogen clearance. These findings will help in better understanding the pathogenesis of *A. hydrophila* and in designing better strategies to control the spread and persistence of this bacteria.

ABSTRACT CODE:PP24

TUBERCULOSIS - CLINICAL ASPECTS AND FUTURE CHALLENGES

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Tuberculosis remains one of the deadliest diseases of mankind caused by Mycobacterium tuberculosis (mtb). Although, TB majorly affects the lungs (pulmonary TB) it can also involve other body parts (extra pulmonary TB). It can also be grouped into active TB infection (TB disease) and latent TB infection. The tests involved in detection of Mtb are Mantoux tuberculin skin test (TST), blood test (known as interferon- gamma release assay IGRA), sputum test and imaging test. Current TB therapy includes first line drugs and second line drugs has several limitations such as long duration, complicated regimen and drug toxicity. Moreover, the occurrence of DR - TB has brought up the urgency to develop another approach to curtail this disease. Presently, BCG (Bacille Calmette-Guerin) is the vaccine for tuberculosis used globally with limitations and its efficacy in preventing pulmonary TB in adults. Thus, various other vaccines undergoing clinical trials include RUTI, M72, MTBVAC and MVA85A etc. In addition to vaccine trials, usage of mycobacteriophage is under research. Furthermore, Host-directed therapy (HDT) is a novel approach that can act as an additional strategy .Also, TB is a serious threat to HIV patients. Hence, timely institution of anti TB treatment using the directly observed treatment (DOTS), short course strategy and Highly active anti-retroviral therapy (HAART).The greatest challenges in the fight against the tuberculosis epidemic involve poor socio-economic circumstances , lack of awareness and resources, HIV infections and M. Tuberculosis drug resistance.

Keywords: Mycobacteriophage, HDT, HIV infections, Drug resistance.

ABSTRACT CODE: PP25

PEPTIDE BASED VACCINE CANDIDATE SELECTED USING IMMUNOINFORMATICS APPROACH ACCORDS BROAD SPECTRUM PROTECTION AGAINST TYPHOIDAL SALMONELLOSIS

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Typhoidal salmonellosis, caused by *Salmonella enterica* serovar Typhi and serovar Paratyphi A, B and C, has been associated with severe illness and high incidence of mortality worldwide. Incessant emergence of antibiotic resistant *Salmonella* strains along with the limitations of the currently available vaccines against typhoidal salmonellosis have underscored the need to look for newer alternatives. Vaccines are one of the best alternatives to combat such infections. *Salmonella* flagella is considered as an important target of innate as well as adaptive immune response. Individual *Salmonella* serotypes alternate between two different antigenic forms, encoded by *fliC* and *fljB* genes, respectively and might use this strategy to escape immune response. In the present study, we have targeted the flagellin epitopes which are common in both of these antigenic forms in *S.* Typhi and *S.* Paratyphi, using various immunoinformatic approaches. After B and T cell epitope prediction and analyzing different physicochemical parameters, interaction of the selected epitope was examined using molecular docking. One peptide epitope, showing best *in-silico* results was synthesized and checked for its immunogenic potential in murine peritonitis model of *S. typhi* as well as *S. paratyphi*; followed by active immunization studies. 75% and 80% mice survival was observed following lethal challenge with *S. Typhi* and *S. Paratyphi* A respectively, along with a significant antibody titer. Reduced bacterial burden in the vital organs along with improved histoarchitecture and significant cytokine levels indicated the protective efficacy of our candidate. Altogether, our findings suggest the potential of proposed vaccine candidate as a promising alternative against typhoidal salmonellosis.

ABSTRACT CODE: PP26

BLOOD TRANSFUSION SENSITIZES IMMUNITY IN DENGUE HEMORRHAGIC FEVER PATIENTS

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Dengue Haemorrhagic Fever is caused by Dengue viruses and it is characterised by extravasation of fluid into interstitial spaces, circulatory collapse and thrombocytopenia in the individual. The prior notions state that sequential secondary infection after a time gap with a different dengue virus serotype than the earlier one leads the patient towards Dengue Haemorrhagic Fever. A patient with clinical condition similar in Dengue Haemorrhagic Fever was referred to Medical College hospital, Jodhpur, Rajasthan where he was given fresh blood containing live white blood cells. Biological and virological analysis of blood was conducted. An increase in the gamma interferon level was observed leading to subsequent recovery from the severe stage of Dengue Haemorrhagic Fever.

ABSTRACT CODE :PP27

IDENTIFICATION OF SECRETORY AND CELL SURFACE-ASSOCIATED PROTEINS OF *LEISHMANIA DONOVANI* FOR EPITOPE PREDICTION AND VACCINE DESIGN

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Leishmaniasis ,a vector-borne disease that affects roughly 350 million people in endemic areas and is one of the most neglected tropical diseases ,with an estimated 1.3 million new cases per year .Visceral Leishmaniasis) VL ,(caused by the Leishmania donovani ,is the most severe and life-threatening form of leishmaniasis .In the absence of therapy ,VL affects the world‘s poorest individuals and has a high death rate .Despite its efficacy ,most chemotherapy regimens are compromised by issues such as high costs ,toxicity ,and long-term and complicated regimens. There is a need for new medications that are both safer and more successful ,and that finally lead to the eradication of the disease .Because most infected people who recover become immune to repeated infections ,there is a good chance of developing a safe and effective vaccine ,as there is so far no licensed vaccine available .The complete proteome of *L .donovani* is a good place to start looking for possible parasite peptides that might elicit an immune response in the human host and could be potentially utilized as vaccine candidates .Antigenic peptides are likely to be found in proteins linked with the cell surface or secretory in nature .We used bioinformatics techniques to identify cell surface-associated and secretory proteins of *L. donovani* such as GPI-anchored proteins ,Trans Membrane Helix) TMH (containing proteins, and secretory proteins .Using IEDB-AR ,we predicted T-cell epitopes in these identified proteins .Our findings imply that identifying distinct immunogenic epitopes opens up a lot of possibilities for developing new vaccines that could provide protective immunity against leishmaniasis and even helping in eliminating the disease.

Keywords :VL *Leishmania donovani* ,GPI-anchored protein ,TM helix proteins ,epitope, vaccine

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Leishmaniasis ,a vector-borne disease that affects roughly 350 million people in endemic areas and is one of the most neglected tropical diseases ,with an estimated 1.3 million new cases per year .Visceral Leishmaniasis) VL ,(caused by the Leishmania donovani ,is the most severe and life-threatening form of leishmaniasis .In the absence of therapy ,VL affects the world's poorest individuals and has a high death rate .Despite its efficacy ,most chemotherapy regimens are compromised by issues such as high costs ,toxicity ,and long-term and complicated regimens. There is a need for new medications that are both safer and more successful ,and that finally lead to the eradication of the disease .Because most infected people who recover become immune to repeated infections ,there is a good chance of developing a safe and effective vaccine ,as there is so far no licensed vaccine available .The complete proteome of *L .donovani* is a good place to start looking for possible parasite peptides that might elicit an immune response in the human host and could be potentially utilized as vaccine candidates .Antigenic peptides are likely to be found in proteins linked with the cell surface or secretory in nature .We used bioinformatics techniques to identify cell surface-associated and secretory proteins of *L. donovani* such as GPI-anchored proteins ,Trans Membrane Helix) TMH (containing proteins, and secretory proteins .Using IEDB-AR ,we predicted T-cell epitopes in these identified proteins .Our findings imply that identifying distinct immunogenic epitopes opens up a lot of possibilities for developing new vaccines that could provide protective immunity against leishmaniasis and even helping in eliminating the disease.

Keywords :VL *Leishmania donovani* ,GPI-anchored protein ,TM helix proteins ,epitope, vaccine

ABSTRACT CODE: PP28

AN AGE OLD BATTLE BETWEEN HUMAN BEINGS AND MULTITUDE OF MICRO-ORGANISMS, WHO WINS? WHAT'S NEXT?

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Anti-microbials a shield used by human beings to battle against microbes that cause infectious diseases, now faces a strong counter from the latter in the form of AMR (anti-microbial resistance). Microbes acquired this resistance by genetic modification, unjustified use of antibiotics as well as insufficient facilities for molecular diagnosis of the diseases. This resistance threatens the human race to return to pre-antibiotic era as such organisms may spread in community, lead to treatment failure, increase mortality, and imposes burden on the healthcare cost. This threat caused by AMR compels the humans to combat the battle through the agent: Deep Neural Network (DNN).

Deep neural network (DNN) are remarkable algorithms in which the nodes and connections of its learning architecture mimics the activity of interconnected neurons of the brain. Neural networks can be trained to learn from examples just like the human brain. Till now, many machine learning algorithms for discovery of new antibiotics fighting resistance have been developed and validated. Most of these algorithms predict accurate and useful results and hence outperform the traditional methods which rely on sequence comparison within the database.

DNN can be an effective approach since it decreases the cost required for screening lead molecules, has higher accuracy and positive rate in identifying new compounds, and also decreases time and labour. Here, we review key features of deep learning, examples of deep learning based drug discoveries, limitations and emphasize the need for more work in this field to equip humans against infectious microbes.

ABSTRACT CODE: PP29

SCREENING OF HERBAL ACTIVE SITE INHIBITOR OF CHITINASE OF SHRIMP PATHOGENIC BACTERIA THROUGH *IN-SILICO* ANALYSIS

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In global perspective, shrimp farming is one of major sector of revenue generation in India. Various delicious food items are prepared by different sea-food sectors which are exported in different countries throughout the globe. During farming, storage and processing bacterial infection of live and dead shrimp is not encouraging in commercial as well as food safety perspective. Bacterial infection of live shrimp leads to rapid spread of the disease and eventual death of the shellfish which ultimately associated with lessened productivity, whereas, bacterial infection of shrimp during storage and processing may leads to rapid spoilage and food borne illnesses. To overcome the dilemma, in the present study, the potent shrimp pathogenic bacteria and their virulent factors were chalked out. It was found that among the enzymes that plays crucial role in pathogenesis/infection, chitinase is pioneer that degrades the chitin-rich shell of shrimp and initiate infection. To restrict chitinase mediated bacterial infection of shrimp, a pool of phytochemical was chosen on the basis their documented preservative potentials and their ability to inhibit bacterial chitinase was evaluated through *in-silico* molecular docking. The potential phytochemical that have capability to bind the active site of chitinase were screened. Their active site inhibition was cross verified through molecular docking of chitinase-phytochemicals with chitin (substrate). The present study may be very much effective to restrict the spoilage of shrimp by the chitinolytic bacteria.

Keywords: Shrimp; Infection; Chitinase; Phytochemical; Inhibitor

ABSTRACT CODE: PP30

ISOLATION, PURIFICATION AND CHARACTERISATION OF MYCOBACTERIOPHAGES

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Note: The work was conducted at Antimycobacterial Drug Discovery Laboratory at ANDC, University of Delhi under the supervision of Dr. Urmi Bajpai, Professor, Dept. of Biomedical Sciences, ANDC, DU.

Antimicrobial infections, Tuberculosis in particular, are some of the greatest challenges that the third world nations, including India are facing today. The slow pace with which new antibiotics develop puts the lives of many in a compromising situation. It is estimated that by 2050, the number of deaths caused due to AMR will surpass that of Cancer, which is one of the largest killers to-date. I present the already controversial concept of phage therapy to combat tubercular and non tuberculous mycobacterial infections in terminally sick patients. Mycobacteriophages can be grouped into various clusters based on the sequence of the tape-measure protein (TMP) gene. It has also been noticed that some clusters (and subclusters) are more important when viewed from the point of treatment of infectious diseases. Clusters A2 and G are of prime importance as bacteriophages D29 and Bo4 belonged to these clusters and have been known since long to lyse and kill Mycobacterium tuberculosis. My work involves collection of environmental soil samples and isolation of mycobacteriophages from them using Mycobacterium smegmatis as a host model. The methods include dilution of environmental samples with phage buffer, followed by enrichment and then plating them on 7H10 double agar plates. The isolated bacteriophages were then subjected to three rounds of purification to obtain a single type of phage exhibiting uniform plaques on the bacterial lawn. The isolated and purified bacteriophages were then amplified and the DNA was isolated. The isolated DNA was then used to put up PCR reactions for classifying the isolated bacteriophages into various clusters. As of now, almost 20 mycobacteriophages have been isolated, with 5 of them belonging to subcluster B1 and one belonging to the cluster G (subcluster undetermined). They have been sent for sequencing for further characterisation. We hope to derive and characterise lysins from these bacteriophages in future.

