8th International Conference

Indian Network for Soil Contamination Research (INSCR)

along with

4th International Symposium on Ciliate Biology



2024 INSCR

Exploring the Microbial World

From Human Health to Environmental Sustainability

organised by

विकसित भारत अभियान
1947 TO 2047

8th International Conference of
Indian Network for Soil Contamination Research (INSCR)
&
4th International Symposium on Ciliate Biology



Exploring the Microbial World

From Human Health to Environmental Sustainability

April 2-5, 2024 | Conference Centre, University of Delhi, INDIA

organised by

under the aegis of DBT STAR STATUS SCHEME

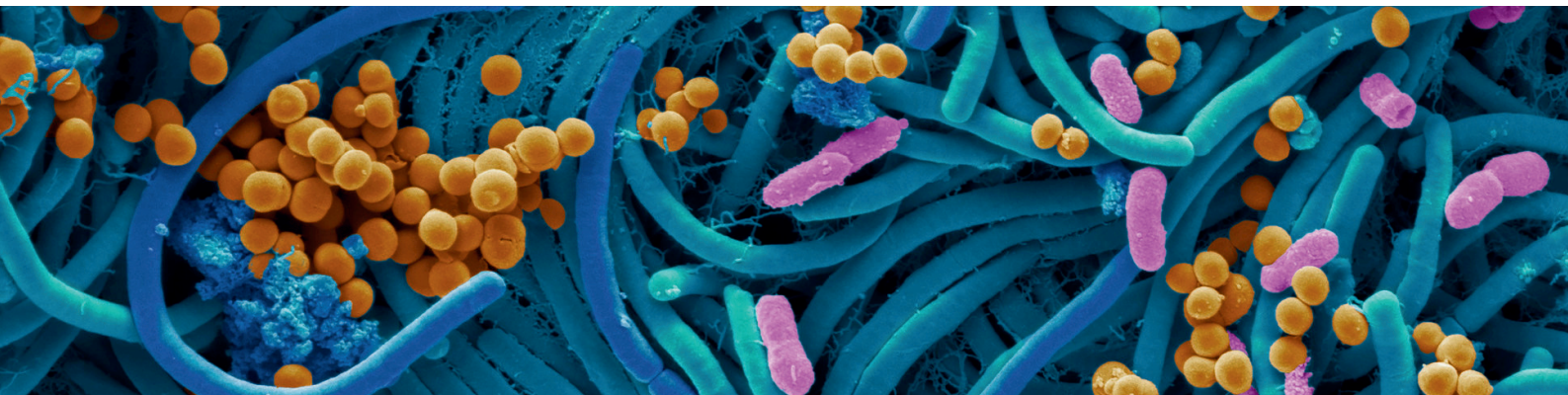
with support from

in association with

About INSCR

Indian Network for Soil Contamination Research (INSCR) was established and registered as a society under the Societies Registration Act XXI of 1860 with registration no. 34693 dated 22nd April 1999. The society organized its first international conference, on the subject of environmental pollution, at Hotel Radisson in New Delhi, in December 1999. The network brought together several key researchers working on different aspects of contamination in soil environments spread across various academy, agricultural, and industrial research institutions.The December 1999 conference was a huge success attracting as many as 200 renowned scientists from various countries, i.e., Australia, New Zealand, Japan, China, Sweden, UK, U.S.A and elsewhere. This paved the way for organizing more meetings to bring together society members and distinguished researchers on a common platform to learn about the latest developments and technologies in soil and environmental research. As of 2022, INSCR has organized seven International Conferences in various parts of India with more than 400 participants each time.

You can also join us and be the next supporter to save the environment!



Vision & Mission of the Conference...



Exploring the Microbial World

Microorganisms play an important role in the existence of human beings. 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.

This year 8th International Conference of INSCR along with 4th International Symposium for Ciliate Biology (ISCB) will emphasize on the role of microbes in achieving the 17 goals of sustainable development which were proposed in 2016 to provide the fundamental necessities including food, cloth, shelter and healthcare facilities to all strata of society. Main highlight of conference is a plenary lecture by renowned scientist and distinguished immunologist Prof. Rino Rappouli, Head, R&D, GSK Vaccines. There will be 10 enriching scientific sessions on different arenas of microbiology and environmental interactions. Additionally, special sessions on Microbial Literacy headlined by Prof. Kenneth Timmis, International Microbiology Literacy Initiative (IMiLI), Entrepreneurship and Innovation in Sciences headed by Managing Director, BIRAC; Women in Science session to celebrate empower and motivate young women researchers and their significant contributions. More than 80 international and national speakers around the globe will share a common platform with researchers and academicians from esteemed Institutes to share their ideas and experiences.

MESSAGE FROM THE CONFERENCE CHAIR



Prof Rup Lal

(Conference Chair and Convenor)
President, INSCR
INSA Senior Scientist
Acharya Narendra Dev College
University of Delhi

Presidential Address

As conference chair and INSCR President, I warmly welcome all the participants to the 8th International Conference of Indian Network for Soil Contamination Research (INSCR) and 4th International Symposium on Ciliate Biology on “Exploring the Microbial World: From Human Health to Environmental Sustainability” organized jointly by University of Delhi, Acharya Narendra Dev College and PhixGen Pvt. Ltd. under the aegis of INSCR from 3rd to 5th April, 2024.

With a record number of participants expected this year, we are delighted and equally excited to share that we have a total of ten scientific enriching sessions in three-day conference. In addition to the scientific program, we have two pre-conference workshops on “Genomics, Metagenomics & Bioinformatics in Microbial Ecology” and “Scientific Writing and Communication” wherein hands-on sessions for young researchers and faculty will be conducted. This year's conference theme includes several outstanding plenary & keynote lectures, special sessions on Entrepreneurship and Innovation in Science”, “Microbial Literacy in Society”, “Women and Science” and other technical sessions. In this conference we bring together renowned and distinguished scientists around the globe, researchers and practitioners from academia, industry, and students to exchange their research ideas and results under various sub-themes of the conference. We have more than 20 international and 65 national speakers and about 500 participants attending the conference in hybrid mode.

I hope that these three days of engagement in the INSCR Conference will leave all the participants with the knowledge, fond memories, and changed enthusiasm and I hope it will be a successful event

We look forward to welcoming you to the online 7th International virtual conference of the Indian Network for Soil Contamination Research.

Best wishes

Rup Lal

MESSAGE FROM THE CONFERENCE

CO-CHAIR



Prof Ravi Toteja
(Conference Co-Chair)
Officiating Principal
Acharya Narendra Dev College
University of Delhi

Dear Esteemed Participants and Researchers,

It is with great pleasure and excitement that I extend my warmest welcome to all of you on behalf of Acharya Narendra Dev College (ANDC), University of Delhi, as we come together for the 8th International Conference on Exploring the Microbial World and 4th International Symposium on Ciliate Biology (ISCB-2024) jointly organized by the Indian Network for Soil Contamination Research (INSCR) and ANDC, along with other colleges of DU. This conference stands as a testament to our collective commitment to advancing scientific inquiry and fostering interdisciplinary collaboration in the realms of microbial ecology and ciliate biology. As we embark on this journey of exploration and discovery, I am confident that our collective efforts will lead to meaningful insights and innovative solutions to the challenges facing our environment and biodiversity.

I extend my heartfelt appreciation to the organizing committee, volunteers, and sponsors for their tireless efforts in making this conference a reality. Your dedication and hard work have been instrumental in creating a platform for scholarly exchange and collaboration. To all the participants, I encourage you to actively engage in the sessions, presentations, and discussions throughout the conference. Your contributions and insights are invaluable and will undoubtedly enrich the discourse and shape the future direction of research in these critical areas. As we come together to share our knowledge, expertise, and passion for scientific inquiry, let us seize this opportunity to forge new connections, cultivate collaborations, and inspire one another to push the boundaries of knowledge further. I wish you all a stimulating, productive, and rewarding conference experience. May this conference be a source of inspiration and empowerment as we collectively strive towards a deeper understanding of the microbial world and ciliate biology.

Warm regards,

Prof (Dr) Ravi Toteja

INSCR OFFICE BEARERS



PRESIDENT

Rup Lal

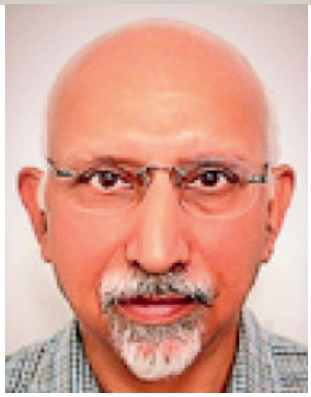
FNA, FNASc, FNAAS
INSA Senior Scientist
ANDC, DU



VICE PRESIDENT

H.C. Agarwal

Retd. Professor, DU



SR.VICE-PRESIDENT

Rajendra Prasad

Patent Consultant, Meritindia



SR.VICE-PRESIDENT

Yogendra Singh

INSA Senior Scientist



JOINT SECRETARY

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Retd. Prof.
Dept. of Zoology, DU



JOINT SECRETARY

Neeta Sehgal

Retd. Prof.
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JOINT SECRETARY

Tanu Jindal

Professor, Amity Institute of Environmental Toxicology Safety & Management, Retd. Scientist, IARI, Retd. Professor, DU
Patent Consultant, MeritIndia
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TREASURER

A. K. Dikshit

Retd. Scientist, IARI

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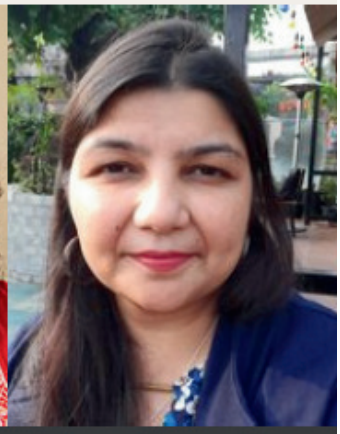


Charu Dogra Rawat
Associate Professor
Ramjas College, DU



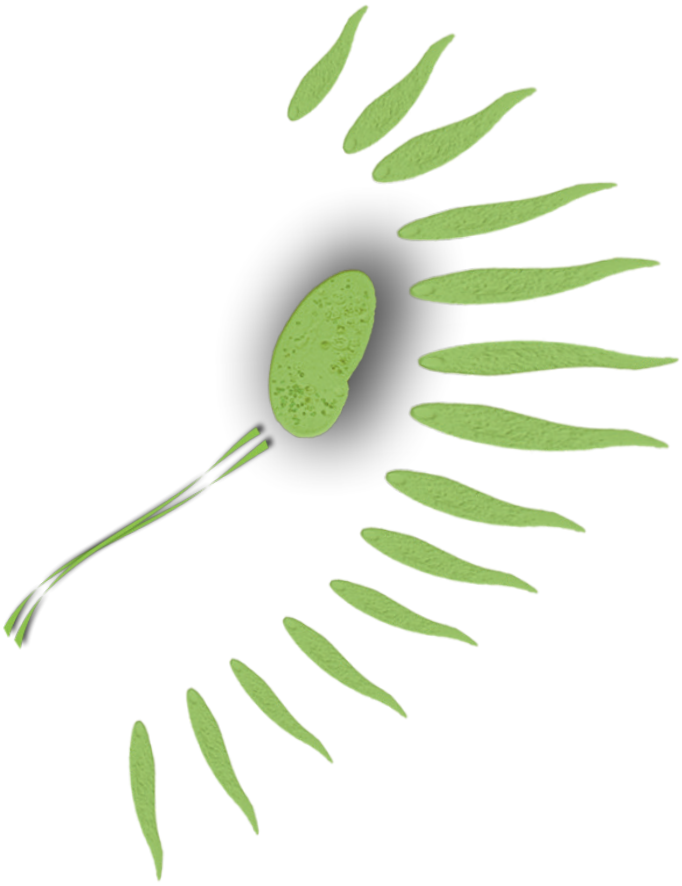
R. K. Negi
Professor
Dept. of Zoology, DU



Atul K Johri
Professor
JNU

INSCR

About ISCB



The Ciliate Biology Forum, Delhi, India has previously organized three International Symposium on Ciliate Biology in the year 2007, 2018 and 2022. This year, Acharya Narendra Dev College is organizing a Symposium in collaboration with INSCR. The symposium aims to achieve the following:

- To provide a platform for the ciliate interest group to exchange information, present latest research findings and establish collaborations
- To enthuse large number of Indian and foreign UG/PG students to take up ciliated protists as their preferred research area
- To provide networking opportunities for students wishing to take up doctoral or postdoctoral research on ciliates

The scientific content shall include a wide gamut of aspects of ciliate biology: Biodiversity, Ecology, Evolution, Systematics, Genomics, Epigenetics, DNA Barcoding, Proteomics, Ciliates and Industry, Ciliates as model organisms in UG teaching and in research, among others. Additionally, there will be a parallel session open for oral and poster presentations. The symposium is likely to have participation of many international ciliate experts sharing their research work. Members of the Ciliate Biology Forum including research scholars will also have the platform to share their current research.

SUPPORTED BY

INDIAN NATIONAL SCIENCE ACADEMY (INSA)

The Indian National Science Academy was established in January 1935 with the object of promoting science in India and harnessing scientific knowledge for the cause of humanity and national welfare

INTERNATIONAL UNION OF MICROBIOLOGICAL SOCIETIES (IUMS)

IUMS is the International Union of Microbiological Societies, founded in 1927 with the aim to mobilize all microbiological societies globally to promote the development of sustainable solutions to control infectious agents while preserving the global microbial diversity and the healthy life of our planet.

INTERNATIONAL SOCIETY FOR MICROBIAL ECOLOGY (ISME)

ISME serves the wider-community and seeks to help and promote microbial ecology in all aspects. Our goal is to serve microbial ecologist and the wider community by supporting research and education.

FEDERATION OF EUROPEAN MICROBIOLOGICAL SOCIETIES (FEMS)

FEMS is made up of an active and diverse network of around 30,000 professionals who are committed to advancing microbiology for the benefit of society in the areas of health, energy, food, materials, and the environment. Set up in 1974, today we are a growing coalition of 55 Member Societies from 40 countries.

SUPPORTED BY

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Department
of Biotechnology
Govt. of India

DEPARTMENT OF BIOTECHNOLOGY (DBT), GOVERNMENT OF INDIA

Vision: "Attaining new heights in biotechnology research, shaping biotechnology into a premier precision tool of the future for creation of wealth and ensuring social justice – specially for the welfare of the poor."

DEPARTMENT OF SCIENCE & TECHNOLOGY (DST), GOVERNMENT OF INDIA

The Department of Science & Technology plays a pivotal role in promotion of science & technology in the country. The department has wide ranging activities ranging from promoting high end basic research and development of cutting edge technologies on one hand to service the technological requirements of the common man through development of appropriate skills and technologies on the other.

सत्यमेव जयते
Department of Science & Technology
Govt. of India

iNSERB
INDIA

SCIENCE AND ENGINEERING RESEARCH BOARD (SERB), GOVERNMENT OF INDIA

ISME serves the wider-community and seeks to help and promote microbial ecology in all aspects. Our goal is to serve microbial ecologist and the wider community by supporting research and education.

INTERNATIONAL MICROBIOLOGY LITERACY INITIATIVE (IMILI)

The initiative aims to provide new materials for the teaching of microbiology in schools in order to create a society that is literate in key aspects of microbiology that are important for knowledge-based everyday family decisions, as well and regional, national and global policy decisions affecting everyone and the planet.

IMiLI
International Microbiology Literacy Initiative



MESSAGES

INSCR 2024

दिल्ली विश्वविद्यालय
University of Delhi

प्रो॰ योगेश सिंह
कुलपति

Prof. Yogesh Singh
Vice-Chancellor

No. DU/VC/2024/371
28th March 2024



MESSAGE

I am delighted to know that Indian Network for Soil Contamination Research (INSCR), Acharya Narendra Dev College and various other colleges of the University of Delhi are jointly organizing the 8th Indian Network for Soil Contamination Research (INSCR) on an appropriate theme of *"Exploring the Microbial World: From Human Health to Environmental Sustainability"* and the 4th International Symposium on Ciliate Biology (ISCB) with much enthusiasm.

I am sure this Joint Conference will allow a platform for distinguished scientists, academicians and researchers from diverse background to converge and exchange their seminal ideas which will eventually pave the way for innovative solution to contemporary challenges in the subject areas of Soil Contamination and Ciliate Biology. The Interdisciplinary nature of the academic discussions will surely help us to find better avenues to address the larger issue of environmental degradation and sustainable development.

I would like to extend warm welcome to the distinguished delegates of the Joint Conference with the hope that this academic confluence will act as a catalyst to further ignite new and innovative thoughts and ideas to address the present situation in a pragmatic manner.

I would like to take this opportunity to extend sincere appreciation to the organizing team of this Joint Conference for their stupendous effort in organization of this event.

Yogesh Singh

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PATRON

Professor R.C. Sobti
(Padmashree Awardee)
M.Sc. (Hons. Sch.), Ph.D., D.Sc., F.T.W.A.S.,
F.N.A., F.N.A.Sc., F.Z.S.,FISC,F.N.A.A.S.,
F.A.M.S., F.P.A.S., F.A.M.I., F.S.C.G.
INSA Sr. Scientist
&
Professor Emeritus
Department of Biotechnology

PANJAB UNIVERSITY
CHANDIGARH, *India* 160 014



I extend a warm welcome to all distinguished attendees of the 8th Annual International Conference of the Indian Network of Soil Contaminated Research (INSCR) and 4th International Symposium on Ciliate Biology, themed "Exploring the Microbial World: From Human Health to Environmental Sustainability". As the patron of this esteemed conference, I am honored to address you on a topic of immense significance in our modern era - microbes in technologies.

For over a century, microbial technologies have been pivotal in addressing a myriad of challenges, spanning from human health to environmental sustainability. From diagnosing and treating microbial infections to the development of vaccines against various diseases, these technologies have revolutionized healthcare practices. Moreover, they have significantly contributed to enhancing food preservation methods such as pasteurization, fermentation, and canning, thereby extending the shelf life of food products.

Furthermore, microbial technologies have played a crucial role in bioremediation efforts, facilitating the cleanup of chemical pollution, waste disposal, and oil spills. The production of essential pharmaceuticals such as antibiotics, insulin, and probiotics, as well as biopesticides and biofertilizers, underscores the versatile applications of microbial processes.

In addition to their contributions to healthcare and environmental sustainability, microbes have emerged as invaluable assets in agriculture and food production. They enhance crop health, increase productivity, and offer solutions to challenges in feeding the world's growing population. Moreover, microbes play a pivotal role in reducing water pollution by breaking down toxins and improving water quality.

Furthermore, the potential of microbes in the realm of energy production cannot be overlooked. From the creation of novel fuels to the generation of clean energy, microbial technologies hold promise for a sustainable future. While research into electricity production directly from microbes is ongoing, microbial catalysts are already being utilized to convert renewable resources into hydrocarbon fuels.

As we convene for this conference, let us delve deeper into the microbial world, exploring its multifaceted applications in human health and environmental sustainability. Let us engage in fruitful discussions, exchange valuable insights, and foster collaborations that will further propel the advancements in microbial technologies towards a healthier, more sustainable future.

Once again, I extend my heartfelt welcome to all participants and wish you a productive and enriching experience at the 8th Annual International Conference of INSCR.

R.C Sobti
(R.C. Sobti)

PATRON

UNIVERSITY OF DELHI
दिल्ली विश्वविद्यालय

प्रोफेसर बलराम पाणी
अधिष्ठाता महाविद्यालय
Professor Balaram Pani
Dean of Colleges



****** MESSAGE*******

It gives me great pleasure to extend my warmest greetings to all attendees of the 8th Indian Network for Soil Contamination Research (INSCR) on *"Exploring the Microbial World: From Human Health to Environmental Sustainability"* and the 4th International Symposium on Ciliate Biology (ISCB) conference.

As the Dean of Colleges at the University of Delhi, I am honoured to witness the convergence of esteemed scholars, researchers, and practitioners in these vital fields. The contributions showcased in the abstract book reflect the dedication, innovation, and scholarly rigor that define our academic community.

The abstracts presented within this compilation encapsulate a diverse range of topics, methodologies, and findings, highlighting the breadth and depth of research being conducted in soil contamination research and ciliate biology. Each abstract represents a significant step forward in our collective understanding of these critical areas of study.

I extend my heartfelt appreciation to the organizers for their unwavering commitment and exemplary coordination in bringing together this esteemed gathering. Your efforts have ensured the success and impact of this conference, providing a platform for scholarly exchange and collaboration.

To all participants, I encourage you to explore the abstracts within this book, engage in discussions, and forge connections that will inspire future research endeavors. Your contributions are integral to advancing knowledge and addressing pressing challenges facing our environment and biodiversity.

I wish you all a stimulating and rewarding experience as you delve into the rich tapestry of research presented in this abstract book.

Warm regards,

Prof. Balaram Pani

Vice regal Lodge, University of Delhi, Delhi-110 007, India, Phones : +91-11-27667066 Fax : +91-11-27667093
Email : dean_colleges@du.ac.in

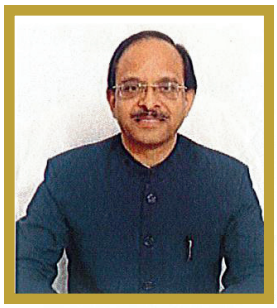
2024 INSCR

CO-PATRON

दिल्ली विश्वविद्यालय
University of Delhi

प्रो॰ श्रीप्रकाश सिंह
निदेशक, दक्षिण दिल्ली परिसर

Prof. Shri Prakash Singh
Director, South Delhi Campus



MESSAGE

It is a matter of immense pride that Acharya Narendra Dev College, INSCR and other colleges of the University of Delhi are jointly organizing the 8th Indian Network for Soil Contamination Research (INSCR) on a pertinent theme *"Exploring the Microbial World: From Human Health to Environmental Sustainability"* and the 4th International Symposium on Ciliate Biology (ISCB).

I feel that purposive research and significant academic deliberations, in the knowledge domains of Soil Contamination and Ciliate Biology, are particularly important in understanding their crucial role in addressing environmental challenges that ultimately affect health and sustainability of our mother Planet, the Earth.

I sincerely hope that this event will give significant opportunity to the scholars and the scientists to come together and delve into the complexities of these fields of knowledge more vigorously through active academic engagement and in the process help in impactful research outcomes.

I extend my heartfelt appreciation to the organisers for their remarkable effort in orchestrating this conference. I hope that academic deliberations in this conference will definitely go a long way in advancement of knowledge in the subject areas of Soil Contamination research and Ciliate Biology in future and help sustainable development.

Prof. Shri Prakash Singh
Director, South Delhi Campus

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CO-PATRON



MESSAGE

It gives me immense pleasure to know that Acharya Narendra Dev College, a Constituent College of the University of Delhi is organising the "8th Indian Network for Soil Contamination Research (INSCR) on the topic *Exploring the Microbial World: From Human Health to Environmental Sustainability"* and the "4th International Symposium on Ciliate Biology (ISCB)".

This conference stands as a testament to the dedication and commitment of the college in fostering interdisciplinary dialogue and collaborative research in the fields of soil contamination research and Ciliate Biology. The significance of these areas of study cannot be overstated, as they hold the key to addressing critical environmental challenges and unlocking the mysteries of the microbial life.

I would like to encourage all the distinguished participants of this conference to engage in meaningful discussions and presentations with scientific fervour while exploring networking opportunities in these knowledge domains. I sincerely hope that your seminal contributions will undoubtedly enrich the discourse and contribute to the collective pursuit of scientific excellence.

I extend my sincere appreciation to Organizing Team of the Acharya Narendra Dev College for their tireless efforts in bringing together researchers, scholars and practitioners from around the globe.

I wish every success for this conference with the hope that it serves as a platform for meaningful exchange, collaboration and generation of novel insights paving the way for transformative advancements in respective knowledge domains.

Best wishes!

Vikas Gupta

(DR. VIKAS GUPTA)

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2024 INSCR

CO-PATRON

PROF. SUDESHNA MAZUMDAR LEIGHTON

Chairperson Governing body | अध्यक्ष शासी निकाय

Acharya Narendra Dev College
University of Delhi | NAAC accredited: A^+ Grade
आचार्य नरेंद्र देव कॉलेज
दिल्ली विश्वविद्यालय | नैक मान्यता प्राप्त 'ए$^+$' ग्रेड



Dear Participants and Guests,

It is with great pleasure and excitement that I welcome you to the *8th International Conference of the Indian Network for Soil Contamination Research* (INSCR) and the *4th International Symposium on Ciliate Biology* (ISCB), hosted by *Acharya Narendra Dev College, University of Delhi*. This gathering of esteemed scholars, researchers, and professionals from around the world promises to be an enriching and intellectually stimulating experience.

As the Chairperson of the Governing Body of Acharya Narendra Dev College, I am immensely proud of the hard work and strides our institution has made towards imparting scientific knowledge and hands-on research training. Our commitment to excellence in education and research has been the cornerstone of our journey. Hosting events like the conference synergizing INSCR and ISCB with its national and international partners underscores our dedication to fostering a culture of innovation and collaboration. Keynote addresses, paper presentations and workshops are planned to explore the latest trends, challenges, and breakthroughs in diverse research fields of the soil ecosystem and its components. It is our sincere hope that this conference will serve as a platform for fruitful discussions, knowledge exchange, and networking opportunities for all participants.

I extend my heartfelt gratitude to the organizing committee, sponsors, and volunteers for their tireless efforts in making this event possible. I would also like to express my sincere appreciation for the distinguished speakers and participants for their valuable contributions and insights.

In closing, I wish everyone a productive and memorable experience at the 8th International Conference of Indian Network of Soil Contamination Research (INSCR) and the 4th International Symposium on Ciliate Biology (ISCB). May this gathering inspire new ideas, collaborations, and discoveries that will advance current knowledge, provide solutions that ameliorate soil health and motivate future researchers among the students and participants!

Jai Hind.

(Sudeshna Mazumdar-Leighton)

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विकसित भारत अभियान

CO-PATRON

DEV BHOOMI
— UTTARAKHAND —
UNIVERSITY
UUS ESTD 2005



Message

Dear Esteemed Participants,

Greetings from Dev Bhoomi Uttarakhand University!!!

It is with great pleasure and excitement that I extend my warmest welcome to all participants of the 8th Annual International Conference of the Indian Network for Soil Contamination Research (INSCR) and the 4th Annual International Symposium on Ciliate Biology (ISCB). As a co-patron of this prestigious events, it is an honor to address such a distinguished gathering of researchers, scientists, scholars, and practitioners.

The theme of this year's joint conference, "Exploring the Microbial World: From Human Health to Environmental Sustainability," encapsulates the profound significance of our collective efforts in understanding and harnessing the power of microbes for the betterment of humanity and our planet. In our quest to unravel the mysteries of the microbial world, these conferences serve as invaluable platforms for the exchange of knowledge, ideas, and innovations. Through interdisciplinary collaboration and scholarly discourse, we aim to advance our understanding of microbial ecosystems, their impact on human health, agriculture, and the environment, and the pivotal role they play in ensuring sustainable development. Over the course of the next few days, I encourage each of you to actively engage in the diverse array of sessions, workshops, and presentations that have been meticulously curated by the organizing committees. This is an opportunity not only to disseminate your research findings but also to gain insights from esteemed colleagues and experts in the field. Furthermore, I would like to express my sincere appreciation to the organizers, sponsors, and volunteers whose dedication and hard work have made this event. Your unwavering commitment to the advancement of science and education is truly commendable.

Wishing you all a stimulating and rewarding experience at the 8th Annual INSCR and 4th Annual ISCB International Conference.

Warm Regards,

Prof. (Dr.) Nabeel Ahmad
Dean, School of Allied Sciences
Dev Bhoomi Uttarakhand University, Dehradun

2024 INSCR

CO-PATRON

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UNIVERSITY OF DELHI
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Phone : 27667706, Fax : 27667447
E-Mail : principal@ramjas.du.ac.in
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Message

Greetings from Ramjas College!

It gives me immense pleasure to welcome you all to the 8th International Conference of Indian Network for Soil Contamination Research (INSCR) and 4th International Symposium on Ciliate Biology (ISCB). The conference entitled **'Exploring the Microbial World: From Human Health to Environmental Sustainability'** has been organized by University of Delhi, Acharya Narendra Dev College, Phixgen Pvt. Ltd. and INSCR. Ramjas College faculty and students are happy to be associated with the elite gathering. The conference focuses on different applications of microbes in agriculture, industries, food production but more importantly in advancing human health and ensuring environmental sustainability. The most interesting part of the conference is a special session on "Women in Science" that has been kept to celebrate the hard work and dedication of women in the scientific field.

I hope that these days of engagement with INSCR and ISCB Conference-2024 leaves all the participants with knowledge, rewarding memories and enriched enthusiasm for pursuing career in the Microbial World. As we convene to exchange our ideas and share insights of the microbial world, we must remain committed to harness the potential of microbes for betterment of human race and protection of our planet.

Hardeep Kaur

Prof. Hardeep Kaur
Principal (Acting)
Ramjas College

Participating Institutes

स्वामी श्रद्धानन्द महाविद्यालय
(दिल्ली विश्वविद्यालय), अलीपुर, दिल्ली-110036
Swami Shraddhanand College
(University of Delhi), Alipur, Delhi-110036

Ref. No. ...SSC/Adv:60/2023-24/2213

Dated.....11/03/2024....

Prof. Rup Lal,
INSA Senior Scientist,
Acharya Narendra Dev College,
University of Delhi



Dear Prof. Rup Lal,

It gives me immense pleasure to be associated with Indian Network for Soil Contamination Research (INSCR) and ANDC, particularly for this International Conference on "Exploring the Microbial World: Human Health and Environmental Sustainability" and 4th International Symposium on Ciliate Biology. I am delighted that SSNC is given the opportunity to be a part of the mega academic event. Microbes are ubiquitous and form an important component of the biological world. Their diverse roles are well known but still much more needs to be explored specially for human well- being and environmental sustainability. Intelligent use of microbes can solve numerous problems related to human health and environment. The conference will throw light on the microbial world for human welfare through the talks of renowned researchers. It will be a great platform for exchange of research ideas and knowledge and will surely be an enriching experience to all the participants. My best wishes for the successful conference!

(Prof. Parveen Garg)
Principal

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Professor Bijayalaxmi Nanda
Principal, Miranda House, University of Delhi

Miranda House is honored to be associated with the 8th International Conference and 4th International Symposium of Ciliate Biology under the theme "Exploring the Microbial World: From Human Health to Environmental Sustainability." This significant gathering, organized in collaboration with the Indian Network for Soil Contamination Research (INSCR), University of Delhi, Acharya Narendra Dev College, and phiXgen, marks a pivotal moment for interdisciplinary dialogue and exploration in the realm of microbiology.

As we convene to delve into the intricate dynamics of ciliate biology, we embark on a journey that spans from understanding the fundamental mechanisms of microbial life to addressing pressing global challenges concerning human health and environmental sustainability. The field of microbiology continues to unfold new dimensions, offering profound insights into the interconnectedness of life forms and ecosystems. Through our collective efforts, we strive to unravel the mysteries of ciliate biology and harness this knowledge for the betterment of society.

I commend the organizers, participants, and collaborators for their dedication and commitment to advancing scientific inquiry and fostering collaboration across borders and disciplines.

May this conference be a platform for fruitful exchanges, meaningful interactions, and groundbreaking discoveries that propel us towards a more sustainable and equitable future.

Professor Bijayalaxmi Nanda
Principal
Miranda House
University of Delhi

हंसराज महाविद्यालय

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मलकागंज, दिल्ली -110007
दूरभाष : 011-27667458, 27667747
ई-मेल : principal_hrc@yahoo.com
वेबसाइट : www.hansrajcollege.ac.in

HANS RAJ COLLEGE

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NAAC ACCREDITED 'A++' GRADE COLLEGE

Message

It brings me great joy to announce the collaborative effort of the Indian Network for Soil Contamination Research (INSCR) and the International Symposium on Ciliate Biology (ISCB) as they come together to host their 8th and 4th Annual International Conferences, respectively, with Hansraj College serving as one of the esteemed organizers. This year, the conference is centered around the theme "Exploring the Microbial World: From Human Health to Environmental Sustainability" and is scheduled to take place from April 2nd to April 5th, 2024, at the prestigious University of Delhi. This event promises to provide valuable insights into the microbial world and the crucial study of environmental sustainability, fostering a global platform for discussion on recent advancements in the field.

The recent pandemic has underscored the significance of understanding the microbial realm, and it is heartening to witness initiatives aimed at enhancing microbial literacy by scientists both within Bharat and internationally. Hansraj College is privileged to partner in the 8th International Conference of the Indian Network for Soil Contamination Research (INSCR) and the 4th International Symposium on Ciliate Biology. As educational institutions increasingly pivot towards a research-oriented paradigm, I am pleased to note that the themes of the Pre-conference workshops align closely with the prevailing circumstances.

Renowned for its state-of-the-art infrastructure catering to the educational and research needs of its students and faculty, Hansraj College consistently encourages student engagement in research endeavors and conference participation, often hosting distinguished speakers in regular seminars. Consequently, this conference presents an ideal platform for students to interact with esteemed national and international speakers of repute.

I extend my heartfelt congratulations and best wishes to all members of the organizing committee, as well as to every student actively participating, for the resounding success of this conference.

Prof. (Dr.) Rama
Principal

Participating Institutes

किरोड़ीमल कॉलेज
दिल्ली विश्वविद्यालय, दिल्ली-११०००७
KIRORI MAL COLLEGE
University of Delhi, Delhi-110007
NAAC Accredited A++ 3.54 CGPA, CYCLE 2 NIRF RANK 9



Professor Dinesh Khattar
Principal, Kirori Mal College

It gives me immense pleasure to write this foreword for the book of abstracts to be presented at the 8th International Conference of Indian Network for Soil Contamination Research (INSCR) and 4th International Symposium on Ciliate Biology on "***Exploring the Microbial World: From Human Health to Environmental Sustainability***" jointly organized by University of Delhi, Acharya Narendra Dev College and PhixGen Pvt. Ltd. under the aegis of INSCR from 3rd to 5th April, 2024.

This event targets researchers, professionals, educators, and students to share innovative ideas, issues, recent trends, and future directions in health, agriculture, and environmental sciences. The conference is preceded by two pre-conference workshops on "*Scientific Writing and Communication*" and "*Genomics, Metagenomics & Bioinformatics in Microbial Ecology*". Young students and researchers will be given hands-on training in various tools used in data analysis.

While the conference has 10 enriching scientific sessions, two special sessions on "Science and Society" to propagate microbial literacy and "Entrepreneurship in Innovative Sciences" are the major highlights. I am pleased to note that researchers and renowned scientists from different parts of the country and abroad are presenting their research.

This conference would greatly benefit researchers, students, and faculty. Young scientists and faculty will find the contents of the proceedings helpful in setting roadmaps for their future endeavors. I wish you great success at the International Conference of INSCR and ISCB.

Dinesh

(Prof. Dinesh Khattar)

Participating Institutes

देशबंधु महाविद्यालय

(दिल्ली विश्वविद्यालय)

NAAC मान्यता A++ प्राप्त संस्थान (CGPA 3.65), एनआईआरएफ 2023 (कॉलेज श्रेणी) 17वाँ स्थान

Deshbandhu College

(University of Delhi)

NAAC Accredited A++ Institute (CGPA 3.65),NIRF 2023 (colleges category) 17th Rank.



Professor Rajendra Kumar Pandey
Principal, Deshbandhu College

Deshbandhu College is known for providing a pedestal to brilliant minds and caters to their interests. The College boasts of a dedicated team of teachers who not only have expertise in their respective fields but also ensure guidance and mentorship throughout a students' academic journey. It fosters an environment for extracurricular activities with a vast number of societies and events. Its rich history and commitment to academic innovation make it a premier institution for academic and extracurricular excellence.

I would like to express my sincerest salutations to all the attendees as we converge at the 8th International conference of INSCR (Indian Network for Soil Contamination Research) and 4th International Symposium on Ciliate Biology (ISCB). We are here today, United by a common goal to discuss and pave the new paths in the soil contamination research. Our collective expertise and dedication in the field of microbial world can help us explore healthy microbiome for human welfare.

The significance of this conference cannot be overstated. It stands as a testament to the power of collaborative efforts and interdisciplinary dialogue in driving forward the wheel of Microbial World's as we know that, microorganism play an immense role in the development of bioactive compounds, fermentation, bioremediation, waste management, biofuel generation, industrial & Agricultural products, education research and much more.

This symposium provide a Platform for the ciliate interest group to exchange information, present latest research findings and establish collaborations and also provide networking opportunities for students wishing to take up doctoral or postdoctoral research on ciliates. Once again, welcome, and let's make this conference a memorable and impactful one.

Welcome to INSCR & ISCB-2024

27/03/24

(Prof. Rajendra Kumar Pandey)

Principal

Participating Institutes

BHASKARACHARYA COLLEGE OF APPLIED SCIENCES

UNIVERSITY OF DELHI

J329+339, Dabri Dwarka Rd, Phase 1, Sector 2 Dwarka, Dwarka, New Delhi, Delhi, 110075



MESSAGE FROM PRINCIPAL'S DESK

PROF. AVNEESH MITTAL
PRINCIPAL
BHASKARACHARYA COLLEGE OF APPLIED SCIENCES, DU

Warm Greeting to all!

It gives me immense pleasure to welcome you all to "8th International Conference of Indian Network for Soil Contamination Research (INSCR) on "Exploring the Microbial World: Human Health and Environmental Sustainability" & 4th International Symposium on "Ciliate Biology" to be held from 2nd to 5th April, 2024.

The notion of sustainable development is based on the premise that humans should be able to fulfill their fundamental requirements while also guaranteeing that future generations can meet their own. Sustainable development aims to strike a balance between economic, environmental, and social concerns. In this view, microbes, which are critical to the survival of life on Earth, can play a significant role. Although most people focus on microorganisms' disease-causing powers, there are various good activities that microbes perform in the environment, necessitating a careful exploration of the microbial world, which may contribute significantly to sustainable development.

This conference, in my opinion, covers all important worldwide aspects of microbiology. If society is sufficiently informed about the ways that microbes can affect our lives and if microbes are used intelligently, then some significant problems facing the world today, such as food, health, well-being, and green energy, can be adequately taken care of. This platform will serve as a venue for the discussion of innovative ideas, issues, and current developments while emphasizing the importance of the microbiological world for sustainable development. Academics and academicians gather at the conference to advance knowledge on the topic. We anticipate having great conversations and exchanging findings with distinguished scientists from across the globe.

I wish you a successful conference on behalf of the whole organizing team.

Prof. Avneesh Mittal
Principal (Offg)

Participating Institutes

GARGI COLLEGE
UNIVERSITY OF DELHI
ACCREDITED WITH GRADE 'A+' BY NAAC



On behalf of the organising committee I extend a very warm welcome to all the participants for the upcoming 8th Annual International Conference of Indian Network of Soil Contaminated Research (INSCR),.Building on the success of previous meetings and learnings from the past distinguished speakers, the present schedule has experts who are the best in their fields. I am confident that you can look forward to sessions that are deeply enriching and stimulating. The organisers are committed to contributing to our understanding of the environment and especially soil which is a critical component of the natural system and contributor to human well-being and the important role the microbes play in its modulation. The pertinent topic of Exploring the Microbial World: Human Health and Environmental sustainability also includes the 4th International Symposium on Ciliate Biology which will enhance our understanding and contribution to work towards sustainable goals.

I add my best wishes for a successful conference and extend a warm congratulations to the organizers who under the able leadership of Professor Rup Lal have planned this conference exemplified by the scientific vigour of INSCR.

Professor Sangeeta Bhatia
Officiating Principal
Gargi College, University of Delhi

Participating Institutes

Sri Guru Tegh Bahadur Khalsa College
(UNIVERSITY OF DELHI)
DELHI-110007

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Ref. No. .....