ABSTRACT CODE: PP31

DESIGN OF PEPTIDES TO INHIBIT THE HOST CELL ENTRY OF HERPES SIMPLEX VIRUS

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Herpes simplex virus (HSV) is known to cause a contagious infection reported across the globe. The existing anti-HSV drugs target viral replication and the resistance to these drugs has become a major concern. Hence, alternative approaches to combating HSV infection have been investigated. In this study, we have employed peptide therapeutics to target viral entry. HSV entry is regulated by the HSV glycoproteins (gC, gB, gD, and gH/gL) and host cell receptor interaction. HSV glycoprotein, gD binds to nectin-1 (host receptor) and triggers the fusion process driven by glycoprotein gB, gH/gL complex. gD-nectin interaction is considered to be crucial for viral entry. No studies blocking the virus entry into the host cells using peptides derived from the nectin-1 host cell receptor as a decoy is reported. Hence, in the present study, we have designed peptides derived from nectin-1 which has a high affinity towards viral glycoprotein gD.

Nectin-1 V-domain known to binds HSV gD. Hence, amino acid sequences from V domain were selected and the secondary structure was prepared by the PEP FOLD-3 server. Selected peptides were docked with the HSV-1 gD glycoprotein by using the ZDOCK server. Further, the stability of HSV-1 gD/peptide interactions was analyzed by performing the molecular dynamic simulation (GROMACS). In the docking study, peptide P1 (20 AA) and P2 (10 AA) showed good interaction with HSV-1 gD. Both the peptides P1 (20 AA) and P2 (10 AA) showed good stability ($< 3A^0$) in MD simulation.

In-silico results showed the strong binding ability of P1 and P2 peptides with HSV-1 gD. These peptides may interfere with HSV-1 gD/nectin-1 interaction and inhibit viral entry into the host cells. Synthesis and testing the antiviral activity of the designed peptides can confirm their potential.

ABSTRACT CODE: PP32

NIPAH VIRUS: A THREAT FOR NEXT PANDEMIC

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Nipah virus (NiV), a zoonotic paramyxovirus of henipavirus genus first identified in Kampung Sungai Nipah village, Malaysia in 1998 among pig farmers. The primary mode of infection is considered to be Pteropus bats (fruit bats), although multiple intermediate hosts are described. Human to human transmission is also possible. This is one of the most lethal and highly dangerous viruses currently known and is on the WHO priority list of pathogens likely to cause outbreaks within a short time. Different strains of this virus found in Malaysia, Bangladesh, India show differing clinical and epidemiological features.This study aims at determining the possible threat and characteristics of Nipah virus for being a pandemic in near future if not contained in a proper manner. For this purpose, the epidemiology, pathology, immunobiology, evolution of the virus, possible diagnostic methods, developing vaccines, treatments and control strategies were examined. Despite its prevalence and yearly emergence in different parts of the world, an effective vaccine has not been developed yet. One of the main reasons for it is that the whole genome sequence of the virus is still unknown and only twenty of these sequences have been identified from humans and ten from bats. Although its transmission is quite lesser in comparison to Covid-19, the mortality rates are much higher. It has been noticed that the duration between each outbreak has significantly decreased in the last few years and human to human transmission has also become a prominent factor. The fact that this virus has been classified as Category C pathogen by the Center for Disease Control & Prevention reveals the threat around the possibility of it turning into a mass disaster. This scenario calls for rigorous research which stands as the only barrier between us and a future pandemic.

ABSTRACT CODE: PP33

GGDEF DOMAIN CONTAINING PROTEINS IN GRAM NEGATIVE BACTERIA: STRUCTURAL INSIGHTS

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In microbiology, the GGDEF domain is a protein domain which appears to be ubiquitous in bacteria and is often linked to a regulatory domain, such as a phosphorylation receiver or oxygen sensing domain. It functions as a diguanylate cyclase which synthesizes cyclic di-GMP. C-di-GMP is an intracellular secondary signaling molecule that controls many virulence factors in bacteria, like exopolysaccharide production, biofilm formation, motility, and cell differentiation. Proteins with GGDEF domain tends to show much diversity amongst Gram negative bacteria. However structural and function aspects of proteins with GGDEF domain are not fully explored. Therefore, mechanistic information on these proteins are scattered. Bacterial genome encodes for multiple proteins with GGDEF domain, in Gram negative bacteria. In this study, our goal will be to perform structural analysis of proteins with GGDEF domains in Gram negative bacteria using bioinformatic tools. The information generated will be useful in the development of antibiofilm molecules targeting proteins with GGDEF domain.

ABSTRACT CODE: PP34

COMPUTATIONAL EXPLORATION OF BROAD SPECTRUM DRUGS FOR THEIR ANTIVIRAL ACTIVITY AGAINST DENGUE

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Recent decades have seen an alarming upsurge of countless viruses around the globe. Out of which, Dengue Virus (DENV) seems to be causing one of the most rapidly growing mosquito-borne diseases – Dengue. Not only has it impacted human health but has also crippled national economies. DENV expresses itself in the form of subclinical to severe flu-like (Hemorrhagic fever) symptoms such as organ impairment, bleeding of nose and gums, CVS failure, and ultimately death. The very first case of severe dengue was recognised way back in the 1950s. One would think that due to its long presence, the science community would have been successful in controlling the disease. However, numerous Asian and Latin American countries still face a colossal amount of cases each passing year. One of the major causes for this widespread is the fact that DENV has four distinct but closely related serotypes, all of which are yet to be subsided with the help of either vaccines or drugs. Although there have been multitudinous attempts at formulating effective drugs, the risk of antibody-dependent enhancement (worsened symptoms during subsequent infections with other serotypes) has severely hindered this development. Hence, in order to combat dengue infection, we computationally screened and filtered out drugs that could be potential inhibitors of three proteins involved in DENV – NS5, NS3, and E protein. The selection process included retrieving drugs from various databases and screening their structures. A total of 33 drugs were then docked against each protein, out of which we were able to produce significant results for 3-4 compounds. Further processing such as toxicity and in-vitro studies can enable us to confirm the efficiency of these promising drugs.

Keywords: DENV, Drugs, Computational screening

ABSTRACT CODE:PP35

TWINNING OF BIOINFORMATICS AND GENOMICS AS A RESORT FOR GENETIC COUNSELORS TO STUDY THE TRENDS OF INHERITABLE OCULAR MELANOMA

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Background: Cancer becoming the leading cause of death globally; accounting for about 10 million deaths yearly, needs immediate attention. It's reported that 10% of all cancer cases are inherited. Intraocular Melanoma runs in family usually due to mutations in signature genes like BAP1, BCL2L1 and many more that are often associated with uveal melanoma but no such stats have been established for other ocular cancers. So, we aimed to explore the relation between uveal and conjunctival melanoma. With advancing bioinformatics; many omics databases help us record genomics metadata profiling of the desired cancer samples. Bioinformatics has made it feasible for genetic counselors to easily study the trends of inheritable cancers among the population.

Approach: Gene expression profiles of GSE143952 (Conjunctival Melanoma) and GSE149417 (Uveal Melanoma) 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 construct PPI network followed by analyses using Cytoscape. Volcano plots were constructed using R to study the expression of genes.

Findings and Future Perspective: Among 63 common DEGs; Genes like MAPK1, PPP2CB, MYC, BAX, and BCL2L1 participated in majority of apoptotic and carcinogenic pathways like RAS signaling, PI3K-AKT signaling pathway. These genes expression were contrasting in both the type of melanomas suggesting that underlying pathways in both cases may be different. Better understanding can be established by doing more miRNA profiling for uveal and conjunctival melanoma as the database lacks a good dataset. Integration of genomic technology with genetic counseling will maximize the utility of genomic possibilities. This can deliver effective and targeted diagnostic and therapeutic strategies for treatment for prospective or affected patients.

Keywords: Genomics, Uveal, Conjunctival, Genetic counselor, Bioinformatics

ABSTRACT CODE: PP36

CURING DENGUE: A REVIEW

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Dengue, a mosquito-borne disease caused by *Aedes aegypti,* has affected a large number of the world population. It has been raised as one of the major threats to public health. The disease is caused by the Dengue virus, a member of the Flaviviridae family having 4 serotypes resulting in the complexity of the disease. As we have undoubtedly heard that the recent pandemic caused by SARS-CoV2 has shaken the whole scientific world which has become an eye opener for the whole research field. Since the virus was mutating frequently; it was impossible to match the pace of designing a compatible drug with its mutation rate so drugs like Remdesivir (reported for EBOLA) came as an appealing resort against COVID-19 to some extent. Analogously, the current outbreak of dengue fever has become a threat globally; showing the urgency of coming up with effective therapeutic strategies against DENV-2. Our work presents an overview of structure and prevalence of DENV, pathogenesis, diagnostic methods and challenges in drug and vaccine development for the same. As we know, drug design projects can fail for a myriad of reasons so, investigating the existing broad spectrum drugs as a prospective candidate compounds against the most virulent serotype DENV-2 can give us some optimistic results. Computational Drug designing techniques play a valuable role in pharmaceutical research, this role makes computational techniques an important part of successful & profitable drug design, so, this approach will help us to reduce the risk owing to the enormous cost involved in the development of drugs.

Keywords: Dengue, Therapeutic, Computational, Serotype.

ABSTRACT CODE: PP37

ISOLATION OF ANTIMICROBIAL AGENT PRODUCING BACTERIA FROM HIMALAYAN FOREST SOIL

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Melanin is a dark color natural pigment synthesized by plants, animals and several microorganisms, and shows a wide range of activities such as photo protective, antimicrobial activity and work as food preservative. Its uses in pharmaceutical, cosmetics and food industries are an alternative approach to minimize the effect of xenobiotic compounds on the environment. In this study, we have isolated three melanin producing bacterial strains from Himalayan forest soil of Uttarakhand. Melanin producing bacteria were cultured on nutrient agar media supplemented with L-tyrosine. Primary screening of antimicrobial agent producing isolates was done by soft agar method and secondary screening by spot lawn method. Melanin and biomass production were observed on the 6th or 7th day of incubation. All three isolates RM1-(1), RM1- (5) and RM1-(13) showed antimicrobial activity against *Staphylococcus aureus* in which RM1- (13) forms greater zone of inhibition (18mm) as compare to other two isolates and positive control. In future study we will do antimicrobial activity of crude extract (melanin) by agar well diffusion and disc diffusion method against other pathogenic bacterial strains including *S. aureus*. Applications of bacterial melanin in pharmaceutical and clinical research as an antimicrobial agent may be a novel use against pathogenic bacteria.

Keywords: Melanin, Xenobiotic, Preservatives, Antibiotics, Pathogens.

ABSTRACT CODE:PP38

THE MENINGO-ENCEPHALITIC STAGE OF HUMAN AFRICAN TRYPANOSOMIASIS

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World Health Organisation aims to eradicate the neglected tropical infectious disease known as Human African Trypanosomiasis or more commonly known as sleeping sickness, by the year 2030. Human African Trypanosomiasis (HAT) is concentrated to the Sub- Saharan Africa region, and is caused by the two “human-pathogenic” sub-species of *Trypanosoma brucei; T. brucei gambiense* and *T. brucei rhodesiense.* It is transmitted by the Tsetse fly. The disease has 2 stages of infection. The Stage 2 is more complex, in both treatment and pathomechanism, and both stages are lethal if left untreated. This poster systematically reviews and interprets the reasons for the complex treatment of Stage 2 or Meningo-encephalitis Stage of Human African Trypanosomiasis, interprets data on recent publication tends on treatment of human african trypanosomiasis and concludes with comments on further developments required to eradicate such complexities.