Dated 20 MARCH'24



Message from Principal's Desk

It is with immense pleasure, that I extend a warm welcome to all the distinguished guests, scholars and experts gathered here for the 8th Annual International Conference of Indian Network of Soil Contaminated Research, INSCR 2024 on ***"Exploring the Microbial World: Human Health and Environmental Sustainability"*** and 4th International Symposium on ***Ciliate Biology***. This conference aims to offer a platform for exchange of innovative ideas and knowledge, challenges and current trends for the delegates at different levels of expertise. The conference also offers opportunities to young Undergraduate and Post graduate students to learn about current environment challenges towards sustainability and its impact on human health.

Conference aims to emphasize upon achieving the 17 goals of sustainable development proposed in 2016 covering all strata of the society. Experts from their respective fields will also discuss the major challenges being faced by the humans such as drug resistance, emergence of new diseases, increase in food production and climate change and more at the conference.

With collaboration between Department of Zoology and multiple colleges from University of Delhi, I'm positive that many fruitful outcomes will be seen that will in turn substantiate our Sustainable Environment Goals. On the behalf of Sri Guru Tegh Bahadur Khalsa College, I congratulate Professor Rup Lal, President INSCR, all participating institutes, organizing committee and the team of volunteers. This conference will certainly catalyze insightful discussions, successful collaborations and pave the way for further. I wish everyone great success and hope they will learn and benefit from this conference and set a roadmap for their future research.

Prof. Surinder Kaur
Acting Principal

Participating Institutes

शिवाजी महाविद्यालय
SHIVAJI COLLEGE
UNIVERSITY OF DELHI
ACCREDITED BY NAAC WITH 'A' GRADE
DBT STAR COLLEGE SCHEME



Dear Delegates & Participants,

It gives me immense pleasure to welcome you all 8th Annual International Conference of the Indian Network of Soil Contaminated Research (INSCR) on "Exploring the Microbial World: Human Health and Environmental Sustainability" & 4th International Symposium on Ciliate Biology to be organized from 3rd to 5th April, 2024.

Exploring the microbial world is a fascinating journey that unveils the intricate relationships between microorganisms, human health, and environmental sustainability. Microbes, including bacteria, viruses, fungi, and archaea, play crucial roles in various ecosystems and have a profound impact on both our well-being and the health of the planet. For example, the balance of gut microbiome is linked to overall health, influencing aspects such as the immune system, metabolism, and even mental well-being. These microbes in the gut aid in digestion, nutrient absorption, and the synthesis of essential vitamins.

Microorganisms contribute to the development and regulation of the immune system. Some microbes have been harnessed for the development of vaccines, antibiotics, and other medical treatments. Understanding microbial interactions is critical for preventing and treating infectious diseases. Microbes are utilized in biotechnological processes, such as the production of pharmaceuticals, enzymes, and biofuels. Advances in genetic engineering enable the manipulation of microbes for therapeutic purposes. Microorganisms are involved in the production of biofuels. Harnessing microbial activities for energy production can contribute to a more sustainable and environmentally friendly energy landscape.

To facilitate the health conditions of the soil to the stakeholders (farmers) through comprehensive sampling for soil health card on 12 parameters namely N,P,K (Macro-nutrients); S (Secondary- nutrient); Zn, Fe, Cu, Mn, Bo (Micro - nutrients); and pH, EC, OC (Physical parameters). Based on this, the SHC will also indicate fertilizer recommendations and soil amendment required for the farm.

I am sure this conference will provide an enriching platform for all stakeholders involved. I on behalf of Shivaji College, wish a grand success to the event and appreciate the efforts of all members of the organizing committee for holding this conference meticulously.

Prof. Virender Bhardwaj
Principal

Participating Institutes



HC HINDU COLLEGE, DELHI | CELEBRATING 125 YEARS *Steered by the past, Moulding the future*

Message from Principal, Hindu College

It gives me great pleasure to be associated with INSCR and other partnering Colleges in organising the 8th International Conference of INSCR and the 4th International Symposium on Ciliate Biology dealing with Exploring the Microbial World: From Human Health to Environment sustainability. Hindu College, in partnership with various International collaborators has been helming various projects on Green Chemistry, and, to be associated with INSCR in alleviating environmental contamination with microbial intervention, will greatly help in the College's resolve to play an important role in sustainable development and protection of the environment.

I wish all the best to all the organisers and participants in the Conference.

Prof Anju Srivastava
Principal
Hindu College



Hindu College, University of Delhi, Delhi-110007
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Participating Institutes

MESSAGE FROM THE CONFERENCE ORGANIZING SECRETARIES

With great pleasure and utmost enthusiasm, we would like to extend a warm welcome to all of the distinguished attendees of this prestigious 8th International Conference of INSCR (Indian Network for Soil Contamination Research) and 4th International Symposium on Ciliate Biology from April 03-05, 2024. This upcoming event has great potential as we get together to collectively explore and unravel the uncharted territories within the realms of scientific inquiry.

Expanding on the great success of our previous events, INSCR 2024 hopes to be an unmatched platform for promoting innovative conversations and progressive dialogues resonating under the guiding theme of 'Exploring the Microbial World-From Human health to Environmental Sustainability'.

We look forward to the convergence of ideas, viewpoints, and innovations from a wide range of eminent experts, seasoned academics, and experienced researchers. Your distinguished attendance and engaged involvement will add an unmatched depth and richness to this scholarly conversation. The carefully selected programme schedule is evidence of our dedication to offering outstanding networking opportunities along with thought-provoking workshops. In this dynamic environment of academic interchange, which serves as the backdrop for our conference, our common goal of scientific innovation and exploration finds the ideal platform.

Our sincere thanks and deep appreciation go out to all of the hardworking organizers and contributors, whose tireless efforts and invaluable contributions have painstakingly moulded and guided the path of this momentous occasion.

We eagerly await an exciting and thought-provoking conference where world-renowned scientists and thinkers will come together to exchange groundbreaking research, present fascinating findings, and jointly push the frontiers of knowledge in the vast domains of Exploring the Microbial World.
Looking forward to our rendezvous at INSCR 2024 and eagerly awaiting the commencement of this groundbreaking scientific research and deep knowledge sharing voyage.

Organizing Secretaries:

Prof. Seema Makhija
Dr. Utkrash Sood
Dr. Mansi Verma
Prof. Pooja Bhagat
Dr. Princy Hira
Dr. Rajeev Singh
Dr. Jasvinder Kaur
Dr. Pushplata

ABOUT

Organizing

INSTITUTES

INSCR 2024





Acharya Narendra Dev College, University of Delhi

Acharya Narendra Dev College (ANDC), constituent college of University of Delhi, stands as a beacon of excellence in higher education, known for its unwavering commitment to academic rigor, holistic development, and societal engagement. Founded in 1991, ANDC has emerged as a premier institution dedicated to nurturing young minds and fostering a culture of innovation and inquiry. Located in the heart of Delhi, ANDC boasts state-of-the-art infrastructure and facilities conducive to learning and research. The college offers a diverse array of undergraduate and postgraduate programs across various disciplines, including Sciences and Commerce, catering to the academic interests and aspirations of a dynamic student body.

At ANDC, academic excellence is complemented by a vibrant campus life enriched with co-curricular activities, sports, and cultural events. The college provides a nurturing environment that encourages students to explore their passions, hone their talents, and develop essential life skills, preparing them to thrive in an increasingly complex and interconnected world. Driven by a dedicated faculty comprising eminent scholars, researchers, and practitioners, ANDC is committed to fostering intellectual curiosity, critical thinking, and ethical leadership among its students. Through innovative teaching methodologies, interdisciplinary research, and industry collaborations, the college equips students with the knowledge, skills, and perspectives necessary to excel in their chosen fields and make meaningful contributions to society.

Beyond academics, ANDC is deeply invested in community outreach and social responsibility. Through various outreach programs, community service initiatives, and partnerships with local organizations, the college actively engages in addressing societal challenges and promoting sustainable development, embodying its ethos of academic excellence with a purpose. As a proud member of the esteemed University of Delhi, Acharya Narendra Dev College continues to uphold its legacy of excellence, innovation, and service, inspiring generations of students to realize their full potential and become responsible global citizens poised to shape the future.



Ramjas College, University of Delhi

The College Campus is among the best in Delhi with a state of the art Library, Computer section, among other facilities. Founded in 1917 by the great educationist and philanthropist, Rai Kedar Nath, Ramjas College is one of the oldest colleges of Delhi. Beginning from the humble precincts of Darya Ganj in Old Delhi, the College today boasts of a spacious campus, state-of-the-art infrastructure and an esteemed faculty of scholars trained at leading universities in India and abroad.

At Ramjas, we believe in holistic education that goes beyond achieving academic excellence, and vocational training. Our philosophy is to realize the overall intellectual, creative, cultural and socio-political growth and development of both the students and the college community in its entirety. The College invites all students irrespective of gender, caste, religion and physical challenges to make us a rich and varied community. The College offers a wide range of courses, extra-curricular activities and technologically advanced facilities accessible to the faculty, the students and the support staff. Here, each individual is encouraged to step beyond the confines of academic and administrative disciplines to explore and intervene in the larger interests of the Ramjas Community that thrives on participation and the desire to venture into newer vistas.



Swami Shraddhanand College, University of Delhi

Swami Shraddhanand College, a constituent College of Delhi University, is run under the trusteeship of Delhi Govt. It is a co-educational institution and imparts instructions in various subjects at both undergraduate and post-graduate levels.Situated in the sylvan ambience of North Delhi, the College has completed 54 years of its existence. From the humble beginning in the Gandhi Ashram building in Narela, the college is now one of the premier institutions of Delhi University. It is equipped with qualified teaching staff, specialized laboratories and adequate library facilities.

The college has extensive playgrounds, which provide an excellent opportunity for budding sportsmen and athletes to participate in various games and sports and to improve their skills and capabilities. Scholarship's and freeships are given to deserving students. Every year a number of prizes are awarded to students on their meritorious achievements in academic and extra-curricular activities.

The students societies / associations play a vital role in improving the academic environs of the college. For each subject, there is a society to stimulate the interest's of the students in the subject and establish its interlinking with the society at large. The societies / associations sponsor lectures, seminars, exhibitions etc., and undertake programmes and activities to make the subject more interesting and more relevant for societal need



Hansraj College, University of Delhi

In the sacred memories of Maharshi Dayanand Saraswati and Mahatma Hansraj who spent their magnificent lives emphasizing the importance of knowledge, The college was founded by the D.A.V. College Managing Committee on 26th July, 1948. This college is one of the largest constituent colleges in Delhi University, dedicated to teaching and research. It has highly qualified academicians who impart education in Science, Commerce, and Arts at undergraduate and graduate levels to more than 6000 students.

With its integrity, encouraging atmosphere, and a vast variety of extracurriculars, the college has consistently demonstrated outstanding performance in all fields. Over the years, the college has built up an impressive infrastructure. It includes a well- stocked Central Library, Departmental Libraries for science subjects and a Book Bank for needy students. The college has six Computer and eighteen Science Laboratories. Its sports facilities include a vast sports field which includes a football field and a basketball court, an indoor sports complex and the only Electronic Shooting Range in the entire University.

Hansraj College has also always kept the needs of its students in frontier and has provided scholarship, guidance programs, mentorship to all students to guide them into their futures.

Hansraj College, while it retains inspiring facets of its proud history, with an equally sharp gaze it looks ahead, assimilating the exciting world of new knowledge as it unfolds in front of it, holding the promise of an experience seeped with exhilarating learning and holistic growth for all those who enter its portals. It has excellent faculty and a wide number of research students, who have been working on phenomenal new works in the future-designed laboratories present in the campus.

And lastly, the quiet, serene ambiance of a lovely campus surrounded by lush green fields and a gorgeous edifice touches your soul as you reach the doors of this institution. Hansraj will never fail to awe one.



Sri Guru Tegh Bahadur Khalsa College, University of Delhi

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. The College is named after Ninth Guru - Sri Guru Tegh Bahadur, who sacrificed his life to uphold secular values, and is an institution with cosmopolitan environment and progressive outlook.

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 19 undergraduate programmes, 12 postgraduate programmes, one postgraduate diploma, 4 undergraduate diplomas, and 8 certificate language courses, making a total of 44 programmes. The teaching-learning process is enriched and made productive by rich experience of teachers and availability of up-to-date resources to students. The process is monitored by Departmental Monitoring as well as by Academic Affairs Committee of the College and the Principal, to make it achieve the learning objectives of the programmes and provide best motivation and experience to learners.



Miranda House, University of Delhi

Miranda House, a renowned institution in the landscape of women's education, has consistently been at the forefront of academic excellence. It is an institution that epitomizes the highest standards of learning and has been recognized for its outstanding contributions to education in India. Our accolades include the prestigious All India Rank One among colleges under the National Institutional Ranking Framework (NIRF) for seven consecutive years from 2017 to 2023, accreditation with Grade A++ by the National Assessment and Accreditation Council (NAAC), and the coveted Star College status awarded by the Department of Biotechnology, Government of India. Established on March 7, 1948, Miranda House, under the visionary leadership of Sir Maurice Gwyer, has played an instrumental role in shaping the history of women's education in India.



Bhaskaracharya College of Applied Sciences, University of Delhi

Bhaskaracharya College of Applied Sciences, named in honor of the renowned 12th-century mathematician, was established in October 1995. With a vision to provide quality education and foster holistic development, the college has been a beacon of academic and professional excellence. In a remarkably short time, the college has garnered prestigious recognition by achieving a NIRF ranking of 22 in college category and receiving an A++ accreditation from NAAC in its reaccreditation cycle 2023

The college offers eleven programs in various disciplines of sciences. A strong emphasis is also laid on extracurricular activities with a diverse array of ECA societies, sports teams, and cultural groups that empower students to explore their passions proving that college is not just a place of education but a vibrant community, a hub of knowledge, and a nurturing ground for future leaders, thinkers, and innovators.

Bhaskaracharya College of Applied Sciences is committed to doing its bit to safeguard the environment. College boasts of a green campus and remains at forefront of adopting future technologies while keeping environment protection and sustainability at the center. Timely environment audits are undertaken and frequent awareness campaigns and seminars are carried out to sensitize students towards conservation efforts. With facilities like 30 KVA solar plant, in house paper recycling unit, bio-toilet, rain water harvesting, dedicated decompost machine, dedicated disposal pits etc. the college ensures its contribution towards leaving a cleaner environment for our youth.



Gargi College, University of Delhi

Gargi College was established in the year 1967 and is a leading South Campus college of the University of Delhi. It is a college for women and offers education in Arts and Humanities, Commerce, Science and Education.Gargi College was named after an enlightened woman named Gargi, figuring in the Brihadaranyaka Upanishada of the Vedic Age. She emerges as an intelligent and bold person embodying the spirit of inquiry juxtaposed with faith as is shown by her penetrating and challenging questions to the great sage Yajnavalkya. In the Upanishad Gargi seems to represent the intellectual potential of the race of Homo sapiens, which continues to manifest itself , in quest of ever-widening fields of knowledge.



Dev Bhoomi Uttarakhand University

Marching with theme of “सिद्धिर्भवति कर्मजा” (success comes with hard work) the rise of Dev Bhoomi Group of Institutions as Dev Bhoomi Uttarakhand University, brings a proud legacy spanning close to two decades. Dev Bhoomi Uttarakhand University encompasses 11 schools including Allied Sciences, Agriculture, Engineering, Management, Pharmacy, Hotel Management, Architecture and Ayurveda and running more than 120 programs. The vision of the university is to foster a society of lifelong learners with the ability of critical thinking, entrepreneurship, leadership and to create an environment for discovery, innovation, discourse, and expression. We at DBUU constantly encourage the next generation to grow, rise and shine like never before.



Shivaji College, University of Delhi

Shivaji College is a constituent college of University of Delhi accredited with grade 'A' by NAAC. It was established in 1961 by Hon'ble Dr Panjabrao Deshmukh, Union Minister for Agriculture and a renowned social activist and farmer-leader. The college caters to 4099 students and have 184 permanent and 2 ad-hoc faculty members. In 2019, Shivaji College was also awarded the financial grant under the prestigious DBT Star College Scheme, by the Department of Biotechnology, Government of India. The college also has Dr. Ambedkar Centre of Excellence (DACE) that provides specialized coaching to the scheduled caste students for the Civil Services examination conducted by the Union Public Service Commission.

The college offers twenty six undergraduate courses in Science, Commerce, Humanities and linguistics, a self-financing course in Bachelors in Business Economics, three post-graduate courses, and add-on courses in German and French. Several faculty members are engaged in major and minor interdisciplinary research projects and more than 20 Ph.D. students have been registered under our faculty members in the past 5 years.

The college lays great emphasis on experiential learning through field visits, summer training programs, institutional, laboratory and industry visits, seminars, conferences and workshops. The college has National Service Scheme (NSS) and National Cadet Corps (NCC) involved in social outreach. Shivaji College believes in holistic growth and development of its students through their participation in different societies and cells. The Women's Development Cell (WDC) strives to contribute towards gender equality and women empowerment and honours individuals working towards women's empowerment at grassroot level and confers on them the Jijabai Achievers Award every year. The Cultural Committee nurtures students with special interests in photography, painting, theatre, dance and music, etc. The Entrepreneurship Development Cell promotes practical application of entrepreneurial skills towards future business opportunities. The SPADE combines theory and applications of economics for practical use in social development. The Shivaji chapter of Enactus hones students with skills for innovation and business principles.



Deshbandhu College, University of Delhi

College was established in the year 1952 by the Ministry of Rehabilitation, in the memory of Late Lala Deshbandhu Gupta - a veteran freedom fighter. Guided by the mantra "Karmanyevadhikaraste" - our motto, the college continues to grow both in size and stature. Today, Deshbandhu is a fully maintained constituent college of University of Delhi and has the distinction of being the oldest and the largest co-educational institution in South Delhi promoting Arts, Commerce and Science courses. To encourage self-learning and to satisfy the thirst for knowledge of the students, the college library has a massive collection of more than 105,000 books, a host of journals and magazines, a spacious reading room, a separate floor for teachers and research scholars, and a book bank section which lends text books to needy students. The college has created a spacious “Web Access Centre” in which 80 computers and servers provided by the Delhi University are housed. The servers have optical fibre connectivity and the college campus is Wi-Fi enabled. In addition there is a dedicated facility for use of computers and Internet connectivity in the library. The college promotes organization of seminars, lectures, workshops, sports activities, N.S.S., N.C.C. and other co-curricular activities. Every student finds his/her expression through College students’ union. A number of scholarships and financial aid is provided to meritorious and needy students every year. The Career- counselling and Placement Cell of the college provide suitable employment opportunities to graduating students through campus recruitment. The College is well-equipped with all infra-structural/academic support that a student requires. The College and the faculty offer a holistic environment to the student and gives preference to their psychological/academic needs. This creates an informal, close knit, friendly and supportive environment that encourages hard work and academic achievement.



Kirori Mal College, University of Delhi

Kirori Mal College, an institution of academic excellence, established in 1954, that has always strived to, and successfully maintained its place as one of the finest within the University of Delhi. We at Kirori Mal believe in providing for our students an environment rich in knowledge and supportive of their extracurricular interests. The college encourages a quest for knowledge that is rooted in an ethical understanding of the world that we inhabit and this enthusiasm for learning along with a desire to evolve into socially responsible beings is reflected not only in the academic atmosphere but also visible in the field of extra-curricular activity. Our tradition of excellence in theatre, art and music only adds to the richness of the academic fabric of the college. You will encounter the unique combination of social activism, creativity and learning in every discipline and every corner of this institution. Over the years, the college has built up an impressive array of academic facilities such as a fully computerized library, a state of the art computer center and an active placement cell. Our endeavor is to make individuals more mature, responsible and socially aware...



Deen Dayal Upadhyaya College , University of Delhi

Deen Dayal Upadhyaya is a constituent college of the University of Delhi. The Government of National Capital Territory of Delhi established the college in the year 1990 in Karampura. The college receives 100% grant from the Govt. of NCT of Delhi and is recognized under 2 (f) and 12 (b) of the UGC Act. We offer nine under-graduate Honours programes in Computer Science, Electronics, Physics, Chemistry, Botany, Zoology, Mathematics, English, Commerce and Bachelor of Management Studies. Further, we also run bachelor's programme in physical science, Life Science, mathematical science and Bachelor in Arts. We also offer Add-on courses in Russian Language and Effective Communication and Personality Development through Theatre (ECPDT) which are very popular amongst students. Recently, we have started a certificate course in French.

Teaching, Learning and Evaluation - Our faculty comprises the backbone of our curriculum delivery system. The college has 94 permanent and 35 temporary (ad hoc) teachers and 18 Guest faculty members. We are extremely cautious in recruiting our faculty. Three of our faculty members have received "distinguished teacher" awards. Each department keeps organizing talks by experts and distinguished resource persons. Our faculty members, including the Principal, have been members of the Academic and Executive councils, Boards of Research Studies, Departmental Committees of Courses as well as syllabi drafting committees. The student strength is 2531 of which 1422 male and 1109 females. Further, the implementation of various quotas ensures that our classrooms are fairly diverse and inclusive. Eighteen teachers have been involved along with sixty students in Innovation Projects sanctioned by the University of Delhi during the last two years. Many of them are Ph. D supervisors and supervising independently and/or jointly research scholars. The college has created a space for setting up a multi-disciplinary research centre with financial support from UGC and other agencies and has space for dedicated research centres for each department.



Hindu College , University of Delhi

Hindu College started with a humble beginning in 1899 and has recently achieved the remarkable milestone of completing 125 years of glorious legacy. It has seen enviable growth over the years which makes it not only one of the most distinguished co-educational institutions of our country, but also the college of first choice in Delhi. It is accredited grade A++ by NAAC, is ranked as 2nd best college in NIRF All India Ranking 2023, is ranked 1st in Arts and Science streams and 2nd in Commerce stream in India Today Best Colleges Ranking, 2023. It offers undergraduate and postgraduate programs in sciences, humanities and commerce. The college has produced many notable alumni in the fields of law, economics, science, psychology, business, philosophy, literature, media, cinema, military, sports and politics.

Hindu College was selected by MHRD for setting Hindu Innovation Council where student-teacher teams work with new innovative ideas. These initiatives are further enhanced through the newly established Research Centre which has more than 20 laboratories with advanced instruments like GCMS, FITR, DSC etc. Hindu College is a Star College under the Star College Scheme, sponsored by the Department of Biotechnology (DBT), Government of India. Hindu College also has a unique ‘Faculty-student Undergraduate Interdisciplinary Innovation Project Scheme’ under which various projects amounting to about Rs. 35 lakhs funded entirely by the college management have been sanctioned. Hindu College also has International Collaboration with NUS, Singapore for prestigious student exchange programs and unique student summits.



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BIONOTES

2024 NSCR

SPEAKERS
INTERNATIONAL

Plenary Speaker



Rino Rappuoli

Scientific Director, Fondazione Biotecnopolo di Siena, Italy

Rino Rappuoli has more than 40 years in the vaccines field. He was CSO at Chiron (2003-2006), Head of vaccine R&D for Novartis (2006-2015) and Chief scientist and head external R&D at GSK (2015-2022). Presently he is the scientific director of the Fondazione Biotecnopolo di Siena, the Italian Institute for Pandemic Preparedness. He is also Honorary Professor, Imperial College, London, and Senior Professor, University of Siena. He is elected member of US National Academy of Sciences (NAS), the American Institute for Medical and Biological Engineering (AIMBE) the European Molecular Biology Organization, the Royal Society of London, and President, International Union of Microbiological Societies. He has published 801 works in peer-reviewed journals.

He introduced novel scientific concepts like genetic detoxification, cellular microbiology, reverse vaccinology, and pangenome. He has developed licensed vaccines among which for acellular pertussis, meningococcus C, and meningococcus B. Dr. Rappuoli is among the world scientific leaders dedicated to the sustainability of global health.

Invited Speakers

Kenneth Timmis



Professor of Microbiology, Technical University of Braunschweig, Germany

B. Sc. (1967) and Ph.D. (1970), University of Bristol, UK; Habilitation in Microbiology and Molecular Biology, Free University Berlin (1979). Postdoc Ruhr University, Bochum (1970-2), Yale University, New Haven (1972-3), Stanford University, Palo Alto (1973-6). Head, Plasmid Group, Max Planck Institute for Molecular Genetics, Berlin (1976-81). Professor, Dept. of Medical Biochemistry, University of Geneva (1981-88). Director, Division of Microbiology, GBF- National Centre for Biotechnology/HZI-Helmholz Centre for Infection Research, Braunschweig (1988- 2011) and Professor, Institute of Microbiology, Technical University of Braunschweig (1988-present,Emeritus since 2011). Visiting Foreign Academician, Oxford Suzhou Centre for Advanced Research (from 2019). Member/Fellow: European Molecular Biology Organisation (from 1983), American Academy of Microbiology (from 1992), Royal Society (from 2008), European Academy of Microbiology (from 2009; President from 2025). Erwin Schrödinger Prize (2001). FEMS-Lwoff Award for Achievements in Microbiology (2023). Editor: Journal of Bacteriology (1987-97), Current Opinion in Biotechnology (1998-2006). Founding Editor-in-Chief: Environmental Microbiology (1998-2022), and Microbial Biotechnology (2007-2021).
Research focus: microbial genetics, microbial ecology, microbial pathogenesis, microbial biotechnology. 351 research papers in international journals practicing peer review; 5 books and book series; 53 book chapters; 49 commentaries/policy articles/editorials; 16 educational microbial humour articles. h-index 121. Current activities and interests: Founder and Chair of Council of the International Microbiology Literacy Initiative; microbial biotechnology for sustainable development; digital DIY primary healthcare

Vipin Chandra Kalia



Professor, Department of Chemical Engineering, Konkuk University, Seoul, Korea

His scientific interests are Microbial Biodiversity, Bioenergy, Genomics; Quorum sensing. He is a Fellow of the National Academy of Sciences (FNASc) and Fellow of National Academy of Agricultural Sciences (FNAAS). He served as Editor in Chief for the Indian Journal of Microbiology (SpringerNature) from 2013-2023. He has received fellowships from organizations in Denmark, France, Korea, the USA, Canada, etc. He is a life member of various Scientific Societies. He has more than 200 publications in Scientific Journals. He has Edited 16 Books. His Google Scholar Citations are 13505 with an h-index of 63.

Max Häggblom



Professor and Chair of the Department of Biochemistry and Microbiology at Rutgers University

He is an elected fellow of the American Academy of Microbiology and the American Association for the Advancement of Science and serves as Editor in Chief of FEMS Microbiology Ecology. His research interests are in microbial ecology and environmental biotechnology, with a focus in the bioexploration, cultivation and characterization of novel microbes including soils, sediments, marine sponges and animal intestinal tracts. The common theme is the “unusual appetites” of bacterial communities, such as the metabolism and detoxification of xenobiotic chemicals or natural products, respiration of rare metalloids, or life in the cold. Work in his laboratory aims to elucidate the physiology, ecology and phylogeny of these bacteria providing a foundation for applications that address the pollution problems facing impacted industrialized and urbanized environments.

Thulani Makhalanyane



Professor, Department of Microbiology and the School of Data Science and Computational Thinking at Stellenbosch University

Thulani Makhalanyane is a Professor in the Department of Microbiology and the School of Data Science and Computational Thinking at Stellenbosch University. He earned his Ph.D. at the University of the Western Cape in 2013 and his research focuses on understanding the ecology of microbial communities in extreme environments. He has coauthored over 80 publications in leading journals including Nature, Science, PNAS and The ISME Journal. Thulani serves on several editorial boards and is currently serves as Editor in Chief for Reviews and Perspectives of The ISME Journal and Senior Editor at mSystems. He also serves on national and international panels representing South Africa in bilateral discussions. Thulani was elected to the board of the ISME Society in October 2018. He is the Director of ISME’s Ambassador Program and is a member of the Executive Advisory Board.



William B. Whitman

Emeritus Professor of Microbiology, Department of Microbiology
University of Georgia

I received my Ph.D in 1978 from The University of Texas at Austin in the laboratory of F. Robert Tabita studying autotrophy in phototrophic bacteria. My postdoctoral studies were conducted in the laboratory of Ralph S. Wolfe at the University of Illinois at Urbana studying methanogenesis. When I started my own laboratory at the University of Georgia at Athens in 1982, we initially focused on developing genetic systems in the methanogenic archaeon Methanococcus as well the pathway of autotrophic CO2 assimilation. Since then, my research has focused on the physiology, systematics and ecology of environmentally important microorganisms. Of special interest is to understand the complete organism, from the biochemical mechanisms it uses to accomplish its day-to-day tasks of living to its interactions with other organisms and its environment. In this context, my work has focused on the methane-producing archaeon *Methanococcus*, DMSP metabolism in the marine bacterium Ruegeria, and the soil and estuarine microbiomes.

Systematics has also been a central part of my work. My laboratory developed one of the most popular methods for determination of the mol % G+C [Mesbah et al. 1989. Int J Sys Bacteriol 39:159-167] and helped describe more than twenty new species. From 1986-2001, I was Secretary of the International Committee on Systematics of Bacteria (ICSB) Subcommittee on the Taxonomy of Methanogenic Bacteria and coauthored its Minimal Standards [Boone and Whitman. 1988. Int J Syst Bacteriol. 38: 212-219]. From 1995-2001, I was an Associate Editor of the International Journal of Systematic Bacteriology. In 2000, I received the Bergey's Award from the Bergey's Manual Trust. In 2006, I joined the Bergey's Manual Trust and became the Supervising Editor of the Manual until 2019. My work as an editor of Bergey's Manual on the Systematics of Archaea and Bacteria has strongly informed my position on prokaryotic systematics. From 2014-2020, I served as Treasurer and member of the Executive Board of the ICSP, and I helped rewrite its statutes [Whitman et al. 2019. Int J Sys Evol Microbiol 69: 584-593].



Hans Richnow

Emeritus Professor, Department Isotope Biogeochemistry
Helmholtz Centre for Environmental Research - UFZ

Since 2004 he was Head of the Department Isotope Biogeochemistry and Head of the Centre for Chemical Microscopy – ProVIS Helmholtz Centre for Environmental Research – UFZ until retirement in June 2022. Now he is Emeritus and guest scientist at the UFZ and senior advisor at his company Isodetect (www.sisodetect.de). He studied Geology at University of Hamburg (Diploma in Geology 1986) and received his PhD (Dr. rer. nat.) in Geoscience at Faculty of Geosciences University of Hamburg in 1991. He complete his Habilitation in Geochemistry 1998 (University of Hamburg, Faculty of Geosciences). 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 350 articles and book chapters and belongs to the frequently cited scientist in Germany. (In Jan 2024 his h-factor was 63 and his work received more than 13.700 citations, source Web of Science, Thomson Reuters).
He is member of the editorial board of Journal of Contaminant Hydrology, Frontiers in Microbiology and frequent reviewer of national and international journals. He serves as 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 the development of stable isotope fractionation concepts for tracking the fate of chemicals in the environment.
- to the analysis of structure, function and activity of microbial communities governing biogeochemical processes.
- to the analysis of the spatial dimension of biogeochemical reaction (e.g. biofilms, metal corrosion, mineral microbe interaction, rhizosphere processes)



Jan Roelof van der Meer

Professor of Microbiology, University of Lausanne, Switzerland

Jan R. van der Meer is a microbiologist from the University of Lausanne in Switzerland. He was trained at the Agricultural University in Wageningen (Netherlands) and later worked at the Dutch Dairy Institute, as well as the Swiss Federal Institute for Aquatic Research, before moving to Lausanne.
His interests are the interactions of bacteria with toxic and polluting substances: how they adapt and how we may be able to deploy their capacities in cleaning up our environment.



Dev Raj Joshi

Associate Professor of Microbiology, Central Department of Microbiology in Tribhuvan University, Nepal

Dr. Joshi earned Masters' degree in Microbiology from Tribhuvan University, Kathmandu, Nepal and Ph D from University of Chinese Academy of Sciences, Beijing, China in Environmental Microbiology. He has over two decades' experience in research and academia. Dr Joshi's primary research interests include phylogenetic and functional microbial ecology of water and wastewater, environmental antibiotic resistance, wastewater-based epidemiology of bacterial and viral pathogens. However, he works on diverse aspects of microbiology using culture dependent and independent microbial molecular tools to study environmental and pathogenic microorganisms. Dr. Joshi has been awarded by "Nepal Vidya Bhusan" Class I and Class II. He is country ambassador of International society for Microbial Ecology since 2018. He chaired first and second edition South Asian Symposium on Microbial Ecology.
Publications:
https://scholar.google.com/citations?hl=en&scioq=Dev+Raj+Joshi&user=_QBeWZgAAAAJ



Chris Bowler

Research Director at the CNRS & Director of the Plant and Algae Genomics Laboratory at the *Institut de biologie de l'École normale supérieure* in Paris

He received his PhD from the University of Ghent in Belgium, followed by postdoctoral studies at the Rockefeller University in New York. In 1994 he established his own laboratory working on signaling in plants and marine diatoms at the Stazione Zoologica in Naples, Italy, and in 2003 he took up his current position in Paris. He has been a member of EMBO since 1995, received the CNRS Silver Medal in 2010, ERC Advanced Awards in 2012 and 2018 and the Grand Prix Scientifique de la Fondation Louis D de l'Institut de France in 2015. In 2016-2017 he was a Fellow at the Radcliffe Institute of Advanced Studies at Harvard University, USA. In 2018 he was elected member of the French Academy of Agriculture, and during the academic year 2020-2021 he held the annual chair as Professor in biodiversity and ecosystems at the Collège de France. His main research interest is the understanding of the response of plants and marine diatoms to environmental signals, through functional and comparative genomics. Since 2021 he is the scientific director of the Tara Oceans project to explore the biodiversity, ecology and evolution of plankton in the world's ocean. In 2023 he was elected member of the Accademia dei Lincei in Italy.



Gunjan Pandey

Senior Scientist at The Commonwealth Scientific and Industrial Research Organisation (CSIRO)

As a senior research scientist within the Industry Environment Program at CSIRO Environment, based in Canberra, my fervour lies in three captivating areas of research that span across diverse domains. Firstly, I'm immersed in applied genomics research, skillfully leveraging the potential of bioinformatics to expedite discoveries and drive applications. Next, my focus shifts towards harnessing the remarkable capabilities of insects as engineers, propelling circular economy endeavors that transform waste into invaluable resources. Lastly, my curiosity drives me to unravel novel gene-enzyme systems with the potential to catalyze a revolution in biotechnology. With these three passions interwoven, my commitment is firmly rooted in shaping a brighter future through the realms of science and innovation, creating impactful outputs across environment, health, food, and biosecurity domains.



Andreas Bechthold

Professor, Director of the Institute for Pharmaceutical Sciences at Freiburg University; Director of the Department of Pharmaceutical Biology and Biotechnology

He is the Director of the Institute for Pharmaceutical Sciences at Freiburg University; Director of the Department of Pharmaceutical Biology and Biotechnology (since 2001). Since graduating in pharmacy studies almost thirty years ago, Professor Andreas Bechthold has now an impressive list of engagements. He is a Professor of Pharmaceutical Biology and Biotechnology at the University of Freiburg, as well as the Dean of Study and member of the managing committee of the Faculty for Chemistry and Pharmacy at the University. He is also a member of both the German-French Ph.D. College ‘Membrane Proteins and Biological Membranes’, and the ‘Spemann Graduate School of Biology and Medicine’ at the University of Freiburg. He has published nearly 200 research articles, reviews and book chapters with nearly 10,000 citations.



Kalai Mathee

Professor of Molecular Microbiology & Infectious Diseases, Florida International University

Professor Kalai Mathee, MSc, PhD, MPH, renowned at Florida International University (FIU), is celebrated for her contributions to microbiology and influential role in academia. As the first FIU faculty inducted into the American Academy of Microbiology, Mathee, a Malaysian native, has achieved notable milestones. Her academic journey spans from the University of Malaya to a Ph.D. in Microbiology and Immunology from the University of Tennessee, Memphis, and a master's in public health from FIU. Mathee's career features several pioneering roles, including being the inaugural chair at FIU's College of Medicine and the first international editor of the Journal of Medical Microbiology. She became the first international Trustee and Council member of The Microbiology Society in January 2024. Her mentorship has impacted over 190 individuals, ranging from professors to middle-school students, contributing to over 170 publications and five patents. Recognitions for her mentorship include the Faculty Award for Excellence in Mentorship (2011) and the New England Biolabs Passion in Science Award (2014). Mathee has delivered over 150 lectures worldwide and engages actively in FIU's School of International and Public Affairs. She has been instrumental in establishing significant programs like the Global Health Conference and Consortium and has significantly contributed to the MLK forum. Mathee's global commitment to education and science is notable.

She was honored with the 2022 Microbiology Society Outreach Prize and has received prestigious awards, including the 2011 President's Council Worlds Ahead Faculty Award and the 2021 FIU Faculty Senate Service Award. Mathee's career epitomizes her dedication to the community within FIU and in the broader realms of microbiology and Tamilar studies. Her resilience, optimism, and perseverance underscore her transformative impact in academia and beyond.



Jana Jass

Professor of Microbiology at The Life Science Center, Örebro University, Sweden

Dr Jana Jass is a Professor of microbiology at The Life Science Center, Örebro University, Sweden since 2005 and Vice Dean of collaboration and lifelong learning. She received her PhD from Exeter University, UK on Pseudomonas biofilms, followed by a Postdoc at Oxford University UK and Umeå University Sweden. Her current research interests include the effects of environmental contaminants on microbe-host interactions and on the emergence and distribution of antimicrobial resistance in different environments. Prof Jass is also on the Board of Directors for the Federation of Microbiology Societies (FEMS), responsible for grants, and co-editor-in-chief of FEMS Microbes



Anil Koul

Professor of Translation Discovery at London School of Hygiene and Tropical Medicine

Prof Anil Koul is currently vice-president and head of discovery research at Global Public Health R&D unit of Johnson and Johnson. Anil is also a Professor of Translation Discovery at London School of Hygiene and Tropical Medicine where he has set up a laboratory to focus on TB translational medicine research. He is currently member of Board of Directors at Janssen Pharmaceutica NV, Belgium, a J&J's European subsidiary, where he has fiduciary responsibility. Anil's key achievement till date has been his role in discovery and development of Bedaquiline - the first drug to be approved in last 45 years for treatment of drug-resistant tuberculosis. Bedaquiline has been conditionally approved in over 64 countries and has reached more than 600,000 TB patients across the world and is on WHO's list of 'essential medicines" both for adult as well as pediatric TB. In 2020 Anil was awarded American Chemical Society's annual "Heroes of Chemistry" award for discovery and development of Bedaquiline. He was awarded in 2017 the 'Sun Pharma Research Award' and in 2004 "Swiss TB Prize" by society of pneumology (Switzerland) for his contributions. Anil was also a member of the J&J team that was awarded 2016's "Prix Galien French prize" for the discovery of Bedaquiline. Anil has published in leading scientific journals such as Nature and Science amongst others and holds more than 30 international patents. During 2017-2019 Anil served as Director of Council of Scientific and Industrial Research (CSIR) - Institute of Microbial Technology, a premier biotechnology laboratory of Ministry of Science and Technology, Government of India. Anil has been on Scientific Advisory Board of CSIR. He is currently a core member of UN's Stop TB Partnership Working Group on New Drugs and in 2023 he has been listed among the "Top 20 Innovators for Bioscience innovations" in India by BioVoice News.



Terry J McGenity

Professor of Microbial Ecology at the University of Essex

Terry McGenity is a Professor of Environmental Microbiology and Head of the School of Life Sciences 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.