ABSTRACT CODE :PP39

EFFLUX PUMP MEDIATED DRUG-RESISTANCE MECHANISM IN MYCOBACTERIUM TUBERCULOSIS

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Tuberculosis ,an infectious disease commonly known as TB ,is one of the world‘s deadliest killers caused by *Mycobacterium tuberculosis) Mtb .(*In our study ,we have attempted to elucidate the working of the transporter proteins in the bacterial cell .It covers one of the resistance mechanisms displayed by the bacteria ,using its efflux pumps present in the plasma membrane. These proteins work as carriers/transporters on the bacterial plasma membrane and provide a channel for importing and exporting the molecules in the bacterial cell .However ,MDR pumps are likely to be evolved as a defence mechanism against harmful substances .We have studied the mechanism of action of Rv1634 ,a multidrug efflux transporter of Major Facilitator Superfamily) MFS (from *Mtb* by computational approach .Initially ,a three-dimensional structure and substrate binding site were predicted for the protein ,since it was not known before. Followed by detection of potential transport channel passing from cytoplasmic end to periplasmic end .Ciprofloxacin and Norfloxacin ,two very well-known antibiotics ,were studied using multiple Molecular Dynamics) MD (simulations to get better insights into active efflux of the drugs across the cell surface .These drugs particularly belong to fluoroquinolone ,a potent group targeting DNA gyrase and topoisomerase IV ,vital enzymes in the DNA replication process .However ,in the case of efflux pumps mediated drug resistance ,the targeted drugs are pumped out of the cell ,making them entirely inefficient for bacterial mortality .The study also found that the differential interaction of these drugs with the protein was probably due to substrate specificity present at the substrate-binding pocket .Furthermore ,the characteristic working mechanism of the MFS proteins was also observed.

Keywords :*Mycobacterium tuberculosis* ,Rv1634 ,Major facilitator superfamily ,efflux pump mediated drug resistance ,fluoroquinolone ,Molecular Dynamics simulation

ABSTRACT CODE: PP40

IDENTIFICATION OF INHIBITOR(S) AGAINST RESISTANT ATP SYNTHASE FROM *MYCOBACTERIUM TUBERCULOSIS*

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Mycobacterium tuberculosis (Mtb) is an obligate aerobe that relies on oxidative phosphorylation for energy and life, but it can also thrive in a hypoxic environment. Both aerobic and anaerobic conditions regulate the altered gene expression. The electron transport chain (ETC), which is associated with ATP synthase, the organism's ATP generating machinery, starts with complex I and finishes with complex IV of the respiratory chain. Since the discovery of bedaquiline (BDQ) against multidrug-resistant tuberculosis, ATP synthase has been a promising anti-TB target. Only the 'c' subunit of ATP synthase is thought to be targeted by BDQ. Recent discoveries, however, have refuted this theory, demonstrating the participation of the 'ε' subunit of the central stalk. *Mtb* ATP synthase's three-dimensional structure is yet to be determined. As a result, we present a homology modeling-based ATP synthase complex structure for the *Mtb*. The ATP synthase complex is amphiphilic, with the F_o area entrenched in the membrane and the F_1 region located in the cytoplasm. The F_o region has subunit 'a' and an oligomer of subunit 'c,' whereas the F_1 region contains three 'α ' and three 'β', (α3β3) subunits linked by a central stalk made up of 'γ' and 'ε' subunits and a peripheral stalk made up of 'b' and (b'δ) subunits. The reported resistance to BDQ has been a major source of worry. As a result, we predicted BDQ's binding site and compared its affinity to inserted mutations reported at positions 28, 61, 63, and 66 of the 'c' subunit. We are also interested in identifying new chemical entities that could act on the mutated bedaquiline site or bind to a different site in *Mtb* ATP synthase.

Keywords: ATP synthase, bedaquiline (BDQ), BDQ resistance, homology modeling.

ABSTRACT CODE: PP41

Bt Crops in Sustainable Agriculture

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Pest management is critically important for sustainable agriculture and food security. Growing Bt (Bacillus thuringiensis) crops is one of the efficient method to control pest. Bacillus thuringiensis is a soil borne, gram positive, facultative aerobic and sporulating bacterium. Bt crops are plants that are genetically modified with Bt gene. Such transgenic crops produce Insecticidal Crystal Proteins (IPC) in their cells which gives them natural protection from several pests belonging to orders Lepidoptera, Diptera, Coleoptera, Nematoda and Hymenoptera. Bt crops provide area-wide suppression of target insect pests and reduce input costs on pesticides. It minimizes the use of the conventional synthetic pesticides which are detrimental for environment and human health. Bt crops give higher yield and they are non-toxic to vertebrates. Environmental Protection Agency (EPA), USA has approved production of several Bt crops like tobacco, corn, potato and cotton. Bt brinjal and Bt soybean has been commercialized in Bangladesh and Latin America, respectively. Bt cotton has been cultivated commercially in India since 2002. Despite some limitations of Bt crops such as high cost of Bt seed and emergence of insect resistance to Bacillus thuringiensis, it is a best integrated pest management strategy and a key step in direction of sustainable agriculture. To broaden the range of insect pests controlled in Bt crops, gene pyramiding is a useful strategy where simultaneous expression of multiple genes takes place in transgenic plants. Gene pyramiding is also a solution towards insect resistance management strategies.

Keywords: Bacillus thuringiensis, Environmental Protection Agency, Bt crops

ABSTRACT CODE: PP42

SEED GERMINATION AND SEEDLING SURVIVAL OF *Phaseolus aureus* GROWN IN SOILLESS MEDIA.

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Staple leguminous crops such as mung, chickpea, arhar are extensively cultivated in India. However, in view of constantly decreasing area of arable land coupled with increasing food demand due to rapidly increasing population, there is a dire need to explore alternatives to soil for cultivating these crops. This study therefore, was aimed at investigating the rate of germination and survival of mung, *Phaseolus aureus* L. (Family – Fabaceae), seedlings in soilless mixtures of seven different compositions, each with a discrete microbiota. The seven potting mixtures T0 – T6 were combinations of Perlite, Vermiculite, Cocopeat, Sand while Seaweed, Arbuscular Mycorrhiza Fungi and *Rhizobium* were added as biofertilizers. The rate of germination was nearly 100% in all the treatments. However at 18 DAS and under incumbent stress conditions like incessant precipitation and uneven sunlight in the month of July, the highest survival percentage of the seedlings raised was observed to be 37.5% in T4 (vermiculite with *Rhizobium* Treatment) and 33.3% in T2 (vermiculite with AMF); whereas, in T1 (perlite with AMF) and T6 (perlite, vermiculite and cocopeat), the survival rate was observed to be lowest, 2.1%,. Consequently, it was concluded that a legume-friendly bacteria such as *Rhizobium sp*. and/or AMF added in a potting mixture with adequate water retention capacity and aeration is most suitable for germinating *P. aureus* seeds, since *Rhizobium sp*. and AMF enhance the rhizosphere microflora and help the plants overcome various biotic and abiotic stresses along with facilitating uptake of nutrients from the rhizosphere. Further studies can be carried out to study the feasibility of using such combinations of soilless mixtures with various microbial inocula to grow crops in marginal lands where soil is either scarce or degraded, under other stress conditions (salinity, alkalinity inter alia) for plant growth, i.e., establishment of the plant beyond the stage of germination as well.

Keywords : Legume, *Phaseolus*, *Rhizobium*, AMF, rhizosphere.

ABSTRACT CODE: PP43

OPTIMIZATION OF COLD-ACTIVE CELLULASE PRODUCED BY PSYCHROPHILIC BACTERIUM *Exiguobacterium sibiricum* (K1) FOR BIOMASS DEGRADATION

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Organic waste constitutes up to 70% biodegradable compounds, which at the same time becomes challenging to degrade quickly and efficiently under cold conditions. Such problems can be overwhelmed by bioprospecting the extremozymes from psychrophiles. However, the use of psychrophiles for the degradation of waste has not been explored much. In the present study, a psychrophilic bacterium *Exiguobacterium sibiricum*, having cellulase, amylase, xylanase, lipase, and protease activity was isolated from the compost sample of Sikkim, India. The bacterial cellulase production was optimized utilizing the response surface methodology, and the enzyme activity was enhanced (3.3 U/mL) with 1% inoculum size at 15˚C, pH 5 and 180 rpm. The extracellularly produced cellulase was used for degradation of organic waste and the degradation study showed that the cellulase was capable of proficiently degrading agroresidual waste. Further, the analysis of cellulose degraded products revealed the significant release of sugars in Gas chromatography-mass spectrometry which can act as a versatile initial material to obtain valuable products. Also, scanning electron microscopy showed structural breakages on the targeted substrate. Hence, such an approach of microbial interventions in agro residual biomass degradation can be benefitable to mankind in attaining an eco-friendly environment and sustaining "green biotechnology" in the future.

Keywords: Agroresidual waste degradation, Cold conditions, Enzyme optimization, Green biotechnology, Psychrophiles

ABSTRACT CODE: PP44

SCREENING, IDENTIFICATION AND CHARACTERIZATION OF FERULIC ACID ESTERASE PRODUCING MICROORGANISM FROM COW DUNG SAMPLES

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Cereals, fruits and some vegetables contain considerable amount of feruloylated polysaccharides. Ferulic acid esterases are the subclass of carboxylic acid hydrolases (EC: 3:1:1:1) that hydrolyzes the ester linkage between cinnamic acids and sugars. The major cinnamic acid occur in the plant world is ferulic acid, that having potential role in therapeutics, food industry and cosmetics.

Certain gut microorganisms could cleave the bond between ferulic acid and polysaccharides. The ruminant's gut microbiome is known to produce ferulic acid esterases to augment the digestion of cellulose, hemicellulose and xylan rich plant components.

In this study to analyze the FAE producing culturable and non- culturable gut microbial diversity from cow dung, ferulic acid esterase producing bacteria were isolated. Ethyl ferulate coated plates were used for the preliminary screening and HPLC have been carried out to confirm the release of ferulic acid from the synthetic substrates. Two of the isolated bacteria showing better ferulic acid release from synthetic substrates were identified as *E coli* and *Pseudomonas aeruginosa* by 16S rRNA analysis. Those isolated bacterial cultures were checked for the enzyme activity in presence of different natural substrates that are known to be having substantial amount of feruloylated polysaccharides. Higher enzyme activity was found in wheat bran (30U/ml), spinach (40U/ml) and tomato (40U/ml).

Further studies are carried out in lab to identify the total FAE producing microbes from selected samples. The metagenome analysis of gut microbiome of different diet pattern may provide the insight into microbial diversity of ferulic acid esterases producing genera and releases free ferulic acid into the lumen.

Keywords: Ferulic acid, Ferulic acid esterases, gut microbiome, diet

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ABSTRACT CODE: PP45

Azospirillum, A PLANT GROWTH PROMOTING RHIZOBACTERIA- A PROMISING INTERVENTION TO SUSTAINABLE AGRICULTURE: AN INDIAN PERSPECTIVE IN CONTEXT TO FINGER MILLET [*Eleusine coracana* (L.) Gaertn.]

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Crop growth and productivity has largely been affected by various abiotic and biotic stresses that occur mainly due to global climate change and progress in agricultural production does not meet the demand of the expanding human population. Therefore, developing improved varieties and designing newer approaches for crop improvement against stress tolerance has become a priority now-a-day. However, most of the crop improvement strategies are directed toward staple cereals such as rice, wheat, maize, etc., whereas attention on minor cereals such as finger millet [*Eleusine coracana* (L.) Gaertn.] lags far behind. Finger millet is a nutritionally rich crop, that is cultivated in semiarid and tropical regions. Its rhizospheric zone harbour diversity of plant growth-promoting rhizobacteria (PGPR). PGPRs are root colonizing bacteria that establish symbiotic relationships with plants and promote plant growth. PGPR promotes plant growth either directly by promoting nutrient availability and acquisition or indirectly by reducing the proliferation of pathogens that hamper plant growth. One such PGPR is *Azospirillum.* Recent results have shown that *Azospirillum*-inoculated finger millet crops enhanced the growth and yield with a great supply of Nitrogen under stress conditions to the crop when applied by seed, seedling, and soil application methods. The present research talks about the phosphorus solubilization, production of phytohormones (IAA, Gibberellic acid, Cytokinin), increased photosynthetic pigments, restoration of vegetation in a harsh environment, enhanced seed quality, alleviate biotic and abiotic stresses, etc. by *Azospirillum* and enhance growth and yield of the crop over the untreated ones.

Keywords: PGPR, finger millet, phytohormones, Azospirillum.