Tista Prasai Joshi

Senior Scientist at the Nepal Academy of Science and Technology (NAST)

Dr. Tista Prasai Joshi is a senior scientist at the Nepal Academy of Science and Technology (NAST) for the last 20 years. She received a M.Sc. degree in Environmental Microbiology and an M.A. degree in Anthropology from Tribhuvan University, and a Ph. D. degree in Environmental Engineering in 2017 from the University of Chinese Academy of Sciences (UCAS) with the UCAS Excellent International Student award. Dr. Tista's research is focused on drinking water quality and purification which appears in many leading journals, such as Water Research, Chemical Engineering Journal, Journal of Hazardous Materials, Science of the Total Environment, Environmental Pollution, and so on. She has been awarded the OWSD-Elsevier Foundation award in Biological Sciences representing the Asia Pacific region in 2019 and UNESCO-OWSD early career fellowship in 2019. Dr. Tista has been decorated with Nepal Vidya Bhusan "Ka" by the honorable President of Nepal in 2017. She was nominated as one of the 50 visionaries of Nepal and was saluted with a medal in 2022. Dr. Tista advocates gender equity in Science and promotes women scientists in Nepal. She is founding member of Women Scientists Forum Nepal (WSFN-NAST) and life member of Women in Science and Technology (WIST) Nepal. She is facilitating many early-career women pursuing their postgraduate and Ph.D. research in her laboratory at NAST.



Kosala Sirisena

Senior Lecturer in the Department of Environmental Technology, University of Colombo, Sri Lanka

He is a Senior Lecturer in the Department of Environmental Technology, University of Colombo, Sri Lanka and currently on his sabbatical leave undertaking a Postdoctoral Research Fellowship at the Department of Soil and Physical Sciences, Lincoln University, New Zealand. He obtained my PhD in Cell and Molecular Biosciences from School of Biological Sciences, Victoria University of Wellington, New Zealand in 2014 with the thesis entitled "Molecular Characterization of Bacterial Diversity in New Zealand Groundwater". Following the completion of my PhD, He had held several postdoctoral research associate roles at esteemed institutions including Victoria University of Wellington, GNS Science, and Lincoln University in New Zealand, as well as Rutgers University and Carnegie Institution of Washington in the United States. Throughout these positions, he had engaged in diverse spectrum of research endeavors, focused on microbial ecology and environmental microbiology across various ecosystems including Antarctic sea ice, New Zealand groundwater systems, hypersaline ephemeral lakes in White Sands National Monument, USA, sedimentary rocks within the Svalbard Islands, thermal springs in Sri Lanka, and the glacier chronosequence at Franz Josef Glacier on the West Coast of New Zealand. Furthermore, he is also serving as the American Society for Microbiology (ASM) Country Ambassador to Sri Lanka and the International Society for Microbial Ecology (ISME) Senior Ambassador to Sri Lanka.



Phoebe Oldach

Head, Global Research Team Lead at Basecamp Research , London, England

Phoebe heads the Global Research Team at Basecamp Research, responsible for developing Access and Benefit Sharing partnerships around the world to build an ethical supply chain of novel microbial genetic diversity. Phoebe brings over 10 years of genomics experience to a team which encompasses specialisms ranging from expedition scientists adept at deploying sequencing labs in remote biodiverse environments, to policy experts at the cutting edge of regulations around the ethical commercialization of biodiversity data, to project managers building long-lasting and impactful global partnerships centered on biotechnology capacity-building and data generation. Through the development of global partnerships and the deployment of cutting edge methods for capturing unexplored microbial diversity, Basecamp's Global Research Program is supporting the development of sustainable synthetic biology solutions for industry and the formation of biodiversity as an asset class.

Prior to work at Basecamp Research, Phoebe worked as a computational scientist at siRNA therapeutics company, Ochre Bio, and obtained her PhD in DNA Replication from Oxford University, and carried out a Fulbright-Nehru Scholarship studying comparative genomics of *Sphingobium* spp in the laboratory of Professor Rup Lal.



Brajesh Singh

Disguised Professor of Soil biology, at Hawkesbury Institute for the Environment, Western Sydney University, Australia. irector, Global Centre for Land-Based Innovation

Brajesh is a Disguised Professor of Soil biology, at Hawkesbury Institute for the Environment, Western Sydney University. Through his fundamental research, he identifies the quantitative relationships between microbial diversity and ecosystem/ host functions and how natural/anthropogenic pressures such climate change affect this. His applied research harnesses the knowledge gained in fundamental research to improve agriculture productivity, restoration success and environmental sustainability. Outcomes from his research have informed multiple policy decisions at national and international levels, and he is currently working with multiple government and inter-governmental bodies including European Commission, United Nation agencies such as Food and Agriculture Authority (FAO) to support the implementation of relevant Sustainable Development Goals. He serves on UN- FAO's Intergovernmental Panel on Soil and is the Chair of FAO- International Network on Soil Biodiversity (FAO-NETSOB).

Prof Singh has published ~ 300 scientific papers including multiples in Nature, Science, PNAS, and these have been cited well above 38,500 times with h' index of 99. He is a Fellow of the Australian Academy of Science, American Academy of Microbiology, Australia Society of Soil Science, American Society of Soil Science. He is a Clarivate Highly Cited Researcher, and a Humboldt Research Awardee and AMI- Horizon Award- Dorothy Jones prize winner.

SPEAKERS
NATIONAL



Amit Kumar Rai

Scientist D at the DBT-National Agri-Food Biotechnology Institute, Mohali, Punjab, India.

He has served as Scientist at DBT-Institute of Bioresources and Sustainable Development, regional centre, Sikkim, India from 2012 to 2023. His current research focus is on fermented foods, microbial biotransformation, bioactive peptides, and enzymes for production of value-added products. He has completed his doctorate from CSIR-Central Food Technological Research Institute, Mysore on application of lactic acid fermentation for recovery nutraceuticals from fish and animal processing by-products. Dr. Amit has contributed in the area of Food Biotechnology for the production of nutraceuticals and functional foods rich in bioactive peptides and isoflavones using microorganisms associated with traditional fermented foods of North East India. Further he has studied microorganisms associated with high altitude region of Sikkim Himalaya and their potential for production of selected industrially important enzymes. To his credit, he has filed four patents and 122 publications including 86 publications in SCI Journals and Edited/Authored 4 books and author 32 book chapters with >3500 citations. His performance has resulted in the bestowment of the Associate Fellow 2023 from Indian National Science Academy (INSA), Young Scientist Award 2022 from International Bioprocessing Association 2019, Scientist of the year 2020 from National Environment Science Academy, India, Young Scientist Award 2016 from Association of Food Scientists and Technologists (India), Young Scientist Award 2015 by Association of Microbiologist of India, Selected Member of National Academy of Science, India - 2022, AU-CBT Excellence Award 2009 by the Biotech Research Society of India, Award for Excellence in Food Biotechnology 2016 from Society of Applied Biotechnology and several best presentation award at National and International conferences. He has supervised 2 PhD students and serving as Editor/Editorial Board member of several SCI Journals.



Ankit Saneja

Scientist at CSIR – Institute of Himalayan Bioresource Technology, Palampur, India.

He received his Ph.D. from the Academy of Scientific and Innovative Research (AcSIR) at the CSIR-Indian Institute of Integrative Medicine, Jammu. He was a postdoctoral research associate at National Institute of Immunology, India, from September 2017 to September 2019. He has received several international awards such as the CEFIPRA-ESONN Fellow, Bioencapsulation Research Grant, PSE Travel Bursary. He has to his credit several international research publications. His research interests includes exploring different types of formulations for various biomedical applications. He has also edited a book Pharmaceutical Technology for Natural Products Delivery published by SPRINGER NATURE.



Veena Pande

Professor, Plant Biotechnology and Biochemistry, Kumaun University, Nainital, India.

Dr.Veena Pande, currently working as Professor, Department of Biotechnology, Kumaun University Nainital is having a proven track record of around 24 years of teaching and research. She has expertise in area of Plant Biotechnology and Biochemistry. She has been associated with the Department of Biotechnology, Kumaun University since its establishment in the year 2000. She served as a Head of the Department of Biotechnology till March 2023. Additionally, she also has other administrative responsibilities such as Coordinator of Institutional Microbiology Programme (since its beginning), Programme Coordinator of BIF centre, Kumaun University (sponsored by DBT, Gov. Of India), Coordinator SC/ST NET Coaching centre , Kumaun University (Sponsered by UGC,since its inception), Dean Students Welfare (DSW), Kumaun University Bhimtal Campus, Bhimtal, District Coordinator, UCOST, Dehradun, Vice Principal, Community College, Kumaun University, Nainital (from its beginning till 2020), Ombudsman, BIAS Bhimtal (starting from1st March 2022), Coordinator, IPR Cell, Kumaun University, Nainital (since 2023) in her credit. She is a life time member of various International and National Academic Societies including Academy of Microscope Science & Technology, Society of Biological Chemists of India, The Indian Science Congress Association, Central Himalayan Environment Association International Symbiotic Society, US., International Mycorrhizal Society, Academy of Microscope Science & Technology, Environment and Social Welfare Society, Khajuraho, India, INTACH, Associate Editor for the journal, SAR Journal of Medical Biochemistry etc. She has successfully completed various research projects mainly as a Principal Investigator which were funded by several funding agencies including G.B. Pant National Institute of Himalayan Environment and Sustainable Development, Uttarakhand Council of Biotechnology (UCB, Govt. of Uttarakhand), UCOST, Govt. of Uttarakhand, CSIR New Delhi, and DIBER, Haldwani

She has received many prestigious award including Lupin Fellow (2010 by ICT, Mumbai), Intellectual Peace award (2010, by All India Intellectual Peace Academy), Bhartiya Shiksha Ratna award (2013, by Global Society for Health & Education Growth, Delhi), Governor's best researcher award (2016 and 2017), ESW Recognition Award (2017, by Environment and Social Welfare Society Khajurao, MP), Bharat Ratna Dr. Radhakrishnan gold medal award (2019, by Global Economic Progress & Research Association, Bangalore), Certificate of Education Excellence & Best Educationist Award (2019, by International Institute of Education & Management), Certificate of Honor (2021, Women's study Center, KU Nainital), Excellence in Research, (2021, by Divya Himgiri in joint collaboration with VMSB UTU, and UCOST), Leading Women Researcher Award (2022 by UCOST Dehradun), Prof. KS Waldiya Research Award (2021 and 2023, by SRICC KU Nainital), STE Women Excellence award (2023, by Save the Enviornment Society, Kolkata) etc. She has one US patent and more than 300 research publications in peer reviewed journals along with 20 book chapters in her credit. Under her guidance 32 students have successfully completed their PhD including two TWAS fellows and around 8 students (one TWAS Fellow) are still pursuing. She has not only participated in various National and International Conferences, workshops, and trainings with different capacities (Invited speaker, chair, co-chair) but also has a vast experience of organizing more than 60 such events successfully till date.



Arun Kumar

Senior Scientist at CSIR-Institute of Himalayan Bioresource Technology, Palampur, Himachal Pradesh, India.

Dr. Arun Kumar graduated with a Ph.D. in Biotechnology under the mentorship of Dr. Sanjay Kumar from CSIR-IHBT, Palampur, H.P. and Punjab University, Chandigarh, India in the year 2013. Thereafter, he joined Prof. AC Kushalappa's group as postdoctoral fellow at Department of Plant Science, McGill University, Canada from 2013-2015. Later on, he moved to USA to join Prof. Shelley Jansky and Dr. Dennis Halterman's group at Department of Horticulture, University of Wisconsin-Madison, USA from 2015-2017. He was awarded with prestigious Ramanujan Fellowship in 2017, and joined School of Agricultural Biotechnology, Punjab Agricultural University, Ludhiana, Punjab, INDIA and worked there until 26th February, 2020. Thereafter, Arun joined CSIR-Institute of Himalayan Bioresource Technology, Palampur, H.P. as a Senior Scientist.

His research interests and long term goals are: (1) to identify enzymes with novel functions and exploit them in healthcare and agriculture industry and (2) to understand the mechanisms of genetic resistance in crops against bacterial and fungal pathogens at the molecular and biochemical levels and exploit this information for crop improvement. He has published 35 peer reviewed articles in national and international journals and holds 4 patents to his credit. One of his technologies on the production of a highly thermostable superoxide dismutase has been transferred to industry (M/s PhytoBiotech Pvt. Ltd., India).

He is member of several national and international societies including Indian Society of Plant Physiology and Biochemistry, Society for Plant Biochemistry and Biotechnology, and International plant proteomic organization.



Jasvinder Kaur

Assistant Professor in the Department of Zoology at Gargi College, University of Delhi, Delhi, India.

Dr. Jasvinder Kaur is currently working as an Assistant Professor in the Department of Zoology at Gargi College, University of Delhi since 2014. She completed her graduation from Acharya Narendra Dev, University of Delhi in 2004 and M. Sc Zoology from Department of Zoology, University of Delhi in 2009. She was a meritorious student and secured university positions in college throughout her education. She specializes in the field of Environmental Biotechnology and Bioonformatics. During her doctoral research, she worked on Genomic Analysis, in-vitro Protein Refolding and Taxonomic Characterization of Sphingomonads. Her current research work is in the field of Drug repurposing.

She has 30 research papers in peer reviewed International Journals of repute to her credit. She has participated and presented her work in several National and International Conferences/ Symposia/ Workshops etc. She has co-authored 14 e-chapters in Biotechnology and Molecular Biology under the MHRD Project National Mission on Education (NME) and post-graduate pathshala, UGC under NME-ICT. She has also co-authored a book the Bioinformatics Manual for undergraduates. Additionally, she has been actively involved in conducting & organizing several workshops and conferences for the students and also Faculty Development Programs for the teachers.

She also holds several academic and administrative positions within her institution.



Pooja Arora

Assistant Professor in the Department of Zoology at Hansraj College, University of Delhi, Delhi, India.

Dr. Pooja Arora completed her master's in Zoology from the University of Delhi and then moved to the highly coveted National Institute of Immunology for her Ph.D. During her Ph.D. she worked towards understanding the factors regulating auto-immunity. Currently, she is working as an assistant professor in her alma mater i.e Hansraj college in the department of zoology. In pursuit to do research, Dr. Arora learned Python programming which she is applying in biological data analysis. She along with her undergraduate students has contributed in several publications related to medically important viruses including SARS-CoV-2, Dengue, and JEV. Today she will talk about her recent work where she used machine learning based approaches to improve the prediction of IL13 inducing peptides.



Atya Kapley

Chief Scientist (Jan 2019 to date)
Head, Environmental Biotechnology and Genomics Division, CSIR-NEERI, Nehru Marg, Nagpur 440 020, India.
Vice President, (upto 2024) Asia, Organization for Women in Science for the Developing World, (OWSD) A program unit of UNESCO

With a research experience of 30 years, Dr Atya has tried to bring in two specific domains into her scientific career (i) Generating knowledge via basic research and (ii) taking science to society. She have worked with developing monitoring protocols for target bacteria in water and used genomic tools to understand the microbial community in sludge, soil and wastewater and developed bioremediation options for polluted niches, the main targets being degraded land and wastewater. Her current interests also include mapping new emerging health concerns targeting multi-drug resistant genes in environmental niche. She has led a number of flagship projects, namely, in-situ wastewater treatment during the Kumbh Mela of 2012, soil remediation and working towards creating a microbial baseline map for the river Ganga. On different fronts, she has coordinated international projects with Finland, Estonia and Portugal to take scientific expertise from different countries and apply in India. Her collaborations also include projects with UK, Netherlands, China, France, Singapore, Denmark and Israel. She has guides ten PhD scholars so far with four ongoing. She published 132 papers in peer reviewed journals. Her expertise in metagenome analysis of polluted niches has let to the deposition of 35 metagenomes in public data base. She is a member of various committees of DBT, DST, CPCB etc. She works extensively to empower women in science.



Helianthous Verma

Assistant Professor, Department of Zoology, Ramjas College, University of Delhi, India

Dr. Helianthous is alma mater of University of Delhi. She did B.Sc. (H) Zoology from Hans Raj College, Masters and Ph.D. from University of Delhi During Ph.D, her work was focused on deciphering the characterization and comparative genomics of sphingomonad species isolated from hexachlorocyclohexane (HCH) contaminated soil. Her Ph.D. specialization is in molecular biology and bioinformatics. She has performed comparative genomics of different bacterial genus such as Novosphingobium, Sphingopyxis, Bacillus and Paracoccus which are environmentally and industrially important genera. Recently, she was involved in comparative genomics of 95 SARS CoV2 genomes which revealed phylogeographical distribution of the virus. In another study, she deciphered the role of mutations in determining the potential molecular drug targets (MDT) for Mycobacterium tuberculosis by performing host-pathogen protein-protein interactions.

She authored 27 research papers in peer reviewed journals and 7 books/book chapters. Currently, she is working on determining marker and highly specific genes in Sphingobium indicum B90A for efficient tracking of this organism in bioaugmentation in-situ field trials.



Junaid Jibran Jawed

Assistant Professor in the Institute of Health Sciences- Presidency University, Kolkata, India.

He has done Ph.D in Infectious Disease and Immunology, Division of Molecular Medicine, Bose Institute. His area of research include Host - pathogen interaction, role of pathogen derived antigen and immunological events during progress and establishment of infection taking Leishmania, Mycobacterium and biofilm forming bacteria as model of pathogens and Identification of molecules with therapeutic potentials against infection. He has worked as an application specialist in Roche applied sciences and molecular diagnostics for 1.5 years. Worked as guest lecturer in the department of Biological Sciences- Aliah University. He has joined as an Assistant Professor – Dept. of Life Sciences Presidency University in 2019. He has 21 research articles which include journals like Pathogen and Diseases, Biomedicine and Pharmacotherapy, Plos Neglected Tropical Disease, Scientific Reports, Langmuir and ACS chemical Biology etc. along with 4 Book chapters. He was awarded Sir Nilratan Sircar Prize for the year 2017 from Bose Institute, DST- Govt. Of India, Prof. Asima Chatterjee Young Scientist Award- 2018 for the contribution in the research area of chemical biology and AMI-Young Scientist Award (Medical and Veterinary Microbiology-2021) by the Association of Microbiologist of India.



Mansi Verma

Assistant Professor in the Department of Zoology at Hansraj College, University of Delhi, Delhi, India.

She earned her Ph.D. in Molecular Biology from the University of Delhi in 2011. Dr. Verma is distinguished as the recipient of the AMI Young Scientist Award, having conducted extensive research on soil-dwelling microorganisms within the Phylum Actinobacteria. Notably, she led the genome sequencing of two economically significant microorganisms, namely *Amycolatopsis mediterranei* S699 and *Sphigobium indicum* B90A. Currently, her research focuses on comparative genome analysis of pivotal human viruses such as Dengue Virus, SARS-CoV-2, and Influenza Virus. Dr. Verma's team is actively engaged in in silico transcriptome analysis of Dengue and Zika viruses. Her scholarly contributions include over 38 research articles published in esteemed international journals, along with 4 chapters of international recognition and 1 of national acclaim. Additionally, she has authored 8 e-chapters under the MHRD Project National Mission on Education through ICT of the Institute of Lifelong Learning, University of Delhi. She has spearheaded several projects as Principal Investigator, earning accolades such as the Bill and Melinda Gates Abstract Award for the ASM FEMS Conference in 2021.



A.A. Mohamed Hatha

Director, School of Marine Sciences as well as Senior Professor and Head of the Department of Marine Biology, Microbiology and Biochemistry, Cochin University of Science and Technology, Kerala, India.

He has more than 25 years of experience in the field of Environmental Microbiology. After a very successful short stint in the industry (as Head of Quality Assurance Division of Seafood Industry where he developed HACCP based production of seafood for the first time in India) he moved into academic and actively pursuing teaching and research for the past 26 years.

A Fulbright Scholar with excellent track record in attracting extramural funding and dissemination of science through publications, Dr. Hatha is passionate about understanding bacterial diversity in the environments ranging from tropics to polar with specific interest in antimicrobial resistance among environmental bacteria. So far produced 25 Ph.D.'s, more than 150 peer research articles and authored/ edited 11 books. Current 'h' index – 35, i10 - 105. Total google scholar citations – 5525 https://scholar.google.co.in/citations?user=oEKULDEAAAAJ&hl=en).

So far completed 12 externally funded major research projects (and 3 ongoing projects https://www.researchgate.net/profile/Mohamed-Hatha-Abdulla) with a total outlay of more than 50 million INR. Dr. Hatha is currently COUNTRY AMBASSADOR OF AMERICAN SOCIETY OF MICROBIOLOGY Dr. Hatha is also a member in the Kerala State Planning Board – working group on science and technology. Dr. Hatha has travelled extensively and visited all the continents including Antarctica (3 times to Arctic and once – 2020 – to the Antarctica). He lead the Indian Arctic Expedition in 2009. Considering the contributions of Dr. Hatha in the field of fish pathology, an isopod fish parasite is named after him (*Norileca hathai*). Dr. Hatha is a Member of the Research Advisory Committee (RAC) of the prestigious National Centre for Polar and Ocean Research (NCPOR), Ministry of Earth Sciences, Govt. of India. Dr. Hatha is a member, Board of Studies of several universities and colleges in India. Dr. Hatha has won the DST-Young Scientist Award early in his career and a Certified Technologist of Export Inspection Agency, Govt. of India.

Dr. Hatha is inducted into the INSA National Committee on 'Scientific Committee on Antarctic Research' – INSA-SCAR



Pratyoosh Shukla

Professor and Coordinator at School of Biotechnology & Coordinator, Centre for Bioinformatics, Banaras Hindu University, Varanasi, India.

He was awarded with Indo-USA Research Professorship at College of Medicine, University of Cincinnati, USA. He has been recently appointed as Visiting Guest Professor in South China University of Technology, Guangzhou China. His research areas include enzyme technology and protein bioinformatics and interdisciplinary areas of biotechnology

He has 24 years of teaching and research experience in reputed universities of India and abroad. He has written 40 book chapters, and published more than 240 peer reviewed publications in reputed high IF 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, Critical Reviews in Biotechnology, Critical Reviews in Food Science and Nutrition, Critical Reviews in Microbiology etc. He has written 9 books including Editor for Springer Briefs in systems biology series. He has carried out more than 15 R&D projects funded by national and international agencies as PI/Co-PI. He has more than 9430 citations with H-index of 56 and i10 index of 156. He was recently also featured among a list of Indian Researchers who were Top 2% in 2019, 2020, 2021, 2022, 2023 –Stanford Study. He was also featured among Top 2% Most Influential Scientists.

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 in Industrial Microbiology, Most Productive Researcher Award, Institute of Science, BHU (2022), 'Faculty Research Awards' 2023 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 6 years from 2014-2020 and presently serving as Board of Governors (BoG) member in BRSI.



Pushp Lata

Assistant Professor in the Department of Zoology, University of Delhi situated in North campus, Delhi, India.

She completed her undergraduate studies at Kirori Mal College, University of Delhi, from 2004 to 2007, and her postgraduate studies in Zoology at the Department of Zoology, University of Delhi, from 2007 to 2009, with a specialization on Cell and Molecular Biology. She completed her molecular biology doctorate at the University of Delhi between 2009 and 2013. She engaged in the sequencing of genomes for economically significant bacteria, such as *Sphingobium indicum* B90A and *Sphingobium lucknowense* strain F2T . Additionally, she conducted a metagenomic diversity analysis of soil gradients contaminated by HCH, contributing significantly to the understanding of microbial communities in such environments. Notably, her work played a key role in isolating new bacteria from HCH-contaminated soil, with noteworthy discoveries including *Flavobacterium ummarensiens* and *Pontibacter indicus*.

She has researched how the bacterial community and lin genes alter throughout the Biostimulation and Bioremediation of soil contaminated with HCH. She has been engaged in metagenomic research on a hot spring in Manikaran and isolated noval bacterium Thermus parvatiensis, India, which is perched atop the Himalayan Ranges. She has also involved in upscaling of Rifamycin production from strain Amycolatopsis mediterranei. She has contributed to over Nineteen research publications published in reputable international journals. Additionally, Dr. Lata has added three chapters to her renown on a national and worldwide scale. She has spoken at numerous conferences as an invited speaker and taken part in over 20 conferences and workshops.



Rajeev Singh

Associate professor in Department of Environmental Science, Jamia Millia Islamia, New Delhi, India.

He is working in the area of Environmental health. He is founder secretary of Bio electromagnetic Society of India. Dr. Singh is member of several scientific and academic bodies. Dr. Singh has organized and participated in several international and national conferences and delivered invited talks. He has published around 100 research papers, chapters in books, conference proceedings etc of international repute. He is also a principal investigator of several major research projects funded by various govt. agencies. He has published a good number of research articles in reputed journals of high impact namely Seminars in Cancer Biology (Impact factor -17), Scientific reports (Impact factor -4.9), Bioresource Technology (Impact factor -11.8), Science of the total environment (Impact factor -10.7), Environmental Pollution (Impact factor -9.98), Cells (Impact Factor -7.6), Chemosphere (Impact factor -8.9), Environmental research (Impact factor -8.4), Fuel (Impact factor -8.0), Biomedicine & Pharmacotherapy (Impact factor -7.4), International Journal of Hydrogen Energy (Impact factor -7.1), Journal of Cancer Research and Clinical Oncology (Impact factor -4.5), Air Quality Atmosphere and Health (Impact factor -5.8), Aerobiologia (Impact factor -2.7), Reproductive Toxicology (Impact factor -3.4), International journal of environmental health research (Impact factor -4.4) and several others. He has edited a number of books published by Springer nature. He is also a reviewer of several high impact journals like Environmental international, PLOS One, free radical research, mutation research etc. Dr. Singh is recipient of Young Scientist Award of Federation of European Microbiological Societies (FEMS), Gold Medal for best oral presentation etc.



Ravi Kumar Asthana

Senior Professor and Head in Centre of Advanced Study in Botany, Banaras Hindu University, Varanasi-221005, India

Prof. Asthana, is throughout First-class distinction with gold medal at graduation. He received scholarships like CSIR JRF, SRF, and RAship. He has undertaken many projects as PI/ Co PI funded by DST, CSIR, UGC and MNRE, DIC-IIT BHU. He is recipient of various fellowships as INSA JSPS (Tokyo), Commonwealth Academic Staff (UK) and INSA - KOSEF (South Korea). He is reviewer of various international journals and has been member of various selection committees. Recognized for outstanding research contributions and was elected as NASI Fellow in 2019 in the area of Drug Discovery, Stress Biology and Environmental technology involving microalgae including cyanobacteria and "Prof. C.N.R. Rao Education Foundation Award for Excellence in Research" by Banaras Hindu University in 2018-19. He has demonstrated prolific scholarly output by filing 3 patents and publishing 73 research articles in peer-reviewed journals (ranging from IF 2- 13). Supervised 21 PhDs and 7 scholars are currently registered. Prof. Asthana demonstrated antimicrobial biomolecules such as lariciresinol-4-O-glucoside, hapalindole-T, maraniol, arachidonoyl dopamine from cyanobacteria, other microalgae and explored ‘stigmatellin Y’ as antifungal biomolecule. Notably, he reported genome-wide expression in Anabaena 7120 under desiccation stress, and achieved significant lipid overproduction (56%) in mass-cultivated D. salina for high-quality biodiesel production. Transcriptomics and metabolomics of microalgae led the identification of candidate genes for crop improvement. His work extends to economic β-carotene extraction, Se-enriched D. salina as food and feed supplement, heavy metal bioremediation, and effective cyanobacterial bloom management. He was Co-ordinator of Industrial Microbiology and Applied Microbiology in the department. Presently, he is heading prestigious department of Botany, Institute of Science, Banaras Hindu University, Varanasi.



Suresh Kumar Dubey

Professor in the Department of Botany, Banaras Hindu University, Varanasi, India.

He is working under major domain of Molecular Microbial Ecology. More specifically his interests include microbial perspectives of methane production-oxidation in rice fields & forest ecosystems, prevalence of antimicrobial resistance (AMR) containing bacteria in environment and their response to drugs, screening & utilization of microbes for their potential role in bioremediation of xenobiotics etc. He has completed various projects funded from DST, DBT, ICMR and DAE-BRNS. He has supervised 13 Ph. D. students and published more than 87 research papers in several journals of international repute. He has won multiple awards for his work, including Biotech Research Society of India Young Scientist Medal 2004, DSTBOYSCAST Govt. of India fellowship 2006, INSA visiting fellowship 2012 and 2017, and JSPS Invitation fellowship 2012, among others. He has visited several frontline research organizations in National & International (Japan, China, South Korea, Sweden, Scotland & England) level to participate in academic discussion/research activities.



Daman Saluja

Senior Professor, Former Chairperson Research Council
Director at ACBR (2006-2010; 2017-2023) and Joint Director of Delhi School of Public Health, IOE, Delhi, India.

AREA OF EXPERTISE Medical Biotechnology
Research Interests: Molecular diagnostics and drug development
ACADEMIC QUALIFICATION: Ph.D. (1986, University of Delhi)
Post-doc NYU Medical Center, NY, USA for more than six years

PROFESSIONAL CAREER
MAJOR CONTRIBUTIONS IN RESEARCH:

- Multiplex PCR-based diagnosis of *Chlamydia trachomatis* and *Neisseria gonorrhoeae*, T vaginalis, Covid-19, Leukemia, and other diseases.
- Licensed two diagnostic protocols for commercialization
- Molecular mechanism of Drug resistance and Drug development in Neisseria gonorrhoeae.
- Understanding gene regulation of cancer progression

Member of the review committee of several journals of Wiley, Springer and Elsevier. Prof Saluja has produced more than 35 Ph.D. students and has several National and International research projects Have 7 Patents, licensed two assays for commercialization. Received several awards throughout career. Publications More than 125 in International journals. Member review committee of several journals of Wiley, Springer, and Elsevier. h index 25, Scopus citation more than 2600. Member task force committee of various funding agencies ICMR, BIRAC, DST, and DBT. Has delivered several Invited talks in National and International symposiums.
Awards: National science talent, INSA Young Scientist, LSS Kumar Memorial Award, Associate of IAS for four years, NIH fellowship, The Biotech Product & Process Development and Commercialization Award', selected for Khorana Technology transfer program (IUSTF)



Shashank Tripathi

Assistant Professor in Microbiology and Cell Biology at the Indian Institute of Science, Bengaluru, India.

He is a Virologist by training. His lab at the Centre for Infectious Disease Research, IISc, uses big data analytic and experimental biology approaches to identify actionable leads against Viral pathogens such as Influenza, SARS-CoV-2, Dengue, and Zika. He is a DBT-Welcome trust India alliance Intermediate Fellow, Infosys Young Investigator, American Society for Virology Global Scholar and an INSA Associate Fellow. Today, he will discuss his group's work on SARS-CoV-2 prognostic markers and host-directed therapy emanating from virus-host big data analytics and validation.



Jyoti Vakhlu

Former Director at the School of Biotechnology, University of Jammu, Jammu & Kashmir, India.

She with over 25 years of dedicated service in academia. Her professional journey commenced as a Research Fellow at the Biotechnology Division of the Indian Institute of Integrative Medicine, Jammu, India, from 1994 to 1997. Building upon this foundation, she transitioned to academia, joining the School of Biotechnology at the University of Jammu, Jammu, India, as an Assistant Professor in 1999. She is deeply committed to both teaching and research, nurturing the minds of budding biotechnologists and making significant contributions to the field. Her expertise lies in Molecular Biology, Recombinant DNA Technology, Genomics, and Metagenomics. Her group has dedicated significant attention to saffron research , aiming to enhance its growth and productivity through innovative approaches. Her group was the first to initiate the work on saffron microbiomics that has now been taken up by the researcher's world over. Her group also attempts at using the microbiome of saffron as a biomarker in absence of genetic diversity in saffron . Other notable aspect of her team's work involves the development of bioformulation based on Bacillus sp. strain D5 (Bar D5) an indigenous saffron bacteria that has demonstrated to double the yield of saffron spice as well as its corms in terms of size of the corm. This bioformulation is ready for commercialization and at present she is looking for the partners to commercialize it. Her team has actively contributed to expanding saffron cultivation beyond traditional areas. They have successfully introduced saffron cultivation in the Poonch district, in Pir Panjal, Himalayas yielding commendable results. These efforts have not only diversified agricultural practices but also fostered socio-economic development by creating opportunities for local communities.

In her professional journey so far she have published around 70 papers in peer reviewed journals of international repute, mentored 10 Ph.D students, 6 M.Phil students and more than 60 masters project students. She has been able to attract extramural funding up to the tune of about 30 million Indian rupees from national as well internation funding agencies, to name few DST,DBT, ICAR, DAAD, ICGEB, Sri Lankan research agency and Austrian research agency .



Anil Kumar

Faculty, Genetics, Cell Signaling and Cancer Biology, National Institute of Immunology, New Delhi

My laboratory at National Institute of Immunology, New Delhi is working towards delineating the complex interaction among microbiota, bacterial infections, inflammation and carcinogenesis. There are increasing research reports which establish the link between human microbiota and carcinogenesis. Pathogenic bacteria and altered microbiota interact with mucosal surface and as a result, epithelial damage can be seen especially in chronic infection conditions. It can be reckoned that gut microbiota-derived metabolites play a key role in epithelial damage and carcinogenesis.

More and more intriguing data are hinting at a much broader link between microbiota, bacterial infections, inflammation and carcinogenesis. The mechanism of this relationship between bacteria and human cancer is not well studied, hence my research group is exploring the role of bacteria, microbiota and their metabolites in cancer causation and treatment.



Dharam Singh

Principal Scientist at CSIR-Institute of Himalayan Bioresource Technology (CSIR-IHBT), Palampur, Himachal Pradesh, India.

He is working in the current institution since 2014. Before that he Master (Biotechnology) from Himachal Pradesh University and PhD (Biotechnology, awarded by GNDU, Amritsar, India) from CSIR-IHBT in 2004-05. He did Post-doctorate (Molecular Biology) from Institute of Molecular Biology, Academia Sinica, Taiwan during 2005-2014. His research group is focused on bioprospecting lignocellulolytic and therapeutic enzymes from microbes of high-altitude Himalayan niches. In addition, his group is actively involved in exploring alternatives to plastic and bioprospected PHA-based biodegradable bioplastic from the Himalayan bacteria. The patented technology for its production has been transferred to two industries too. He has published over 60 research papers in international peer-reviewed journals such as PNAS USA, J Biomed Sci, Bioresource Technology, J Bacteriol, Food Chemistry, J. Environ. Manage, Frontiers Microbiol, Scientific reports, Process Biochem, Genomics, FEMS Microbio Letters, Biotech J, Critical Review Biotech, Food Res Internal, International Journal of Biological Macromolecules, Extremophiles, and Probiotics and Antimicrobial Proteins etc. Also, he has handled more than twelve research projects and filed two patents. He has guided 08 students for PhDs and currently 06 students are pursuing PhDs. Three post-doctoral fellows were guided, and one is currently being pursued. He has been awarded Distinguished Postdoctoral Fellow Award, IMB, Academia Sinica, Taiwan in 2009. Also selected “Assistant Director” State Forensic Science Laboratory, Junga, Shimla, Himachal Pradesh through the Public Service Commission in 2009. In 2008 awarded with “Young Scientist International Travelling Fellowship” by Japan Society for Promotion of Science (JSPS, Japan) for participation in the JSPS-DST Asian Academic Seminar 2008 held at Jawaharlal Nehru Centre for Advanced Scientific Research, Bangalore, India. In 2007, awarded “International Travelling Fellowship” by Institute of Molecular Biology, Academia Sinica, Taiwan for the year 2007. Earlier in 2005, he was selected as Scientist Gr. IV(1) at Regional Research Laboratory (CSIR lab), Jorhat, India (2005).



Baljeet Kaur

Professor in the department of Computer Science, at Hansraj College, University of Delhi, Delhi, India.

She completed her graduation in Mathematics from University of Delhi, followed by masters and PhD from Utkal University. After working in the Education and Research department at Infosys, she joined Hansraj College. Her research interests include machine learning, pattern recognition and big data analysis. Her post doctorate study involved the study and building of decision models for multiple modalities for depression detection. Currently she is working on depression detection and multimodal multiobjective optimization problems. She also contributes towards understanding

and building efficient classification models for biological data. She has supervised work related to SARS-CoV-2 and Japanese Virus Encephalitis which is published. She has also developed and published an effective Machine Learning model to classify coding from non-coding RNAs. She also contributes to selecting effective biomarkers for classification of various biomolecules.



Ankur Mutreja

Scientist (Project Lead) at MSD-Wellcome Trust Hilleman Labs, New Delhi, India

Dr Ankur Mutreja is an experienced global health professional passionate about science and innovation for making the world free of epidemics and pandemics. Dr Mutreja has worked in academic research (universities, research institutes), biotech industry (pharma, biotech) and public health (WHO and UN) in the area of vaccines, diagnostics and WASH for infectious disease. He has extensive experience in identifying strategic partnerships and translating scientific research into tangible products or services for the best impact.

Dr Mutreja has led a translational research team at the Department of Medicine, University of Cambridge; has worked as a Project Leader at the MSD-Wellcome Hilleman Laboratories (HL); and also as an Advanced Marie Curie Fellow for bridging Academia and Industry at the Novartis Vaccines. Dr Mutreja has made crucial input to the R&D and translation of several vaccines. With an excellent publication record, including in Nature and Science, Dr Mutreja is a Fellow of Royal Society of Biology and also serves in honorary and board positions at several institutions and organizations around the world.



Manoj Kumar

Senior Scientist, working at CSIR-Indian Institute of Toxicology, Lucknow, Uttar Pradesh, India.

His areas of Specialization includes Food Microbiology, Microbial Toxigenesis, Fungal Biology and Bioremediation. His group is working on the rhizospheric microbes to utilise them in bioremediation of toxic metals. Currently, they are characterising microbes capable of metal accumulation and biotransformation into less or non-toxic forms and less leaching in the environment. We have isolated several strains of fungi and bacteria with arsenic biotransformation capabilities with beneficial effects on the plants. His aim is to study the molecular mechanism of uptake, biotransformation, accumulation and tolerance of toxic elements by these microbes. Group also investigating the role of Arsenite Transporters (Acr3) and Ycf1/Vmr1 in arsenic tolerance and accumulation in fungi. They are characterising bacterium capable of producing new and safe insecticidal toxins against specific insect parasites in plants and animals. More specifically, they are looking into the mechanism of toxicity of bacterial toxins and their interaction with target insects, biosafety and fate. Publications: More than 30 publications in reputed journals like Environmental Pollution, Microbiological Research, Ecotoxicology and Environmental Safety etc.



Janmejay Pandey

Assistant Professor in Department of Biotechnology, School of Life Sciences at Central University of Rajasthan, Bandarsindri, Kishangarh –Ajmer, Rajasthan, India.

Dr. Pandey is an active researcher in the field of Applied Microbiology & Biotechnology. His primary area of research focuses on identification of gene(s) and gene cluster(s) involved in microbial metabolism and synthesis of bioactive secondary metabolites. He received M.Sc. in Biotechnology from Kurukshetra University, Kurukshetra, 2002 and completed PhD. in Microbial Biotechnology from Institute of Microbial Technology – (IMTECH CSIR), Chandigarh, India in 2009. During doctoral studies, he worked as visiting scholar at Ecole Polytechnique Federal de Lausanne (EPFL), Lausanne, Switzerland and Commonwealth Scientific and Industrial Research Organisation (CSIRO), Canberra, Australia. After obtaining the Ph.D. degree, he joined Gordon Centre for Integrative Sciences, University of Chicago, Chicago- IL, USA as a Postdoctoral Scholar in 2009 and later moved to School of Medicine, Georgia Health Sciences University, Augusta- GA, United States of America. He returned to India in June 2012 and joined Central University of Rajasthan, Ajmer-Rajasthan as an Assistant Professor in Department of Microbiology. Subsequently, he joined Department of Biotechnology at Central University of Rajasthan in March 2013. To date, He has authored 30 research articles, 5 review articles in journals of high impact factors and international reputes. He has also contributed 14 book chapters. His work has been cited in ~ 1450 citations. He is a reviewer for several international journals. His current research interests include studies on (i) diversity of extremophilic actinobacteria towards isolation, characterization of novel bio-actives and therapeutics; (ii) genomics and bioinformatics guided discovery of microbial pathogen specific small molecule inhibitors, (iii) plant -microbe interaction for mitigation of biotic and abiotic stress in arid, semi-arid regions of Rajasthan. He is currently also serving as the Deputy Ambassador in India for the FEMS Internationalization Program.