ABSTRACT CODE :PP46

TWO BACTERIAL INOCULANTS *Arthrobacter psychrochitiniphilus* AND *Pseudomonas trivalis* IMPROVE GROWTH AND YIELD OF ONION

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Soil isolate ,*Pseudomonas* sp .C5pp has been reported to degrade Carbaryl as the sole source of carbon and energy .The metabolic pathway responsible for degradation and the enzyme involved have already been elucidated .Carbon source dependent enzyme activity studies have suggested the degradation enzymes are inducible .The gene annotation and nucleotide sequence of super-contig revealed that genes involved in Carbaryl utilization are arranged in the form of three gene clusters) upper ,middle and lower .(In addition to that ,the *in-silico* analysis using BPROM and SAPPHIRE has been used to predict probable promoters for genes involved in Carbaryl degradation .The co-transcriptional analysis was performed using gene specific primers and cDNA prepared from Carbaryl and salicylate grown cells .In the presence of Carbaryl all the genes encoding the enzymes for degradation are induced) genes from upper ,middle and lower operon were co-transcribed as polycistronic-mRNA .(While in the presence of salicylate ,only genes of middle and lower pathway were transcribed as polycistronic-mRNA .Therefore ,the co-transcriptional analysis study confirms the operonic arrangement of the genes from three pathways involved in the Carbaryl degradation by the strain *Pseudomonas* sp .C5pp.

Keywords :Carbaryl degradation ,*Pseudomonas* sp .C5pp.

ABSTRACT CODE: PP47

EXPLORATION OF MANGROVE ENDOPHYTIC BACTERIA AS AN EFFECTIVE PHOSPHATE SOLUBILIZERS

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The present study aimed to explore potent phosphate solubilizing endophytic bacteria from the mangrove ecosystem. In total 87 isolates were obtained from the leaf and root samples of mangrove. The isolates were screened for their phosphate solubilizing ability. The activity was optimized by studying the effect of carbon, nitrogen, pH, and incubation time by one of the most potent isolate-S23. Also, pot studies for the plants like cluster bean and sorghum were performed to analyse the potential of phosphate solubilisation.

Keywords: mangrove ecosystem, endophytic bacteria, cluster bean, sorghum

ABSTRACT CODE: PP48

UTILIZING THE POTENTIAL OF MICROBIAL CONSORTIA FOR MANAGING ARSENIC CONTAMINATION IN RICE

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Arsenic (As) is a hazardous metalloid that is found in nature and persists in the environment. This ranks first among inorganic toxicants because of its extremely carcinogenic qualities. Its distribution in the environment causes major human health difficulties all over the world. In soil, As occurs in three predominant forms i.e. arsenite (As3+), arsenate (As5+) and organic arsenic. The main staple crop, rice, is more susceptible to As uptake. Heavy metal tolerant rhizobacteria are commonly used in bioremediation mechanisms viz. oxidation, reduction and methylation. The interaction of Debaryomyces hansenii (NBRI-Sh2.11; MN629349) with rice plant under As stress condition improved the physiological and nutrient status of rice along with reduced As accumulation in grain (~40% reduction) as compared to As alone treatment. The present study involves the characterization of arsenic tolerant bacterial strains compatible to the yeast strain D. hansenii for development of microbial consortia in order to have reduced arsenic uptake in rice. Developed bio formulation will be useful for alleviation of As stress in arsenic contaminated areas.

Keywords: Arsenic, Bioremediation, Rice, Yeast, Consortia

ABSTRACT CODE: PP49

NEW STRATEGIES INTEGRATION TO TACKLE SHEATH BLIGHT DISEASE IN RICE MAT NURSERY

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Rice is a very Crop of India as well as west Bengal. The crop is affected by number of diseases. Out of those Sheath blight disease caused by Rhizoctonia solani ,The pathogen Rhizoctonia solani is the the causal agent we proved Koch's postulates and under humid conditions this pathogen found to be escaping from soil to canopy And we found canopeo based automated disease quantification methodology found to be accurate and effective and it was found that 100 gram seed density found to be less effected by Rhizctonia solani lowest disease severity 29.72% corresponding to 534.95 cm2 of affected area of 1800cm2 ,in search for best agent to control this pathogen we secerned variety of biotic and abiotic agents and their combinations to to found best one in inoculated treatments highest FGCC and 69.81% and lowest canopy temperature (26.63%) found in cucl2 treatment (T5) biochemical defence enzyme expression shown peroxidase (54%) and polyphenol oxidase (52%) and super oxide dismutase has (67%) negative correlation with disease incidence and they(defence enzymes) also had very high positive correlation with each other ,in root system reconstruction analysis studies revealed most of the root system characteristics found to be best in Trichoderma viridae treated seedlings 56% negative corelation found between second order root length and disease severity , in histopathological study some amount of infection cushions found on most of the treatments however in pseudomonas fluorescens and riboflavin treated seedling no infection development observed ,87% corelation found between disease scoring by FGCC and IMAGEJ methodology so CANOPEO based methodology was adopted for disease scoring and treatment screening as this is quick and accurate and it was found PF+TRICHO+PSB combination is the best as it produced lowest (7.4%)disease severity this treatment is followed by SSP+MOP+CUCL2 +PF+TRICHO+PSB (9.86%).

Keywords : Rice, Sheath blight, *Trichoderma virdae*, *Rhizoctonia solani*

ABSTRACT CODE: PP50

PAENIBACILLUS POLYMYXA AS A NEW PLATFORM FOR THE PRODUCTION OF SUSTAINABLE ADVANCED BIOFUEL

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Rapidly increasing world-wide energy need and environmental issues like pollution, ozone layer depletion and climate changes, demand for alternative renewable energy resources over fossil fuels. At present, microbial platforms such as bacteria, yeast, and algae are the main focus for sustainable production of biofuels. Advanced biofuel molecules like isopropanol, butanol, isobutanol, 2-methyl-1-butanol, 3-methyl-1-butanol production are on high priority over conventional biofuel*, i.e.* bioethanol. These higher chain alcohols have many advantages over bioethanol such as low hygroscopicity, higher energy content, higher octane value, less volatile and compatible with existing machinery system. These properties make them good substitute for gasoline. In nature microbes do not produce or produce very less amount of biofuel molecules. Various microorganisms have been genetically engineered for production of advanced biofuels, for example *Clostridium* species for production of butanol, *E. coli* for production of isopropanol, n-butanol and isobutanol, *Bacillus* species for production of ethanol and isopropanol, cyanobacteria *Synechococcus* species for production of isopropanol. *Paenibacillus polymyxa* is a non-pathogenic gram-positive and facultative anaerobic bacterium widely found in nature. *Paenibacillus* strains produce up to 60 g/L of 2,3-butanediol by fed-batch fermentation as shown in our lab. 2,3-Butanediol and isobutanol pathway shares the same intermediate precursor *i.e.* acetolactate which makes *Paenibacillus* an advantageous strain for isobutanol production. Another advantage is that this pathway is redox balanced as 2 NADH required for producing one molecule of isobutanol from two molecules of pyruvate is derived from 2 NADH produced during glycolysis. Isobutanol production has not been demonstrated in *Paenibacillus* species earlier, hence we are proposing *Paenibacillus polymyxa* as a new platform for production of isobutanol, an advanced biofuel molecule.

ABSTRACT CODE: PP51

PRODUCTION, CHARACTERIZATION, AND APPLICATION OF EXOPOLYSACCHARIDE EXTRACTED FROM A POTENTIALLY NOVEL GLACIER BACTERIUM Mucilaginibacter sp. ERMR7:07

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Mucilaginibacter sp. is known as an exopolysaccharide (EPS) producer. In present study, a potentially novel species of genus Mucilaginibacter was used for the extraction of EPS. Statistical optimisation by Response Surface Methodology (RSM) produced 1320 mg/mL EPS at 20°C) pH 7.4. The molecular weight of the extracted ERMR7:07 EPS was 3045.09 Da as determined by MADI-TOF/TOF-MS. Structural characterization by monosaccharide composition, methylation, Fourier-transform infrared spectroscopy, and Nuclear magnetic resonance analysis revealed that the ERMR7:07 EPS was a linear polysaccharide with the sugar backbone of α-D-Glciv(1→4)α-D-Glciii(1→3)β-D-Glcii(1→6)α-D-Glci. The extracted EPS provided 97.91% viability to mesophilic Escherichia coli under freezing conditions (-80 °C) for up to 7 days. Additionally, ERMR7:07 EPS showed metal ion biosorption ability for Cu2+ (8.36 mg/g), Fe2+ (4.47 mg/g), Mn2+ (0.12 mg/g), and Zn2+ (0.103 mg/g). Owing to these properties, the extracted EPS can be explored for its application as a cryoprotective agent and as a medium to remove toxic metal ions.

Keywords: Production, exopolysaccharide, glacier bacterium

ABSTRACT CODE: PP52

ISOLATION AND CHARACTERIZATION OF LIPASE PRODUCING BACTERIA FROM BAKERY SOIL SAMPLE

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Soil is the major reservoir for the variety of microorganisms such as bacteria and fungi which produces different hydrolytic enzymes. The ability of these microorganisms to produce hydrolytic enzymes makes them potential candidates for hydrolysis of complex polymeric substrates. The effective production of lipase has been performed after screening different habitats for lipase producing bacteria and the optimization of their culture parameters. The present study was focused on the isolation of bacteria from bakery soil followed by screening for lipolytic activity on 1% tributyrin agar media and maximum lipase production by optimizing different parameters such as pH, temperature, incubation time, agitation and substrate specificity. Out of 12 bacterial isolates, 9 isolates were found to be positive for lipase production and an isolate named KBSlip-3 showed maximum lipolytic activity. The optimum pH, temperature and incubation time for KBSlip-3 was 7.5, 37°C and 24 hours respectively. To determine maximum lipase activity different nutrient sources as carbon, nitrogen and metal ions were assessed. The phylogenetic analysis of 16S rRNA sequence data of this isolate showed 96% sequence similarity to a Bacillus sp.

Key words: Extracellular enzyme, lipase, bakery soil, optimization, soil bacteria

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ABSTRACT CODE: PP53

MICROALGAE: AN INHERENT SOURCE FOR WASTEWATER TREATMENT AND A POTENTIAL FEEDSTOCK FOR BIOFUELS AND OTHER VALUABLE PRODUCTS

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Microalgae have gained huge attention due to their wide ranging applications such as bioremediation and production of high-value products. Microalgal biomass, a rich source of lipids, carbohydrates, proteins, pigments and antioxidants can be an excellent feedstock for various industries such as biofuels, food nutrition (human and animal), pharmacology, cosmetology and as biofertilizers in agriculture. Similarly, wastewater which is one of the major environmental issues and microalgae having the ability to utilize wastewater contaminates for their growth is an essential and promising biological agent for wastewater treatment. Using microalgae not only helps in bioremediation but also helps in reduction of operating cost for commercial cultivation of microalgae for various end-products.

Several wastewater resources like river, industrial, and domestic water discharge were successfully treated using different microalgae. It was observed that *Chlorella vulgaris* and *Chlamydomonas* are the most efficient species for COD, BOD and TSS removal in terms of nitrate and phosphorus. *Nannochloropsis* sp., *Neochloris oleoabundans, Scenedesmus obliquus* and *Dunaliella tertiolecta* have been considered as promising candidates for fuel production in terms of quantity and quality of fatty acids. *Chlorella* sp., *Scenedesmus* sp. and *Nannochloropsis* sp. in wastewater have the potential to accumulate high levels of lipids and starch. For instance, *Scenedesmus rubescens* and *Neochloris vigensis* having the ability to remove 11% and 25% of the total phosphorous from synthetic water and in return gave 16 and 20% of lipids concentration respectively. The algae food market is ruled by *Chlorella vulgaris* and *Arthrospira platensis* and extracts of *Dunaliella salina* (β-Carotene), *Haematococcus pluvialis* (astaxanthin) or *Crypthecodinium cohnii* (docosahexaenoic acid) are specifically exploited due to food safety regulations of the European Food Safety Authority. Additionally, the biomass obtained after treatment of wastewater is rich in nitrogen, phosphorous and potassium along with other micronutrients which in turn make them into a great biofertilizers. No doubt, microalgae are a useful feedstock to treat wastewater and get valuable products without causing any adverse environmental effect and an integrated process of wastewater treatment with algal biomass production and utilization in a biorefinery mode can be a sustainable and commercially viable preposition.

Keywords: Microalgae, bioremediation

ABSTRACT CODE: PP54

EFFECT OF PHYSICOCHEMICAL STRESSES ON C-PHYCOCYANIN FROM *PHORMIDIUM* SP. CCC 112 ISOLATED FROM CALICUT, KERALA

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The market demand for C-phycocyanin has been increasing because of the versatile applications in natural food colorant, dietary supplement, cosmetics and others. Stability of the pigment is one of the major factors that determines the productivity of the industrial process as loss of the characteristic colour and other properties during various processing diminish its commercial value. It is assumed that cyanobacterial strain found at adverse environment may possess stable C-PC. Therefore, in the current study, *Phormidium molle* CCC 112 isolated from Kerala, India and maintained in the germplasm of CCUBGA, IARI, New Delhi was evaluated for the C-phycocyanin stability under different physicochemical stressors. Initially, one step purification of C-phycocyanin via anion exchange chromatography was performed that resulted in analytical grade purity of 5.29 with 44.7% recovery. Spectral characterization of the pure pigment was done through UV/Vis spectroscopy by scanning over a wavelength range of 250-700nm that recorded sharp peak at 620nm. SDS-PAGE analysis of the pure pigment showed two distinct bands of around 17 and 19 kDa corresponding to the α and β subunits of phycocyanin. Further, the purified pigment was subjected to different temperature regimes, pH conditions as well as graded concentrations of H_2O_2 for 1 hour. The relative concentration (C_R%) of C-PC was found to be 95.31 ± 2.07% and 51.95 ± 1.61% at 40°C and 60 °C, respectively. The pigment was quite stable over a broad spectrum of pH with maximum C_R% found at pH 6 (91.98 ± 3.28%) with respect to initial C-PC content. Gradual decrease in the C-PC amount was observed with the increase of H_2O_2 concentrations. Functionality of C-PC after different treatments was also assessed by measuring its fluorescence property via fluorescence spectrophotometer that showed a decrease in relative fluorescence in the stress exposed C-PC than the control. However, the C-PC obtained from the present strain, *Phormidium molle* CCC 112 was found to be relatively stable at high temperature and broad pH range.

Keywords: Chromatography, C-Phycocyanin, Stability, Cyanobacteria.

ABSTRACT CODE: PP56

BIOMETHANE AND BIOMETHANOL PRODUCTION THROUGH THE INTEGRATIVE PROCESS FROM BIOWASTE

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In this study, potato peels as a biowaste were subjected to anaerobic digestion (AD) to produce biogas, which was subsequently used as a substrate for methanol production by methanotrophs. AD resulted in high yields of up to 170 L of methane/kg total solids (TS) from 250 mL substrate (2% TS, w/v). Under optimized conditions, maximum methanol production of 5.24 and 3.60 mmol/L from raw biogas was observed in *Methylocella tundrae* and *Methyloferula stellata*, respectively. Immobilization of methanotrophs on banana leaves showed loading of up to 156 mg dry cell mass/g support. *M. tundrae* immobilized on banana leaves retained 31.6-fold higher methanol production stability compared to non-immobilized cells. To the best of our knowledge, this is the first study on immobilization of methanotrophs on banana leaves for producing methanol from potato peels AD-derived biogas. Such integrative approaches may be improved through process up-scaling to achieve sustainable development.

Keywords: Biowaste, Methane production, Methanotrophs

ABSTRACT CODE: PP57

EXPLORING RECENT ADVANCEMENTS IN MICROBIAL DEGRADATION OF WASTEWATER PESTICIDES

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Bioremediation is a cost-effective and eco-friendly technology that utilizes microorganism's metabolic potential to remove the contaminants from the polluted environments. The process of remediation generally takes place in non-sterile and open environment by the action of diverse microbes. A complex interaction occurs between microorganisms and the degradation process is mainly dominated by bacteria but the presence of fungi, protista and other microbes also affects the process. Bioremediation technologies can be divided into in situ or ex situ. In the in situ process, the remediation of contaminants takes place on the site whereas in the case of ex situ, the contaminants are treated away from the actual contaminated site. Wastewater and domestic sewage mostly contain degradable organic compounds, most of which are broken down into simpler compounds by microorganisms. However, the industrial sewage and runoff water from agricultural land contain complex synthetic organic compounds like pesticides which are not easily degraded during the treatment process. Widespread and indiscriminate use of pesticides (e.g., Cypermethrin and other pyrethroid pesticides) has resulted in the contamination of soil and water systems with these toxic compounds. While most of the microorganisms are unable to survive in the presence of such toxic compounds, only a handful of them are able to use the organo-toxicants as the carbon source. Thus, harmful complex organic pollutants such as pesticides can be degraded into simple harmless compounds with the use of potent microorganisms including bacteria. This paper intends to explore the microbes involved in biodegradation of pesticides present in wastewater systems, their degradation pathways and the influencing factors.

Keywords: Sewage, Biodegradation, Wastewater treatment

ABSTRACT CODE: PP58

PIGMENT PRODUCTION BY MICROORGANISMS: NATURAL COLORANTS WITH ANTIMICROBIAL ACTIVITY AND ENZYME PRODUCTION

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Pigments are secondary metabolites produced by plants and microorganisms as the adaptive mechanisms to withstand the adverse environment conditions such as light, heat and pH. Some pigments are also associated with medicinal properties and are successfully used for preventing and treating microbial diseases and display distinct antimicrobial effect against many pathogenic bacteria. These features along with growing concern for the environment have created the necessity for the use of natural dyes over synthetic dyes, which are being used extensively in dying and textile industries, paper manufacturing industries causing great harm to aquatic animals, humans and to the environment by polluting air, soil, and water. Therefore, this study focusses on natural pigment production. Microbial pigments are also of industrial interest because they are often more stable, highly producible and easily available. Soil being the rich source of microbes, often explored for pigment producing bacteria and fungi. However, this is the first report where pigment is extracted from colored bacterial and fungal growth seen on uninoculated nutrient media plates stored in refrigerator for 7-8 days. Pigment producing isolates were identified and characterized by morphological and molecular identification methods. Pigments were purified, characterized by GC-MS, and evaluated for dyeing ability, antimicrobial activity against human pathogenic bacteria, and ability to produce amylase, lipase, protease, and cellulase enzymes. Thus, the current study can be useful step not only for the lab scale production of pigments, but their use can be explored in dying and textile industries, large scale enzyme production, and antimicrobial activities.

Keywords: Natural dyes, Pigment production, Textile dyes

ABSTRACT CODE: PP59

IMPACT OF FLUOROSIS ON SOIL HEALTH IN NALGONDA DISTRICT, TELANGANA, INDIA

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Nalgonda district (17.05°N; 79.27°E) the fluorosis capital of India usually contains dental and skeletal deformities. National programme for prevention and control of fluoride (NPPCF) says the old Nalgonda district's limits, 17 mandals out of 59 were severely affected and 31 moderately affected by fluorosis. Government providing water from the Krishna River in now-a-days, hence the present generation is safe. Even though the soil health in the district is affected by fluorine as dental, skeletal and non-skeletal fluorosis, making it one of the worst affected around 8,397 people suffering with skeletal fluorosis are getting pension in the district. The present study reveals that the Narketpally mandal (Yellareddygudem village) of Nalgonda district is having more toxic level (11.4) of fluoride compared all other mandals. And also have the threat of disease in the same mandal.

Keywords: Nalgonda, Fluoride, Soil Health

ABSTRACT CODE: PP60

FUNGI MEDIATED VALORIZATION OF PULP AND PAPER MILL SLUDGE BY BIOACCUMULATION OF HEAVY METALS, AND CONTEMPORARY PRODUCTION OF VALUE-ADDED ENZYMES AND SUBSEQUENT VERMICOMPOSTING: A PIONEERING APPROACH TO BOOST THE CIRCULAR ECONOMY

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The ever-increasing demand for paper led to the overproduction of pulp and paper mill sludge, which comprised a significant quantity of pollutants. The paper mill sludge mixed with the agricultural waste (60:40) was subjected to solid-state fermentation by utilizing three fungal genera; namely, *Aspergillus fumigatus, A. niger*, and *Trametes hirsuta*, to bioaccumulate sludge laden heavy metals (mg/g) [*A. fumigatus*: Pb-2.41, Cd-1.09; *A. niger*: Pb-2.25, Ni- 1.75, Cr-1.63, Zn-1.62, Cd-1.17, Cu-0.74; *T. hirsuta*: Cr-1.02, Cd-0.89] and the concomitant production of a high valued enzymatic cocktail (U/ml) [cellulase: endoglucanase (271), exoglucanase (268), β-glucosidase (261); amylase (249); pectinase (185); xylanase (181)]. The mixed, treated sludge now bring forth for vermicomposting, using *Eisenia fetida*, and it was found that the amount of several plant growth-promoting minerals (g/kg) were significantly increased [P (127.78), Ca (71.88), N (9.69), K (5.81), Mg (5.65), and Na (5.52)]. CHNS analysis of the mixed sludge showed a significant drop in carbon quantity (%) [37.69 (initial)-22.48 (after enzyme production)-8.97 (after vermicomposting)]. This study has enough potentiality to manage the environmental pollution associated with sludge and channel this sludge toward the production of valuable enzymes and vermicompost.

Keywords: Sludge, Fungal genera, Bioaccumulation, Enzymatic cocktail, Vermicompost

ABSTRACT CODE: PP61

BIOCHEMICAL CONVERSION OF SUGARCANE BAGASSE INTO XYLOBIOSE AND ETHANOL :AN INTEGRATED BIOREFINERY APPROACH

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Endo-xylanases are commercially essential enzymes required for xylo-oligosaccharides (XOS) production. Xylo-oligosaccharides are established prebiotics that confer health benefits to humans by selectively stimulating host gut microflora. Xylobiose is reported to have the highest prebiotic potential among XOS with varying degrees of polymerization (DP). Fungal species are well known for their ability to degrade lignocellulosic material by secreting a cocktail of lignocellulose-deconstructing and hydrolytic enzymes. In this study, we isolated and screened 26 fungal strains, which were ranked using the Weighted Aggregated Sum Product Assessment (WASPAS) model based on their growth, protein secretion, xylanase production, xylan hydrolysis, beta-xylosidase activity, and xylose formation. F25 isolate was ranked no. 1, which showed the highest potential for the production of XOS from beechwood xylan. Xylanases produced by F25 isolate were also able to make XOS from hemicelluloses extracted from different lignocellulosic materials such as sugarcane bagasse, wheat straw, rice straw, and corn cob. After optimization of physico-chemical parameters for XOS production, we achieved 80% hydrolysis of SB xylan. The hydrolysate contained 65.71% xylobiose, 16.71% XOS with $DP \geq 3$, and 17.55% monomeric sugars. Xylobiose was purified by activated charcoal chromatography and 96.90% purity was achieved with a 77.02% purification yield. The purified xylobiose showed antioxidant properties by scavenging ABTS and DPPH free radicals. Purified xylobiose was consumed by *Bifidobacterium adolescents* and *Lactobacillus brevis* as a sole carbon source and these strains were able to produce lactate and acetate under anaerobic conditions. The process can be integrated with ethanol production for the establishment of commercially viable integrated biorefinery plant, which in turn can pave the way for both energy as well as food security.