Parminder Kaur Narang

Associate Professor in the Department of Zoology, SGTB Khalsa College, University of Delhi, Delhi, India.

She, since past 18 years is teaching Cell Biology, Ecology and Physiology along with other papers. She did her M.Phil in the field of Aquatic Biology from Department of Zoology, University of Delhi and further did her Ph.D. from School of Biotechnology, KIIT University, Odisha, in the field of Bioinformatics. She has published her papers in journals of international repute. Dr. Narang has also contributed modules towards the e-content under PG-pathshala, NMEICT, UGC. She has also been the jury member of the Inspire Award National Level Exhibition and Project Competition (NLEPC) by DST, Government of India, for 4 consecutive years. She has participated in more than 20 Conferences and workshops and has been the invited speaker for many conferences. She is now enthusiastically working in the field of comparative genomics, carotenoid enzymes and microalgal studies.



Om Prakash

Associate Professor and Deputy head of Symbiosis Centre for Climate Change and Sustainability at Symbiosis International (Deemed University), Pune, Maharashtra, India.

He served as Curator of the anaerobic facility of the National Centre for Microbial Resource (NCMR) of the National Centre for Cell Science (NCCS) Pune for 11 years. He received his M.Sc., PhD and postdoctoral training in microbiology from University of Delhi and Florida State University, Tallahassee, FL, and Georgia Institute of Technology, Atlanta, USA respectively. He has worked as a Research Faculty in the Translational Science Laboratory (TSL) College of Medicine, Florida State University, under an ICMR-supported long-term fellowship and as a Visiting Fellow in ARO-Israel under the 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). are anaerobic microbiology, climate change, biomethanation, methanotrophy and environmental health are His area of interest. Till date he has published 85 research articles with more than 4100 citations.



Nabeel Ahmad

Dean at School of Allied Sciences and Professor in the Department of Biotechnology at Dev Bhoomi Uttarakhand University, Dehradun, Uttarakhand, India.

He has over 15 years of teaching, research and administrative experience. His research areas are mainly focused on nanobiotechnology, Flexible Electronics with Nanosensor and Bioprocess Engineering. He has published more than 40 research papers in National and International peer reviewed journals including Nanomaterials, RCS Advances, 3BioTech, and many more. He has served as Editor in three books on nanobiotechnology namely 3 D Printing Technology in Nanomedicine, Intelligent Nanomaterials for Drug Delivery Applications and Emerging Nanotechnologies for Medical Applications published by Elsevier Pennsylvania USA. He is also serving as eminent member of Editorial Board of Journal of International repute. In addition to that, nine patents are also in his credit on nanobiotechnology and discussion is going on to transfer the technology to three organizations to commercialize the same. The same has already been highlighted in the National news papers. Dr. Ahmad has been invited to deliver experts lecture in various Universities including University of Malaysia, and national and international conferences organized by Indian network for soil contamination research, Association of Microbiologist of India and many more. Dr. Nabeel Ahmad is the recipient of prestigious fellowship including the Teachers Associateship for Research Excellence (TARE) fellowship under Science and Engineering Research Board (SERB) Department of Science & Technology (DST) New Delhi. He is the Fellow of Linnean Society (FLS) London.



Sanjukta Subudhi

Microbiologist and working as senior fellow & Area Convener at TERI, New Delhi, India.

She leads the 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, bioethanol, biojet fuel, from 1st, next generation feed stocks) and green biochemicals (2,3 Butane Diol, lactic acid, value added volatile fatty acid, lipase, bioflocculant, carotenoids, PUFA, Pre and probiotics). Her in depth research contributions are recognized in the form of 62 high impact factor peer reviewed international journal publications, 4 patents, 1 position paper, 1 white paper, 4 book chapters and over 100 international conferences (>1674 citations, h-index, 22, I10 index, 33).
She has established Tata Chemicals Ltd (TCL) -TERI Centre of excellence at TERI, as the lead project coordinator. She is the Bioeconomy expert member of Indian Federation of Green Energy (IFGE), and is a task force expert in Environmental biotechnology and Bioenergy domain (DBT-BioCARe, Ministry of Science and Technology, govt. of India). Dr Subudhi is the member of several professional bodies (BRSI, AMI) and has edited several international peer reviewed journal and books (Springer, CRC Press) as guest editor. She has deliberated as bioenergy expert at G20-RIIG Bioeconomy' (Research and Innovation Initiative Gathering) international conference organized during 23-24 March/2023 on the theme; 'Building towards sustainable and circular organized by DST, DBT, MoST, govt of India).
Dr Subudhi has worked in several bilateral and multilateral collaborative research projects with overseas research institutions: PTB, Germany, Michigan State University, U.S; Helmholtz Centre for Environmental Research (UFZ, Leipzig, Germany); Korea Maritime and Ocean University (Busan, South Korea); Queensland University (Brisbane, Australia); Curtin University; University of South Australia (Perth, Australia), Saitama University, (Tokyo, Japan); Feng Chia University (Taichung, Taiwan); Green Chemistry Centre of Excellence, University of York, (York, UK); Finnish Meteorological institute, Helsinki & Tampere University, Tampere, (Finland), AIST , Japan.



Yogendra Singh

Director in Delhi School of Public Health, Institution of Eminence, University of Delhi, Delhi, India.

Dr. Yogendra Singh is currently Director, Delhi School of Public Health, Institution of Eminence, University of Delhi. He obtained his PhD. from V.P. Chest Institute, University of Delhi. He has been working on various aspects of Tuberculosis and anthrax. He has published more than 160 papers. He is a fellow of three major academies of India (NASI, INSA and IAS). He has received many awards including J C Bose Fellowship. Today he will talk about the role of Protein modification in bacterial survival and pathogenesis.



Shailly Anand

Assistant Professor, Department of Zoology at Deen Dayal Upadhyaya College, University of Delhi, Delhi, India.

Dr. Anand is currently working as an Assistant Professor in the Department of Zoology at Deen Dayal Upadhyaya College, University of Delhi since 2012. She completed her graduation from Ramjas College, University of Delhi in 2006 and M. Sc Zoology from Department of Zoology, University of Delhi in 2008. She was a meritorious student and secured first position in college throughout her graduation and post-graduation. She specializes in the field of Cell & Molecular Biology. In appreciation of being the university rank holder, she was awarded the University Teaching Assistantship for a period of 4 years from 2008 to 2012 in the Department of Zoology, University of Delhi along with her Ph.D. coursework. She has 14 research papers and articles in peer reviewed National and International Journals of repute to her credit. She has also contributed 11 e-chapters in Biotechnology and Molecular Biology under the MHRD Project National Mission on Education through ICT of the Institute of Lifelong Learning, University of Delhi. She has participated and presented in several National and International Conferences/ Symposia/ Workshops etc. Her current research work is in the field of metagenomics and molecular microbiology. Additionally, she has been actively involved in conducting & organizing several workshops/ training programs/ summer camps for the students and also Faculty Development Programs for the teachers. Since 2018, she has been organizing rural Outreach Programs at Bani (Bani School Innovation Camp, BaSIC) and Biar (Biar Initiative: A School Outreach Program for Enrichment, BIϕSCOPE) villages in the interiors of Hamirpur District of Himachal Pradesh in association with Prof. Rup Lal (NASI Senior Scientist Platinum Jubilee Fellow at The Energy and Resources Institute, New Delhi). She also holds several academic and administrative positions within her institution.



Sudesh Kumar Yadav

Director and scientist at CSIR - Institute of Himalayan Bioresource Technology, Himachal Pradesh, India.

Dr. Sudesh Kumar Yadav is an outstanding scientist and contributed significantly in the area of biotechnology, metabolic engineering, bioprocessing and nanobiology for crop improvement and production of value added molecules. He has extensively worked on understanding the regulation of key metabolic pathways of crops like tea, stevia, rice and horsegram as well as developed several technologies for value added products from agricultural waste biomass. He has already published more than 200 research papers, 17 patents, 3 books, 28000 citations, 55 h-index. Listed by Stanford University among the top 2% scientists of the world. He is fellow of national academies such as The National Academy of Sciences, India; National Academy of Agricultural Sciences. He is recipient of S. Ramachandran National Bioscience Award, NASI-Reliance Industries Platinum Jubilee Award, and “Recognition Award’ by NAAS.

He has also been conferred Indian National Science Academy (INSA)-Young Scientist Award, 2008; The National Academy of Science, India (NASI)-Platinum Jubilee Young Scientist Award, 2009; Council of Scientific and Industrial Research (CSIR)-Young Scientist Award, 2010; BOYSCAST Fellowship, 2008 by DST, GoI; NAAS-Associate, 2013; Prof. Hira Lal Chakravarty Memorial Award of Indian Science Congress Association (ISCA), 2012-2013; Haryana Yuva Vigyan Ratna Award, Haryana Govt., 2011-12.



Thandavarayan Ramamurthy

INSA-Senior Scientist in the ICMR-National Institute of Cholera and Enteric Diseases (NICED), Kolkata, India.

Dr. Ramamurthy is working as an INSA-Senior Scientist in the ICMR-National Institute of Cholera and Enteric Diseases (NICED), Kolkata. Afer completion of Ph.D in Marin Microbiology from the Annamalai University in 1988, he was awreded Guest researcher followship by the Japna Human Health Science Foutation to work at the National Children's Medical Research Center and International Medical Center of Japan, Tokyo. He joined as Assistant Director in NICED in 1997 and superannuated as Scientist-G in 2015. He worked as DBT-THSTI National Chair until 2020. He severed as in member in several National and International committees. He is the elected Fellow of the Indian National Science Academy, National Academy of Sciences, West Bengal Academy of Science and Technology and American Academy of Microbiology. He has published more than 300 papers and several book chapters.



Urmi Bajpai

Professor in Department of Biomedical Science at Acharya Narendra Dev College, University of Delhi, Delhi, India.

She has a PhD in Microbiology from the University of Delhi, South Campus. Prof Bajpai has a teaching experience of 25 years and is a pioneer of undergraduate research in the college. Her research focus is on TB drug Discovery and her lab is exploring antimycobacterial solutions in bacteriophages and small molecule inhibitors as candidates for multi-target therapy in *M. tuberculosis*. Prof Bajpai is the Co-founder of the 'International Bacteriophage Research Consortium (IBRC)' built in collaboration with Open Health System Laboratories (OHSL), USA; Projects advisor and Director of the Phage Program at Open Source Pharma Foundation (OSPF, Bangalore), Consultant on phage lysins with a Mumbai-based Life Science Start-up. She Was featured among 35 Vigyan Vidushis in the country as Future Hopes by Vigyan Prasar, Department of Science & Technology (DST), Government of India. 2023. She is 'SBRT Fellow' Awardee by the Indian Bacteriophage Society for Distinguished and Sustained Contribution to Bacteriophage Science Communication in 2022. She was also featured in the list of #365IndianWomenInSTEM, curated by TheLifeofScience.com. 2021. She has received Indian National Science Academy (INSA) Teacher Award. 2018 and Excellence Award for Teacher in Service in College' for exemplary service to the University of Delhi. 2017. She was also awarded with Meritorious Teacher Award, Directorate of Higher Education (DHE), Govt of NCT of Delhi. 2014



Vipin Gupta

Environmentalist & Scientist, Ministry of Environment Forest and Climate Change (MoEF&CC), Government of India, New Delhi, India

Dr. Vipin Gupta completed his graduations and post graduations in Zoology from Hans Raj College, University of Delhi and obtained his Ph. D from Department of Zoology, University of Delhi. After his Ph.D., he started his Post Doctorate work under the National Mission for Clean Ganga project coordinated by NEERI. His key research domains are Environmental Microbiology, Computational and Systems Biology, Bioinformatics, Genomics, Metagenomics, Proteomics, and Antimicrobial Resistance. His major research focuses on clinical and non-clinical strains of Acinetobacter baumanni and prediction of novel drug target approach for the bacterial pathogens.. He was awarded Young Scientist award 2022 by Association of Microbiologist of India. He has authored more than 40 research articles published in peer-reviewed high impact journals and several book chapters. He has served as the associate editor for Indian Journal of Microbiology (Springer) and currently an editorial board member for journals like Springer Nature, BMC biotechnology & Medicon Microbiology. Dr. Gupta is also member of various scientific societies like Association of Microbiologist of India (AMI), International Society for Microbial Ecology (ISME), Indian Network for Soil Contamination and Research (INSCR). He was involved with designing and conduction of various courses on Computational Biology in many eminent institutes and universities of India. He has conducted more than 100 workshops on computational biology and art of scientific writing in various universities and colleges at national and international platforms. Dr. Vipin Gupta is working as deputy Director in Ministry of Environment, Forest and Climate Change, Govt of India and currently involved in the regulations of Environmental Protection Act, representing MoEFCC in various NGT and High court constituted committees and other environmental related issues of the state of Uttarakhand



Yogesh Shouche

Deput Director at SKAN Research Trust Bengluru and Honorary Scientist at National Center for Cell Science (NCCS), Pune, India.

Dr. Yogesh Shouche is currently working as Deputy Director at SKAN ResearchTrust Bengluru. He started his career as scientist National Centre for Cell Science (NCCS) in Pune, India. After working on different aspect of microbial, especially bacterial diversity of various ecological niches, his thrust area of research is now to understand succession of microbial communities in human gut during development and their role in health and diseases. He is working since 25 years in the field of microbial ecology, microbial molecular taxonomy and biodiversity; published more than 400 publications in journals of relevant area; reviewed publications in International journals like FEMS Ecology, International Journal of Systematic and Evolutionary Microbiology and Microbial Ecology. He is also on Editorial board of prestigious journals like Current Science, PlosOne etc. He is fellow of Maharashtra Academy of Sciences, Indian National Science Academy and National Academy of Sciences India.

In 2009, he was given a responsibility of establishment of Microbial Culture Collection (MCC). It is now known as National Center for Microbial Resources (NCMR), it currently holds more than 150,000 bacteria and fungi in its collection recognized by WFCC (World Federation of Culture Collection). MCC is also recognized as International Depositary Authority (IDA) and is Designated Repository by Ministry of Environment, Forests & Climate Change, Government of India under the Biological Diversity Act 2002. In September 2018, Department of Biotechnology extended the mandate of this repository to include Anti Microbial Resistant microbes.
After successful career at NCCS for 32 years, he joined Azim Premji University from 1st March 2022 and from August 2023 he took over as Deputy Director of SKAN Research Trust. He was also on the member of the Executive Boards of International Society for Systematics of Prokaryotes till August 2023 and presently on Executive Board of World Federation of Culture Collections. As a recognition of his contributions , recently a genus of has been named in his honor Shouchella . Interesting after recent re classification this genus now contains well known probiotic species. Bacillus clausii is now Shouchella clausii.



Utkarsh Sood

Assistant Professor, at the Department of Zoology, Kirori Mal College, University of Delhi, Delhi, India.

He graduated from Hansraj College and did his Master's in Zoology from the Department of Zoology, University of Delhi.
After that, during his doctoral research, he worked on the complete and comparative genomic analysis of clinical and nonclinical isolates of Pseudomonas aeruginosa. He was awarded a Ph.D. degree in November 2018 by the University of Delhi. He has more than 35 publications to his credit in highly reputed journals. He has also contributed 2 genus chapters in the prestigious Bergey's Manual of Systematics of Archaea and Bacteria. He has conducted hands-on sessions on microbial ecology, genomics, and metagenomics in more than 30 workshops under the American Society for Microbiology, the Federation of European Microbiological Societies, the International Society for Microbial Ecology, and DST. He has also co-founded a startup PhiXGen Pvt. Ltd. that works on bacterial biomolecules. He is now enthusiastically working in the field of comparative genomics, microbiome and metagenome studies, and secondary metabolites of bacteria.



Sunil Pabbi

Professor at ICAR-Indian Agricultural Research Institute, New Delhi, India.

Prof. Sunil Pabbi, M.Sc. Honors and Ph.D. (Microbiology) from Panjab University, Chandigarh, India was professionally employed at ICAR-Indian Agricultural Research Institute, New Delhi- 110012, INDIA and served in Centre for Conservation & Utilization of Blue Green Algae & Division of Microbiology for over 36 years before superannuating in July 2023. His major research contributions are 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 private companies leading to its large-scale adoption 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 an Indian patent granted for the same. Dr. Pabbi has so far carried out 15 different research projects and has over 164 publications (both national and international), authored two 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. Dr. Pabbi is a member of several National/International societies in the field of biology and is presently PRESIDENT, Association of Microbiologists of India. He is on the editorial board of Scientific Journals of repute and is also nominated as Distinguished Honorary Advisor and Expert member, Board of studies of several universities in India. Dr. Pabbi also served as Chairman/member of various Committees of Govt./State Departments, organizations such as ICAR, BIS, CSIR, Ministry of Agric. & Farmers Welfare, Research Institutions etc.

His current research interests include application of microalgae in bioindustry and bioenergy, nutraceutical and functional food preparation including proteomics and metabolomic studies in microalgae.



SK Barik

Professor at North-Eastern Hill University, Shillong and Director of CSIR-National Botanical Research Institute, Lucknow, India.

SK Barik is Professor at North-Eastern Hill University, Shillong. He was Director of CSIR-National Botanical Research Institute, Lucknow till recently. An accomplished ecologist and biodiversity researcher Prof. Barik has been working in the Himalayan region for the past 35 years. His works on plant-microbe interaction and restoration of degraded ecosystems using microbial technologies have high application value. He is a fellow of INSA, NASI and NAAS, and recipient of several national level awards for his research in biodiversity and plant sciences.



Sinosh Skariyachan

Assistant Professor in Microbiology, St. Pius X College Rajapuram-Kannur University (Aided by Govt. of Kerala), Kerala, India.

Specialization: M. Sc (Microbiology); M. Sc (Bioinformatics)- Bharathiar University, Coimbatore, TN; Ph. D (Biotechnology)-Visvesvaraya Technological University, Belagavi, Karnataka. Qualified ICAR- NET (Agri. Micro)
Experience: 19 Years in teaching and research
Area of expertise: Medical, Environmental and Food Microbiology, Bioinformatics and Computational Biology, Computational Drug Designing, Chemo-informatics, Immuno-informatics and Computational Systems Biology

Major contributions:

- Identified several potential natural lead molecules against prospective molecular targets of multidrug-resistant bacteria and viruses by structure-based virtual screening approaches.
- Modeled and validated novel drug targets of several pathogenic bacteria and viruses by computational biology approaches.
- Screened novel chromophoric and fluorophoric therapeutic metabolites from symbiotic bacteria associated with marine sponges towards drug-resistant bacteria.
- Isolated several thermophilic bacterial consortia from extreme environments and formulated novel microbial consortia that showed enhanced degradation to low and high-density polyethylene and polypropylene

- Awards: National Level Best Teacher Award by Microbiologist Society of India (2022-23); Bill and Melinda Gates Foundation Abstract Award for Scientists (2021) by ASM and FEMS, Young Scientist Award- Association of Microbiologists of India (2016); Young Investigator Award from India and South East Asia by International Society for Infectious Diseases (2016); World's Top 1 % of Reviewer in Biology & Biochemistry by Web of Science-Publon (2018 & 2019); Conference grant award by EMBL-EMBO, FEMS, DST-SERB, ISID, ASM, Best mentor award by KSCST, IISc, Bangalore (2014), Best research paper awards: More than 25 Conferences

- Recognitions: Associate Editor: Computers in Biology and Medicine (IF: 7.7; Elsevier); Academic Editor: Plos One, Guest Editor: Frontiers in Microbiology, Editorial Board Member: 5 SCI journals. Reviewer: More than 130 SCI journals

- Publications: 85 SCI indexed international journals (Citations: 1766; h index=22; i10 index=36); 16 Invited book chapters, 01 text book, 85 conference papers, 05 Articles in scientific magazine and periodicals. Patents: 01

- Life member in more than 20 Scientific and Professional Societies

- Plenary/invited speaker: More than 40 National//International Conferences and symposiums
- Guided more than 80 projects in UG/PG/PhD level



Rup Lal

INSA Senior Scientist at Acharya Narendra Dev College, University of Delhi, New Delhi, India.