Keywords: Ethanol, Lignocellulose, Xylo-oligosaccharides

ABSTRACT CODE: PP62

PURIFICATION AND CHARACTERIZATION OF FOUR FILAMENTOUS CYANOBACTERIA BASED ON MORPHOLOGICAL STUDY FROM THE INDIAN SUNDARBANS

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A total of twenty-five samples were isolated from the estuarine habitat of the Indian Sundarbans covering Jharkhali, Patharpratima, Bhagabatpur, Namkhana, Kakdip. All the samples were well maintained in the laboratory conditions. Out of twenty-five samples four samples were purified to make axenic culture for alpha diversity study of cyanobacteria of Indian Sundarbans. Purification was performed by different subculture techniques with addition of different antibiotics (Penicillin-G, streptomycin sulphate, chloramphenicol, cycloheximide) in different concertation in ASN-III culture media. Results of the morphological analysis showed that each strain differed from other by their filament type, cell length, size and motility. Filaments of all the strains were thin, unbranched, long, straight often wavy and trichrome of the strains were cylindrical, isopolar, uniseriate. Presence of thin, colourless mucilaginous sheath was observed in all the strains. In S19 and S23 cells were longer than width whereas in S9 and S15 cells tended to be isodiametric. Cell shape of the strain S9 was cylindrical, barrel shaped, trichrome clearly constricted; length ranged from 0.428-0.519 µm and width 0.332-0.412 µm. In S15 cell shape was slightly larger than S9; the cell length ranged from 0.854-0.942µm and width 0.626-0.716 µm. Trichrome of S15 was slightly constricted. The cells of S19 were longer than their breadth; length ranged from 1.5-2 µm and width 0.450-0.500 µm. The cells of S23 were elongated and gradually narrowed. Cells of S23 were much larger than their breadth; length ranged from 3.1-4µm and width 1.3-2µm. In S23 trichrome was slightly constricted whereas S19 showed no trichrome constriction. According to the latest classification system of cyanobacteria based on morphological analysis the purified strains were allotted to Pseudanabenaceae family.

Keywords: Cyanobacteria, Estuarine, Mangroves, Sundarbans

ABSTRACT CODE: PP63

PROBIOTIC POTENTIAL OF LACTIC ACID BACTERIA WITH ANTIMICROBIAL ACTIVITY AGAINST SOME HUMAN PATHOGENIC STRAINS

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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 10 isolates were isolated from various plants of *Cocoa criollo, Cocoa forastero, Saccharum officinarum, Fragaria ananassa, Borassus flabllifer and Opuntia ficus indica* from various locations of Gujarat. They were withstanding with broad spectrum antibiotics so it should 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 all isolates showed antagonistic effects against the pathogens. Gujarat is at 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 CODE: PP64

REMOVAL OF POLYAROMATIC HYDROCARBON CONTAMINANTS APPLYING INDIGENOUS MICROBIAL-BASED MIXED BIOFILMS FROM SUNDARBANS TIDAL MANGROVE FOREST

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This study focused on intertidal biofilms of the Sundarbans and the manner by which these biofilms can be exploited for the removal of polyaromatic hydrocarbon (PAH) contaminants. Six heterotrophic as well as phototrophic stably-growing, robust and well-formed biofilms were selected each representing the different geographical locations: (Pg) Purba Gurguria, (Mt) Maipit, (Pp1 and Pp2) Patharpratima, (Nk) Namkhana and (Kk) Kakdwip. These indigenous biofilms were cultivated in two sets of the patented biofilm-promoting culture vessel possessing hydrophilic glass surface and hydrophobic polymethyl methacrylate (PMMA) surface, containing liquid media spiked with 16 priority PAHs. Heterotrophic biofilm-mediated 97-100%, whereas phototrophic biofilm showed 32-100% removal efficiency of individual PAHs was attained in all media. Significant differences were observed between mean residual PAHs obtained from the liquid media of PMMA and glass flasks cultured with phototrophic biofilms. Residual amounts of acenaphthene (Ace), anthracene (Ant), benzo(a)pyrene (B(a)P) and benzo(g,h,i)perylene (B(g,h,i)P) showed notable differences in their sequestration when cultivated with both the biofilms in flasks having hydrophobic and hydrophilic surfaces. The residual amounts of PAHs obtained from biofilms of both heterotrophic and phototrophic microorganisms cultured in PMMA and glass flasks also displayed a significant difference. Hydrophilic culture of phototrophic biofilm Pp1 and hydrophobic culture of heterotrophic biofilm Pp1 and phototrophic biofilm Kk showed higher PAH sequestration. Morphological analyses of these PAH degrading biofilms showed presence of purple sulphur bacteria, diatoms, cyanobacteria (*Gleocapsa* sp., *Chloroidium* sp., *Microcystis* sp. and *Phormidium* sp.) as well as *Closterium* sp. like green algae. Composition, structure and abundances of indigenous heterotrophic microbial communities in PAH-sequestering biofilms by amplicon-based metagenomics revealed bacterial phyla including *Proteobacteria*, *Bacteroidetes*, *Firmicutes*, *Actinobacteria*, *Chloroflexi* and *Planctomycetes* as well as members of *Ascomycota* phylum of fungi. The dominance of *Candida tropicalis*, *Clostridium butyricum*, *Sphingobacterium multivorum* and *Paecilomyces fulvus* were established.

Keywords: Polycyclic aromatic hydrocarbons, Sundarbans, Sequestration, Biofilm, Microbial community

ABSTRACT CODE: PP65

PSYCHROTROPHIC PLANT BENEFICIAL BACTERIA FROM THE GLACIAL ECOSYSTEM OF SIKKIM HIMALAYA: GENOMIC EVIDENCES FOR THE COLD ADAPTATION AND PLANT GROWTH PROMOTION

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Commercial biofertilizers tend to be ineffective in cold mountainous regions due to reduced metabolic activity of the microbial inoculants under low temperature. Cold-adapted glacier bacteria with plant growth-promoting (PGP) properties may prove significant in developing cold-active biofertilizers for improving mountain agriculture. With this perspective, the cultivable bacterial diversity was documented from East Rathong glacier ecosystem lying above 3900 masl of Sikkim Himalaya. A total of 120 bacterial isolates affiliated to *Gammaproteobacteria* (53.33%), *Bacteroidetes* (16.66%), *Actinobacteria* (15.83%), *Betaproteobacteria* (6.66%), *Alphaproteobacteria* (4.16%), and *Firmicutes* (3.33%) were recovered. Fifty-two isolates showed multiple *in vitro* PGP activities of phosphate solubilization (9-100 μg/mL), siderophore production (0.3-100 psu) and phytohormone (IAA) production (0.3-139 μg/mL) at 10 °C. Genome analysis of four representative bacteria of diverse genera predicted many genes involved in the bacterial PGP activity. Comparative genome study highlighted the presence of PGP-associated unique genes for glucose dehydrogenase, siderophore receptor, tryptophan synthase, phosphate metabolism (PhoH, P, Q, R, U), nitrate and nitrite reductase, TonB-dependent receptor, spermidine/putrescine ABC transporter etc. in the representative bacteria. Overall, this study signifies the psychrotrophic bacterial diversity from an extreme glacier environment as potential tool for improving plant growth under cold environmental stress.

Keywords: Bacterial diversity, Biofertilizers, Plant growth promoting genes

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ABSTRACT CODE: PP66

DETERMINATION OF TIME SINCE DEATH: AN UNPRECEDENTED APPROACH TOWARDS ENVIRONMENTAL SUSTAINABILITY BY MICROBES

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Microbes perform diverse role to make earth a sustainable ecosystem. Recycling of the primary elements which are the basic component of all living organism is the most significant and required role of the microorganisms. Thanatomicrobiome is fast developing field that links microbial profiling with forensic applications. The resultants of biodegradation or decomposition of complex organic material is compounds of carbon which can easily be utilized by other organisms. Microbiomes after death of a host can act as a biomarker in estimating Time since death or Post Mortem Interval. It can also help in locating the location or decomposition location of the cadaver. The different stages of degradation are represented by the different succession of microorganisms which help in estimating time since death. Various methods can be used for estimation such as extraction at various degradation stages, CFU count and various biochemical tests. Community dynamics of thanatomicrobiome can not only provide lead to decomposition location but also assist in determination pf PMI, though environmental factors and technical issues makes the dynamics interpretation a tough one. Future implementation of thanatomicrobiome could provide new insights into time and availability at a place of forensic samples.

Keywords: ecosystem, microbiomes, Time since death, forensic, decomposition

ABSTRACT CODE: PP67

PROBIOTICS: A POTENTIAL MITIGATION STRATEGY AGAINST ENVIRONMENTAL POLLUTANTS IN FOOD

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Exposure to environmental pollutants such as persistent organic pollutants (POPs), polycyclic aromatic hydrocarbons (PAHs), phthalates and heavy metals via food is increasingly associated with microbial dysbiosis as well as myriad of human disorders. With burgeoning evidence of probiotics as a potential dietary intervention against diseases like obesity, type 2 diabetes, Alzheimer's disease, etc., lactic acid bacteria (LABs) can be considered as a promising mitigation strategy against exposure to these pollutants. In this study, we investigated the binding efficiency of various *Lactobacillus* strains to PAHs in aqueous medium using high performance liquid chromatography (HPLC). 10^9 CFU/ml LAB population were used to study the binding ability of each strain to benzopyrene at a concentration of 10 µg/ml. Three strains *L. rhamnosus* LGG, *L. plantarum* NCIM 2387, *L. fermentum* 95.8 were observed to efficiently remove benzopyrene from aqueous medium with binding efficiency of approximately 99% for each strain. These results revealed that *Lactobacillus* could be used as a potential dietary strategy against the detrimental effects of PAHs.

Keywords: Environmental pollutants, *Lactobacillus* sp., Polycyclic aromatic hydrocarbons

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ABSTRACT CODE: PP68

SCREENING OF FUNGI FOR EFFICIENT DEGRADATION OF MAJOR PHTHALATE ESTERS (PAES)

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Phthalate esters (PAEs) or phthalic acid esters (PAEs) are a group of compounds including dialkyl or alkyl aryl esters of 1, 2-benzendicarboxylic acid (phthalic acid). Among PAEs, di-n-butyl phthalate (DBP) and di-2-ethylhexyl phthalate (DEHP) are mostly used as plasticizers and in manufacture of toys, cosmetics etc. They are known to have teratogenic, endocrine disrupting and carcinogenic effects due to which, are listed as priority pollutants by environmental regulatory bodies such as U.S. Environmental Protection Agency (USEPA). Chinese and Indian agricultural soils are reported to be contaminated with these compounds. Microorganisms, especially fungi have been known to degrade PAEs by producing enzymes like esterase and laccase. The present study screens different fungal isolates for enzyme production using standard protocols. It was found that, of 13 isolates growing on DEHP, twelve produced esterase, except for a laccase- producing strain CDEHP1. Similarly, fourteen of 15 DBP degrading isolates exhibited esterase activity. However, SDBP2 tested positive for laccase production. Radial growth was measured on basal salt medium containing individual PAEs as sole C source. SDEHP2 showed maximum growth of 48 and 83.3 mm after 7 and 14 days respectively, on DEHP supplemented plates. SDBP4 exhibited maximum radial growth on plates containing DBP (50.7 mm after 7 days and 83.7 mm after 14 days). The study paves way for screening fungi for efficient bioremediation of PAE contaminated soils.

Keywords: Enzyme activity, Fungal isolates, Phthalate esters

ABSTRACT CODE: PP69

BIOREMEDIATION - AN APPROACH TOWARDS HUMAN AND ENVIRONMENT WELFARE

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Bioremediation is a branch of biotechnology where living organisms like microbes and bacteria are used to clean contaminated environment such as soil contaminated by acidic mining drainage and agricultural chemicals, groundwater, underground pipe leaks, subsurface material, oil spills and crime scene clean-ups. Bioremediation stimulates the growth of certain microbes, by altering the environment conditions, that use contaminants and target pollutants (including wastewater, industrial waste and solid waste). These microorganisms digest the toxic compounds using their enzymes and convert them into small amounts of water and gases like carbon dioxide and ethene. Bioremediation can be used to treat contaminants like oil, petroleum products, solvents and pesticides. Heavy metals like cadmium, chromium, lead and uranium are non-biodegradable and become present in the environment due to anthropogenic activities like industrial emissions, electronic waste, and ore mining. or natural factors like weathering, soil erosion, and forest fires. Bioremediation can be used to reduce the mobility of these material in the subsurface, reducing the potential for human and environmental exposure. For bioremediation to be effective, the right temperature, nutrients and food also must be present. Bioremediation may be done "in situ"–at the site of the contamination (where polluted sites are treated in a non-destructive and cost-effective manner) –or "ex situ"–away from the site (where polluted sites are vacated; this process is costly). Addressing Environmental pollution is the need of the hour due to increased human activities on energy reservoirs, unsafe agricultural practices and rapid industrialization. Bioremediation is beneficial in this scenario as it doesn't require as much equipment, labour, energy and money as other clean up methods. Also, we don't have to transport them elsewhere for treatments and very few by-products Waste is created.

Keywords: Bioremediation, *in situ* bioremediation, *ex situ* bioremediation

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ABSTRACT CODE: PP70

GENETIC ENGINEERING OF *BACILLUS SUBTILIS* FOR DECONTAMINATION OF HEXACHLOROCYCLOHEXANE (HCH) DUMPSITE SOILS

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In past attempts have been made to remediate and reclaim the persistent organic pollutant hexachlorocyclohexane (HCH) contaminated soils. Bioremediation strategies included microbial remediation, phytoremediation, rhizoremediation, enzymatic degradation etc. which have been practised in controlled or uncontrolled systems. These approaches, however, are limited by many challenges; for instance, microbial remediation is constrained by availability of robust microorganisms that can sustain in the field conditions, growth of microbes to raise high cell number inoculants, degradation efficiency of the microbes etc. and thus, pose many hurdles in the development of sustainable bioremediation technology. In this regard, genetic engineering of *Bacillus subtilis*, widely used as a cell factory in agriculture owing to its highly efficient protein secretion system and adaptable metabolism, is undertaken. HCH catabolic *lin* genes, *linA* (encoding dehydrochlorinase) and *linB* (encoding haloalkane dehalogenase) that produce enzymes catalysing the initial steps of HCH degradation are amplified from *Sphingobium indicum* B90A, a model organism of HCH catabolism that degrades the most persistent and recalcitrant b-HCH isomer as well. *LinA* and *linB* genes are independently cloned in pYS5 vector, a recombinant vector plasmid containing Protective Antigen (PA) gene promotor sequence of *Bacillus anthracis*. A 29-amino acid Signal Sequence (SS) is also cloned preceding the gene sequence for facilitating secretion of the proteins. *LinA* and *linB* genes are also cloned in pPROEX HTc expression vector for checking expression of the genes and raising antibodies against their proteins. All clones (SS + *linA* and SS + *linB* in pYS5 and *linA* and *linB* in pPROEX HTc vector) were confirmed by restriction digestion and sequencing. LinA and LinB recombinant proteins are purified using Ni^+-NTA His tag affinity column, extracted from SDS-polyacrylamide gel and injected into mice to raise the antibodies. Analysis of SS + linA/B + pYS5 clones for secretion of functional Lin proteins are underway. Genetic engineering of *B. subtilis* for HCH degradation and its application in the HCH dumpsite soils will provide a proof-of-concept for decontamination of other polluted sites worldwide.

Keywords: HCH, Bioremediation, *Sphingobium indicum* B90A, *Bacillus subtilis*

ABSTRACT CODE: PP71

METAGENOMICS IN THE NEW GENERATION SEQUENCING ERAS

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The nature harbours billions of microorganisms, which are omnipresent in our biosphere, and they occupy diverse habitats ranging from Glacial deserts, hot springs, ocean bottoms to hypersaline environments. Most of these microbes are unculturable by standard techniques, thus it is necessary to use culture independent techniques to research on them. Metagenomics (also referred as eco-genomics) is a novel field developed to explicate the collective genomes of the uncultured microorganisms mainly using methods of molecular genetics, bioinformatics, proteomics, and metabolomics. The rRNA 16S, which represents 80% of total bacterial RNA, has several variable regions appropriate for PCR amplification and sequencing, is used for the identification of unexplored bacterial community. Techniques like Denaturing Gradient Gel Electrophoresis (DGGE) or Terminal Restriction Fragment Length Polymorphism (T-RFLP) are used to analyse these microbial communities. Next generation sequencing (NGS) helps to work out the DNA sequence of whole genome during a single sequence run, and from these data, information on resistance and virulence, as well as information for typing is obtained. There are no requirements of bacterial cloning of DNA fragments and electrophoresis, since NGS libraries preparation process are carried out in a cell-free system and the sequence output is directly distinguished. The NGS studies follow some common phases such as sample and metadata collection, DNA extraction, library construction, sequencing and read pre-processing followed by quantitative analysis and functional binning. Another important aspect for any successful metagenomic study is that the extraction of high-quality DNA from the environmental samples. The extraction methods are chosen carefully supported the medium and therefore the DNA population of interest. In the presentation, the techniques used for the microbial studies will be discussed further.

Keywords: Metagenomics, PCR amplification, DGGE, T-RELP, NGS

ABSTRACT CODE: PP72

A STUDY ON ROLE OF ABIOTIC AND BIOTIC COMPONENTS IN BIOREMEDIATION

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Increasing environmental pollutants due to various anthropogenic activities are of great concern nowadays since they affect the health of both terrestrial and aquatic ecosystems. Pollutants such as pesticides, heavy metals, fertilizers are non-biodegradable and persist in the environment for a longer duration affecting the health of living organisms. In this context, bioremediation technology is gaining considerable attention. Bioremediation technology involves various living organisms for the removal of toxic pollutants. An attempt has been made to discuss detoxification methods adopted by various microorganisms and to understand how these detox-mechanisms can be exploited to clean up the environment in a natural way. Finally, various environmental factors that regulate bioremediation processes and the methods to improve the rate of bioremediation have been mentioned. This comprehensive study may help to understand the fundamental aspects and future perspectives of microbial remediation of pollutants which could help in commercial success of waste management processes.

Keywords: Detoxification mechanism, Environmental pollutants, Microbial remediation, Waste management

ABSTRACT CODE: PP73

RECENT ADVANCES IN METHODS OF SPECIES IDENTIFICATION: DNA BARCODING

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Biodiversity plays a vital role in maintaining ecosystem health and function as a consequence of functional variations among organisms that permit resource partitioning and facilitation. Approximately 1.2 million species have been described, which is the around 10-15% of total biodiversity present on the earth. For describing remaining diversity an accurate method for taxonomic identification is required. The DNA barcoding is a powerful taxonomic tool to estimate and understand the world's biodiversity. DNA barcoding utilizes one or more standardized short DNA region for taxon identification. With the emergence of new sequencing techniques, such as Next generation sequencing (NGS), Oxford Nanopore Technologies (ONT)'s MinION™ sequencing and Pac Bio sequencing, DNA barcoding has become more accurate, fast and reliable. The consortium for barcode of life (CBOL) present various working group to identify the universal barcode gene, such as COI in metazoans; rbcL, matK, and ITS in plants; ITS in fungi; 16S rRNA gene in bacteria and archaea, and creating a reference DNA barcode library. An attempt has been made to summarize the various proposed DNA barcodes for animals, plants, fungi, bacteria, virus, and protists with special emphasis on ciliates. The paper also discusses the strength, limitation, and recent advancement in DNA barcoding approach.

ABSTRACT CODE: PP74

THERMOSTABILITY OF *THERMOACTINOMYCES VULGARIS* PROTEASE

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Microbial protease play an important role as metabolic catalyst and hence are used in various industrial market. The extra cellular protease stability in wild-type strain of *Thermoactinomyces vulgaris* were characterized in presence of casein substrate. The thermostability of protease was determined at different temperatures and time intervals, in the absence and presence (10 mM) of a divalent cation, Mn^{2+}, which enhances its catalytic activity at 60°C, 17% and 28% inactivation was recorded after 20 min and 30 min of heat treatments, respectively, in the absence of Mn^{2+}; while 12% and 13% inactivation was recorded after 20 min and 30 min of heat treatments, respectively in its presence. Similarly, at 65°C, 25% and 32% inactivation was observed after 20 min and 30 min of heat treatments, respectively in the absence of Mn^{2+}; while 13% and 20% inactivation was observed after 20 min and 30 min of heat treatments, respectively in the presence of this divalent cation. However, at 70°C, 80°C and 90°C, similar patterns of thermostability of protease were observed in the absence and presence (10 mM) of Mn^{2+}. The thermal inactivation pattern of extracellular protease of *T. vulgaris* on the temperature treatment of this enzyme for 30 min at 50°C, inactivated it to the 11% and 17% in the absence and presence (10 mM) of Mn^{2+}, respectively. Suggesting that the thermophilic protease of this thermophile is thermolabile, as it was not completely thermostable even at its growth temperature.

There was gradual increase in the specific activity of the enzyme in the control cultures (without chloramphenicol) over 24 h period of growth, when assayed either in the absence or presence (10 mM) of Mn^{2+}. The chloramphenicol treated cultures, on the other hand, exhibited a gradual decrease in the specific activity of protease, showing about 23% and 39% decrease in the enzyme activity after 24 h of growth in the absence and presence (10 mM) of Mn^{2+}, respectively. The results revealed that a slight increase in the level of extracellular protease of *T. vulgaris* in the absence of chloramphenicol and a decrease in its specific activity in the absence of protein synthesis (i.e., in presence of chloramphenicol added in the culture medium at 8 h of growth at 50°C), indicated a rapid turnover of this enzyme. This rapid turnover counteracts the destructive effect of heat and thus permits the organism to grow at elevated temperatures. These in-vitro observation of extracellular protease of *T. vulgaris* can be used for high-temperature catalytic reaction in various industrial enzymatic processes.

ABSTRACT CODE: PP75

ASTROBIOLOGY: A SEARCH FOR MINIATURE LIFE BEYOND EARTH

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The astonishing movements and patterns of the sky ignited in the minds of the sapiens the creation of myth to explain astronomical events. However, in the modern world, this curiosity led to the establishment of the branch of science well known as ‘space microbiology’. Life in space would seem impossible due to its exceptional architecture (microgravity, vacuum, extreme thermal conditions, high velocity and radiation) but there are extremophiles that can not only endure these extremities for years, but also reproduce in space! Imagine a world where life exists in those conditions where humans cannot set their foot without those fancy equipments. NASA has been searching for these worlds as early as 1975. Wait till you learn about the method which was used to study this phenomenon in the Kibō module, where the color change depicted their survival. Why do you think finding life on another celestial body is imperative? So, are you curious to reveal the changes in microbes which will make you believe how these creatures can play a beneficial role for mankind?

ABSTRACT CODE: PP78

POTENTIAL USE OF MICROBES FROM POLAR REGIONS IN THE BIODEGRADATION OF POLYCHLORINATED BIPHENYLS

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The purpose of this poster is to bring to the attention of its viewers, the tremendous feat that is biodegradation of one of the most notorious and persistent organic pollutants called Polychlorinated Biphenyls, or PCBs. These man-made organic compounds were heavily used between the years 1930 and 1980. They were employed in a variety of appliances such as capacitors, hydraulic systems, transformers, etc. on a large scale. The Stockholm Convention has banned the production of PCBs all over the world. However, they are present in all the major parts of the world even now (owing to their large amounts and handsome half-lives), hence posing potentially lethal health hazards to living beings. They are lipophilic compounds which means that they accumulate in the fatty tissues of lower organisms, and are thus magnified as they are consumed by the top predators like polar bears, seals, humans, etc. Inside these organisms, they cause the dysfunction of bodily systems such as reproductive system, immune system, endocrine system; they are also found to cause cancer. Today, almost everyone has PCBs in their system; these compounds are also found in the breast milk of mothers. This will continue to pose as a mortal threat even to the upcoming generations. The methods employed to treat PCBs are usually really expensive and cumbersome. However, bioremediation of PCBs is an efficient alternative. Psychrotolerant Arctic and Antarctic microorganisms can be employed in the *in-situ* treatment of these compounds. The biodegradation of these chemicals is carried out in two steps, namely anaerobic reductive dechlorination and aerobic oxidative degradation. Promising territories for the aforementioned methodology are the Antarctic and Arctic regions, since microbes found in such extreme environments are heavily researched upon, and are found to have biodegradative properties. Prior researchers have been successful in identifying some polar microorganisms which have PCB-degrading properties but some abiotic factors which play an important role in any biochemical process might have been overlooked. Hence, it should be of prime concern that the research methodology should be altered, focussing on the abiotic factors affecting the bioremediation process, and novel ideas should be pondered upon, including the introduction of these polar microbes to temperate regions. This research is still in its origin years and more funds should be granted in order to improve the methodologies employed, so a sustainable solution to a biohazardous threat to the existing and future generations can be worked upon.

ABSTRACT CODE: PP79

EXPLORATION OF POTENTIAL BIOACTIVITY OF ENDOPHYTIC FUNGI OBTAINED FROM THE MANGROVES OF KUTCH, GUJARAT, INDIA

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Mangrove harbours a large number of unique fungal communities known as manglicolous fungi. These fungi, especially an endophytic fungi, which reside within living plant tissues are considered to be a major source of novel bioactive compounds. An antimicrobial spectrum of mangrove root endophytic fungi obtained from Kutch, Gujarat was investigated. Human bacterial pathogens such as *Escherichia coli, Staphylococcus aureus, Bacillus cereus, Pseudomonas aeruginosa, Klebsiella pneumonia*, *Proteus vulgaris*, *Enterobacter* sp., *Enterococci sp*., *Salmonella typhi* and *Shigella sp.* was taken into study. Three of the fungal isolates showed broad spectrum activity against the pathogens. Ethyl acetate treated extracts were found to show better activity compared to crude extracts. The study suggested that the isolated endophytes can be an exceptional source of bioactive compounds.

ABSTRACT CODE: PP80

EXPLORATION OF CONJUGATED LINOLEIC ACID (CLA) PRODUCING PROBIOTICS FROM TRADITIONAL FERMENTED FOOD OF NORTH-WESTERN HIMALAYAN REGION AGAINST OBESITY

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Obesity is one of the major metabolic diseases prevalent in our society. Many recent studies have suggested that the composition and diversity of gut microflora in humans are highly linked to obesity. In Lahaul valley, people have been consuming fermented food like Churpe, Curd, Cheese, and Lugri for a long period. The present study focused on the isolation of conjugated linoleic acid (CLA) producing probiotic from the fermented foods and isolated 114 distinct bacterial morphotypes; 54 strains were selected based on their probiotic attributes and safety assessment. Taxonomically, the isolates ranged among 11 distinct genera and 13 different species, quantitatively assayed using gas chromatography-mass spectrometry. Among the selected isolates, *Lactiplantibacillus plantarum, Latilactobacillus curvatus,* and *Enterococcus faecalis* strains were observed to produce CLA isomers (cis-9, trans-11). Further, in-vitro and in-vivo investigations has to be performed to establish the role of indigenous probiotic strains against obesity.

Keywords: Fermented foods, Conjugated linoleic acid, Probiotics, Lactic acid bacteria, Obesity

ABSTRACT CODE: PP81

BIOACTIVE POTENTIAL OF *STREPTOMYCES* SPP. AGAINST DIVERSE PATHOGENIC FUNGI

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In the ongoing Covid-19 pandemic, fungal infection has emerged as a severe threat to the human health. Fungi not only harm the humans but also damage food grains, vegetables and fruits across the world. Pathogenic fungi are rapidly getting resistant nearly against all the available drugs. Adding to this problem is the fact that most chemical fungicides in use are reported for the disruption of mammalian endocrine and reproductive systems, and potential neurotoxicity along with entry into the food chain, leading to bioaccumulation. So there is a dire need for the detection of new bioactive molecules against these pathogens. Natural compounds are always good reserves of bioactive molecules having broad range of antimicrobial activities. Genus *Streptomyces* of actinobacteria is a prolific source of novel secondary metabolites for drug applications. During our previous studies, different *Streptomyces* strains were isolated, taxonomically characterized using 16S rRNA gene, screened for production of bioactive compounds and these were identified using GC-MS, LC-MS, and NMR techniques. In the present study, we are focusing on the extraction of bioactive compounds from these strains and analyses of their antifungal potential against the diverse pathogenic fungi. Screening of antifungal activity will be perfomed using disc diffusion assay, MTT assay and broth microdilution method for MIC determination. Furthermore, investigation will be focused on the effect of extract treatment on the structural integrity of the plasma membrane of treated pathogens using SEM/TEM microscopy and Flow cytometry. Due to treatement of antifungal extract, reactive oxygen species accumulation takes place in treated fungi, which will be measured by bioluminescence assay. In nutshell, findings from the present study using *Streptomyces* spp. may help to control the pathogenic and crop destroying fungi.

Keywords: *Streptomyces* spp., Bioactive potential, Pathogenic Fungi, MIC determination, MTT assay, Flow Cytometry(FACS), Bioluminescence Assay.

ABSTRACT CODE: PP82

NEW SURPRISES FROM A URANIUM TOLERANT BACTEROIDETES SOIL BACTERIUM, *CHRYSEOBACTERIUM* SP. STRAIN PMSZPI

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Microbes residing in metal enriched environment provide valuable insights into the microbial adaptation and survival strategies. A *Bacteroidetes* soil bacterium, *Chryseobacterium* sp. strain PMSZPI, isolated from uranium enriched site exhibited superior tolerance to uranium and other heavy metals. The 3.8 Mb large genome of the strain was sequenced and 3346 protein coding genes were predicted which included genes largely important for metal resistance and efflux. Transporters like P type ATPases, polysaccharide synthesis genes for biofilm formation and phosphatases for metal precipitation were annotated. In the absence of flagella and pili, PMSZPI moved over solid agar surfaces by a unique form of motility, known as gliding motility resulting in formation of spreading colonies which is a distinctive feature of members of Bacteroidetes phylum. All the genes reportedly important for bacteroidetes gliding motility were found in this strain. We present here, the interesting interaction between gliding motility and cellular organization in PMSZPI spreading colonies. The colony spreading was higher under nutrient deficient conditions and was reduced at high agar concentrations and presence of motility inhibitor like 5-hydroxyindole. *In situ* structural analysis of spreading colonies revealed closely packed cells at center of colony while the cells at the edges were interconnected and periodically arranged in hexagonal lattices. This periodic arrangement of the cell population in the spreading colonies attained through gliding motility possibly resulted in bright structural coloration or iridescence when illuminated. Cells exposed to uranium had reduced motility and iridescence and enhanced biofilm formation. The findings obtained here shed interesting light on how features like the motility process, formation of biofilms, and structural coloration might contribute to the adaptation of PMSZPI in stressful metal enriched environment.

ABSTRACT CODE: PP83

METAL TOLERANT MICRO-ORGANISMS: AN EMERGING BIOREMEDIATION TECHNIQUE - A REVIEW

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Over the time purity of water is deteriorating massively at a high pace due to various types of contaminations, like excretion/discharging of the various heavy metals into the water bodies. Major sources are effluents from industries, chemicals used in agricultural and various anthropogenic activities. Problem arises as these heavy metals are non-biodegradable leading to bio-accumulation in various parts of the plants and animals and it lead to bio-magnification. A research shows metals like iron, magnesium, zinc, copper, nickel, chromium and cadmium predominates in the list and is much above the prescribed limits. Through atomic absorption spectrophotometry microbes like *Bacillus pumilus, Bacillus subtilis, Pseudomonas aeruginosa, Serratia liquefaciens* are found to have adapted better in high metal concentration. They help in decreasing the heavy metal concentration or convert them into less toxic forms through various mechanisms like biosorption, bioaccumulation, oxidation/reduction, precipitation and bioleaching. The process involves various enzymes like Chromate Reductases (ChrA,YieF), Nitoreductases (NfsB,KefF), periplasmic cytochrome etc. which have broad/narrow specificity. Various resistance mechanism are also involved like extracellular/intracellular precipitation, complexation, chelation etc. in response to heavy metal toxicity. Even after knowing various chemical and physical techniques, bioremediation technique have gained much interest of researchers as it being more efficient, eco-friendly, less cost involving, demand less monitoring and heavy equipments. This is not just a simple technique but a whole process that will lead to a sustainable and healthy environment and biota.

ABSTRACT CODE: PP84

REVIEW ON ORIGIN AND TRANSMISSION OF SARS-CoV2

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SARS-CoV2, a virus belonging to the family Coronaviridae, is the latest virus to have caused a global pandemic. As of 7th September 2021, there have been 221,134,742 confirmed cases of COVID-19 globally. SARS-CoV2 is believed to be a zoonotic virus with bat origin, due to its astonishing genomic similarities with the BatCoV RaTG13. Although the intermediate host of this virus is still unknown, the Malayan pangolin is believed to be the primary suspect. Human to human transmission of the virus is via direct contact through respiratory droplets, aerosols or contaminated surfaces. While the origin of the virus is still unclear, the spread of the virus is believed to have started from a wet seafood market in China. By the end of December 2019, China informed WHO of an outbreak of 'pneumonia like cases', which was later confirmed to be caused by the newly discovered SARS-CoV2 virus. Since the outbreak unfortunately overlapped with the Chinese Lunar New Year, cases spread rapidly within the Hubei province, leading to implementation of strict lockdowns. However, the virus swiftly spread to neighbouring countries and was declared as a pandemic by WHO on 11th March 2020. In India, the first case of COVID-19 was discovered on 30th January 2020 from Kerala. The first wave of COVID-19 in India reached its peak in September 2020 with around 100,000 cases per day. In March 2021 the second wave, suspected to be caused by the highly infectious delta variant (B.1.617.2 lineage), arrived with an almost fourfold increase in daily number of cases reported. As of today the third wave of the virus is predicted to hit India around October-November 2021. This pandemic has affected the economies of most countries including India, disrupting all aspects of life.

ABSTRACT CODE: PP85

SARS-CoV2: INFECTIONS AND IMPLICATIONS

USAGE AND EFFECTIVENESS OF COMMON HERBS FOR THE MANAGEMENT OF COVID-19: AN ONLINE CROSS-SECTIONAL SURVEY BASED STUDY

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Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV2) causes COVID-19 which is an infectious disease primarily affecting respiratory systems. Various medications and vaccines are being approved for COVID-19 emergencies. Since the emergence of SARS-CoV2, the scientific community has been working restlessly to hunt out short-term therapeutic approaches to scale down the spread and curb the COVID-19 related morbidity and mortality. Herbal treatment has been practiced indigenously across the globe to cure and control various infections, diseases and syndromes. Various herbal remedies are mentioned in the alternative systems of medicine to suppress the symptoms and complications related to Covid-19 with minimal or no side effects. The online surveys can be an easy and efficient way of real time communication and data collection during the Pandemic. Therefore, we have conducted an online survey in India by using survey administration software - Google forms to assess the usage and effectiveness of major herbs that are used in almost all the Indian households - *Curcuma longa (*Turmeric), *Ocimum sanctum (*Tulsi)*, Allium sativum* (Garlic), *Cuminum cyminum (*Cumin), *Syzygium aromaticum* (Clove)*, Piper nigrum* (Black pepper) and *Zingiber officinale* (Ginger). These herbs have various bioactive compounds that show therapeutic efficacy against various symptoms of the infection and can also inhibit the replication of SARS-CoV2. They may also have various antiviral, immunostimulant and SARS-CoV2 Main protease (M-pro) inhibiting properties that can help in suppressing the symptoms and other complications, thereby reducing the severity of the infection. Our online survey demonstrated that these herbal therapeutics may not prevent the infection but definitely increases the immunity of an individual and acts as a supportive therapy, if consumed regularly.

Keywords: Therapeutic, Antiviral, Immunostimulant

ABSTRACT CODE: PP86

STRUCTURAL CHANGES IN TNAA, GADB AND TDC GENES OF HUMAN GUT BACTERIAL COMMUNITY LEAD TO VARIATIONS IN NEUROTRANSMITTER LEVELS DURING DEPRESSION

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A philharmonic orchestra between gut microbiota and neurotransmitters is the key to good physical and mental health. Disturbances in the gut microbial ecosystem can adversly impact the homeostasis of the host physiology. Depression has also been associated with gut dysbacteriosis in the past decade as a major cause. This is due to the bidirectional communication linking the gut microflora and the brain that forms the Gut-Brain Axis. The levels of neurotransmitters like Serotonin, Dopamine, and Gamma-Aminobutyric Acid (GABA) are known to decrease in case of depression. These neurotransmitters are majorly synthesized in the gut and changes in the gut microbiome or their metabolites can lead to decreased levels of these neurotransmitters which can further elevate or ameliorate depression. Metagenomics studies of the gut microbiome variability under various stress conditions or dysbiosis has so far focussed on the disparity in the alpha and beta diversity of microbes. Attempts have been made to identify variations in gene structures responsible for the biosynthesis of dissimilitude metabolites during depression. Three genes namely, tnaA, tdc, and gabB responsible for the synthesis of Indole, Tyramine, and GABA, respectively were selected. Present study indicate that the variations in these gene structures are responsible for diverting the biosynthetic pathways of neurotransmtters implicated in depression.

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