He is the Fellow of American Academy of Microbiological Sciences (FAAM), Indian National Science Academy (INSA), National Academy of Sciences (FNASc), National Academy of Agricultural Sciences (FNAAS), Academy of Microbiological Sciences (FAMSc). He was Ambassador to ASM (2012 to 2015) and serving as Senior Ambassador for ISME and FEMS, Advisor to IMiLI-SAC (International Microbial Literacy Initiative-South Asia Centre) and Honorary Director PhiXgen Pvt Ltd, Adjunct Professor, Career Point University, Hamirpur, visiting Prof Kumaun University, Nainital and NASI Senior Scientist Platinum Jubilee Fellow at TERI.

Prof Rup Lal has over 40 years of experience in teaching, administration and research. He has supervised 75 PhD thesis, edited /authored seven books and published over 270 research papers with more than 10,000 ISI citations and h-index of 50.

Professor Lal is the recipient of various prestigious fellowships and awards like Alexander von Humboldt Fellowship, DBT Overseas Fellowship, Indo-US-ASM Professorship in Microbiology, Endeavour Executive Fellowship, Moselio Schaechter Distinguished Service Award from ASM, Prof. S.R. Vyas Memorial Award, Prof. B.N. Johri Award and Life Time Achievement Award from the Association of Microbiologists of India. During the past more than a decade he is propagating microbial literacy among masses and even school children. He has also been actively involved in conducting several workshops across the country to train young students in the field of computational biology.



Rakshak Kumar

Senior Scientist specializing in Environmental Microbiology at CSIR-Institute of Himalayan Bioresource Technology (CSIR-IHBT), Himachal Pradesh, India.

He has spearheaded research in high-altitude microbiology. With a Ph.D. from North Eastern Hill University and postdoctoral experience at CSIR-Institute of Microbial Technology and Sikkim Central University, his work focuses on harnessing microbial communities from extreme Himalayan environments for societal and industrial benefits. Notable achievements include innovative approaches to organic waste management, crop cycle optimization for Shiitake mushroom production, and bacterial applications for plant growth promotion. His efforts have led to the development of technologies for accelerated compost degradation, benefiting crop yields in cold hilly regions. Dr. Kumar's research initiatives have also contributed to the establishment of SFURTI clusters, generating livelihood opportunities for over 1150 individuals. With 57 research articles in international journals and mentoring seven Ph.D. students, his contributions continue to drive advancements in environmental microbiology.



Radha Prasanna

Head, Principal Scientist, Division of Microbiology, ICAR-Indian Agricultural Research Institute, New Delhi, India.

Dr. Radha Prasanna has made significant and pioneering contributions towards exploring cyanobacteria and their interactions with other eubacteria and fungi besides plant-cyanobacteria interactions and their role in elicitation of plant metabolic machinery and modulating the plant-soil microbiome of crop plants through their multifaceted abilities as plant growth promoting, biocontrol and biofortifying agents. Novel microbial formulations including Cyanobacterial Biofilms have been developed as technologies, which can provide 20-30% N savings, stimulate crop growth, yields, soil nutrient availability and enrich produce.

Her major inputs to agricultural microbiology have been towards diversifying the role of cyanobacteria in crops other than rice and their significant role as plant growth promoting inoculants for wheat, maize, cotton, legumes and vegetable crops and as biocontrol agents against phytopathogenic fungi in vegetable crops. She and her team have undertaken comprehensive analyses of the taxonomic and niche-specific diversity of cyanobacteria in diverse agro-ecologies of India, developed biochemical and molecular markers and protocols for evaluating their establishment in soil and colonisation in plants. For protected cultivation, cyanobacteria-amended nursery mixes as disease, soil health restoration and nutrient management options for enhancing vigor, yield and quality of produce has been optimized. Several first-time reports were generated through prospecting cyanobacteria as valuable sources of novel genes and metabolites.

She has published more than 300 research papers [h index-65; Number of citations: 12975] and deposited more than 300 sequences in the NCBI. She is the recipient of Fellowship of NAAS (2005) and Academy of Microbiological Sciences (FAMSc 2019), ICAR Panjabrao Deshmukh Outstanding Woman Scientist Award (2012), Hari Krishna Shastri Award (2017) and Best Teacher Award (2008), which highlight her passion and excellence in teaching and research.



Prashant S Phale

Professor at IIT Bombay in Biosciences and Bioengg, Mumbai, India.

MSc in Biotechnology form MS U Baroda, 1987.

Ph D from IISC Bangalore, Biochemistry department in "Microbial metabolism of naphalene and naphathoic acid".. 1994.

Post doc at Blozentrum, Univ Basel, switzerland ...On structure-function relationship in outer membrane proteins 1994-1998.

Post doc at Harvard medical school, Harvard University on.. mamalian ion channels 1999 - 2000.

Faculty at IIT Bombay since may 2000...at Biosciences and Bioengg.

Broad research area: Microbial metabolism of aromatic pollutants and pesticides.



Pinaki Sar

Professor at Indian Institute of Technology Kharagpur, Kharagpur, India.

Pinaki Sar is an environmental microbiologist investigating environmental microbiomes and their biotechnological potentials using a combination of multi-omics and geo-analytical approaches. He is a professor of Biotechnology at Indian Institute of Technology Kharagpur, Kharagpur, India.

Pinaki Sar has obtained his Ph D from Banaras Hindu University, Varanasi, India and joined the prestigious Dr K S Krishnan Research Associate program of the Department of Atomic Energy, Govt. of India at Bhabha Atomic Research Centre, Mumbai in 2000. During his post-doctoral research he has worked extensively on bacteria-radionuclide interaction and developed biosorbents for bioremediation of nuclear waste. He has started his independent academic and scientific carrier at Birla Institute of Technology and Science, Pilani, India; and subsequently moved to IIT Kharagpur, Department of Biotechnology in the year 2004. He has worked as an international researcher at the Rice University, Houston with the BOYSCAST fellowship from Govt. of India. His research interests focused on deciphering environmental microbiomes and geo-/bio-interactions, defining environmental constraints of microbiome composition and function, and identifying organisms/bioprocesses relevant for biotechnological applications (e.g., carbon capture and utilization, bioremediation). His current areas of work include Microbial genomics and Metagenomics; Deep Biosphere; Geomicrobiology; Microbial CO2 capture and utilization; Biodegradation of plastics and bioremediation of landfill wastes.



Nirjara Singhvi

Assistant Professor at Dev Bhoomi Uttarakhand University, Dehradun, India.

She completed her PhD in 2021 from Department of Zoology, University of Delhi under the supervision of renowned microbiologists Prof. Yogendra Singh and Prof. Rup Lal. In her doctoral research, she has majorly focused on the proteomic architecture of rifamycin producer, Amycolatopsis mediterranei and decipher the molecular mechanism of antibiotic export in the mutated strains. She actively participate in International and National Conferences and has organized several computational biology workshops, conferences and symposium in collaboration with AMI-ISME-INSCR societies and various institutes. She was invited to Tribhuvan University Nepal for conducting the workshop on proteomics. She has been awarded with travel grant by International society for microbial ecology, The Netherlands to attend AMI annual conference 2018. She was awarded with INSCR best poster and ISME best oral presenter awards in various international conferences. She is also the member of microbiology societies like AMI, and INSCR. She is actively working in field of proteomics, comparative genomics, system biology and structural biology. She has published her research work in various reputed and peer reviewed journals like Journal of Proteomics, mSystems, Journal of Biomolecular Structure and Dynamics, Infection, genetics and Evolution and many more.



Natesan Manickam

Chief Scientist at CSIR-Indian Institute of Toxicology Research, Lucknow, India.

He is currently heading the 'environmental biotechnology division' and is coordinator of 'environmental toxicology' group.
Current research focus of him includes Identification of chemical residues from different environmental matrices, bioremediation of persistent toxicants, eco-toxicology risk assessments, microbial genomics, and profiling of antimicrobial resistance from waste and river water streams. He was coordinator of national missions like Namami Gange (Clean Ganges-River) for specific river stretches. In an effort to restore the contaminated hazardous sites, he has also developed two microbial technologies and licensed them to NRDC, New Delhi.
He was member of genetic engineering appraisal committee for 2 terms (for biosafety and approval of genetically modified crops/organisms etc).
He is a Task Force member in different committees of Department of Biotechnology (DBT), Ministry of Environment, Forest and Climate Change (MOEF& CC), under government of India.
He is also International Scientific Council member at Rovaltain Foundation, France.
More than 50 publications in international peer reviewed journals.
10 PhDs supervised
He has been awarded with,

- Long term DAAD fellowship award
- DFG-INSA fellowship award



Namrata Misra

CEO, Bhubaneswar City Knowledge Innovation Cluster, GoI
Advisor: KIIT TBI and Associate Professor at KIIT School of Biotechnology, Bhubaneswar, Odisha, India.

Dr Misra has a decade of experience in contributing to the innovation and startup ecosystem in various capacities at KIIT TBI. As one of the founding members of KIIT TBI, She has played a vital role in its growth journey, witnessing the transformation from a 10-member team to our current strength of 110 members, nurturing over 400 startups. She is currently serving as Chief Executive Officer since Aug 2023 in Bhubaneswar City Knowledge Innovation Cluster, an initiative of the Office of the Principal Scientific Adviser to the Government of India and Advisor, KIIT TBI.
During her tenure as the Head of Technology Incubation at KIIT TBI, she oversaw tech-driven startup incubation operations, managed numerous programs, and ensured the successful development of technologies from concept to commercialization. She was also responsible for incubation policy formulation, securing government and private funding, and ensuring compliance with state and central ministries.

Since 2016, she has served as the Co-coordinator of the BIRAC Regional Centre @KIITTBI, focusing on catalyzing innovation in the East & and North East regions. she has actively collaborated with R&D institutes, universities, and colleges in Odisha to cultivate an authentic innovation culture and mentor nascent incubation managers.
In addition to her leadership roles in the innovation and incubation ecosystem, she has maintained an active presence in research, specializing in bioinformatics and computational biology as an Associate Professor in KIIT School of Biotechnology, KIIT University. Her contributions have resulted in around 60 international journal publications, the development of numerous cutting-edge computation tools, databases, web servers, and the Editor of two scientific books (Springer & Elsevier). She has also served as the principal investigator for two DST-sponsored research grants. Her dedication to STEM has been recognized with prestigious awards, including the "Odisha Young Scientists Award 2019" by the Science & Technology Department of the Government of Odisha and the "Women Excellence Award-2022" by the National Environmental Science Academy.



Mrutyunjay Suar

Director General of R&D and Innovation at KIIT University, Bhubaneswar and the CEO of KIIT Technology Business Incubator (KIIT-TBI), Bhubaneswar, Odisha, India.

An entrepreneurial professor with PhD in Molecular Microbiology from University of Delhi and trained as postdoc at the Institute of Microbiology, ETH Zurich, Switzerland. He returned to India and established the School of Biotechnology in 2007 under KIIT University which became a Centre of excellence awarded by Department of Biotechnology, Government of India.

He also established KIIT technology Business Incubator (KIIT-TBI), promoting deep tech start-up companies. Under his leadership, KIIT-TBI nurtured more than 430+ start-ups in last 13 years and created 7000+ 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 startups and helped them through their journey from ideation to enterprise creation. Under his leadership, KIIT TBI receives the best TBI of the year award-2017 from Hon'ble President of India and the best IP driven Incubator of India award from the Ministry of Industries.

Currently, he is also the Chairman of Bhubaneswar City Knowledge Innovation Cluster Foundation (BCKIC), an initiative of the office of the Principal Scientific Adviser (PSA) to the Govt of India and creating the Science, technology and innovation ecosystem in Odisha and North East states. Under his leadership, BCKIC is setting up Technology and Innovation Hubs in all the eight states of North East with support from various ministries. Main purpose of these hubs will not only promote technology innovation but also will facilitate technology validation and deployment activities.

Received several recognitions including Fellow of Royal Society of Chemistry (FRSc), 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 was also nominated for Global Entrepreneurship leadership Symposium at HAAS Business School, USA and visited UC Berkley.



Kashyap Kumar Dubey

Professor and Dean School of Biotechnology at Jawaharlal Nehru University, New Delhi, India.

He is working in the area of biopharmaceuticals, process development and removal of antineoplastic compounds from aqueous waste. He is running two research project sanctioned from ICMR-DHR, CRG-DSTand completed Six projects funded by DBT (Horizon2020) on Clean Water for Health, BIRAC- DBT (PACE), BRICS-DST, UGC and SERB on microbial process development. He has been significantly published in the area of biomanufacturing and hospital aqueous wastewater treatment. He is having motivation towards development of low cost decentralised technology for onsite treatment of hospital aqueous water.



Jyoti Prakash Tamang

Senior Professor in Department of Microbiology of Sikkim Central University and Director of Research and Development Cell of the University.

Professor Dr. Jyoti Prakash Tamang is an Internationally recognized food microbiologist of fermented foods and beverages. Professor Tamang is the pioneering researcher in ethnic fermented foods and beverages of the Himalayan regions of India, Nepal and Bhutan; North East India and also of South East Asia for last 38 years focusing on history, gastronomy, microbiology and multi-omics approaches for microbiome and health benefits. He did MSc (Gold Medal) in 1985, PhD in 1992 from North Bengal University, Post-doctorate from National Food Research Institute, Tsukuba, Japan in 1995 and another Post-doctorate from Max Rubner Institute of Nutrition, Karlsruhe, Germany in 2002. Prof. Tamang was the International Centre for Integrated Mountain Development Mountain Chair for 2019-2022. He is Fellow of Indian National Science Academy (FNA), Fellow of National Academy of Sciences India (FNASc), Fellow of National Academy of Agricultural Sciences (FNAAS), Fellow of Indian Academy of Microbiological Sciences and recipient of Bio-Science Award of Department of Biotechnology. He has 38 years of teaching ad research experiences, and also more than 18 years of administrative experiences as Registrar, Dean and acting Vice-Chancellor. He has published more than 200 research publications including 9 books, 31 Book-chapters with more than 10,000 citations and 52 h-index. He produced 16 PhD students and 7 Post-doc. He has one patent. Prof. Tamang is also the Chairman of Scientific Panel on Alcoholic Beverages of FSSAI (Food Safety and Standards Authority of India), Government of India.



Jitendra Kumar

Managing Director of Biotechnology Industry Research Assistance Council (BIRAC), Department of Biotechnology, Government of India

Dr Kumar holds a PhD degree in Biotechnology from Institute of Microbial Technology, Chandigarh. Subsequently, he moved to University of Illinois at Chicago, where he worked on leukaemia. He also holds an MBA degree from the Fisher College of Business at Ohio State University, US.

After returning from US, he joined as a Vice- President of Life Science Incubator at IKP Knowledge Park, Hyderabad where he was involved in actively mentoring incubatee companies, creating pipeline of entrepreneurs through innovative models of team building around the technologies, working with public R&D laboratories and universities to create entrepreneurial models of commercialisation.

Later, he took charge as the Managing Director of Bangalore Bioinnovation Centre (BBC) with a focus on incubating innovations in agriculture, food and nutrition, biofuel/bio-energy and pharma/healthcare. He has worked closely with Department of Biotechnology, Government of India and the Department of Electronics, IT, BT and S&T, Government of Karnataka, to create a vibrant Life Sciences Innovation cluster in Bangalore. He is also a guest faculty at University of Agricultural Sciences, Centre for Human Genetics, Manipal Institute of Regenerative Medicine (MIRM) and Indian Institute of Science in Bangalore. He is a member of various Central and State Government Committees and advises on policy matters related to startups, innovation and entrepreneurship in Life Sciences. Currently, he is a member of CII national committee on Biotechnology, Member of Association of Biotech Led Enterprises (ABLE), Member of committee for Karnataka Start-up policy and Member for Government of India supported Bangalore Innovation cluster under the aegis of Indian Institute of Science, Bangalore.

He is an Internationally acclaimed thinker and advisor on Biotech Innovations and entrepreneurship. He has been invited as a speaker at various conferences in USA, South Korea and the Netherlands to represent India and Karnataka. He has inspired thousands of youths to start and build successful Biotech ventures. He has around 20 years of experience in research and innovation management in the area of life sciences. He has around 25 peer reviewed publications and around 45 products have been launched under his mentorship.



Iddya Karunasagar

Advisor, Research and Patent at Nitte University. Food and Agriculture Organisation. Karnataka, India

Iddya Karunasagar obtained his Masters and Ph.D degrees in Microbiology from Mysore University. He joined University of Agricultural Sciences (UAS), College of Fisheries, Mangalore as Assistant Professor, rose to become Professor, and Head of Division of Fisheries Science. He was appointed the first Director of Research of Karnataka Veterinary, Animal and Fisheries Sciences University. Indian Council of Agricultural Research (ICAR) awarded him National Professorship.

During 1999-2005, he served as drafting member of Joint FAO/WHO Expert Meeting on Microbiological risk assessment (JEMRA). He then moved to the Food and Agriculture Organisation (FAO) of United Nations and was based in Rome as Senior Fishery Officer, where he led a Team on fish safety and quality and was based at FAO Headquarters in Rome. He played a key role in several FAO/WHO food safety risk assessments, which led to the development of international food standards at Codex Alimentarius Commission. He represented FAO in meetings of Codex Committee on Food Hygiene and Codex Committee on Fish and Fishery Products. He was Lead Technical Officer for several food safety projects in Asia, Europe, Africa, South Pacific, Caribbean Islands and Latin America. He played a pivotal role in the development of WHO Five Keys for Safer Aquaculture Products.

After his retirement from FAO, he has been working as international consultant supporting projects funded by the Asian Development Bank, UNIDO, International Trade Center of United Nations. He was Member of WHO Advisory Group on critically important antimicrobials for human medicine. He has been working also with World Organisation of Animal Health on topics related to antimicrobial use in food producing animals. He is associated with Nitte University, Mangalore, which has been designated the FAO Reference Center for Antimicrobial Resistance and Aquaculture Biosecurity.



Amulya K. Panda

Director at Panacea Biotech Ltd, New Delhi and Former Director of National Institute of Immunology, New Delhi, India.

Dr. Amulya K. Panda has B. Tech degree from HBTI, Kanpur and Master degree in chemical engineering from IIT Madras on 1986, He did Ph. D from IIT Delhi and worked at National Institute of Immunology, New Delhi from 1990 to 2021. He retired from NII as its Director on May 2021. He was a visiting scientist at the Dept. of chemical engineering, University of California at Berkeley, USA. His area of expertise in bioprocess engineering encompassing fermentation, protein purification and formulation of biologicals using polymeric nanoparticles. Inclusion body refolding method developed by Dr. Panda is recognized worldwide for high throughput recovery of bioactive protein from E. coli.

He was awarded the Young Asian Biotechnologist Prize from the Society for Biotechnology, Japan, for the year 2004. He has published 165 research papers, 12 book chapters and has guided 25 Ph. D students and around 60 master students and have 38 pending/granted patents. He was the president of the Association of Microbiologist of India (AMI) in 2017. He has been a Fellow of the Royal Society of Chemistry (FRSC) since 2020. Currently he is overseeing the vaccine and biological research and manufacturing activities at Panacea Biotech Limited, Delhi.



Hira Paul Gangnegi

Retired professor (March 2019) from University of Delhi.

Dr. Hira Paul Gangnegi is a retired professor (March 2019) from University of Delhi. He completed his M.A., M.Phil, and PhD from the Department of Buddhist Studies, University of Delhi and been the (HOD) Head of the Department of Buddhist Studies from 2014-2017. His study focused on cultural heritage of Mahayana Buddhism in Tibet and Himalayan Region, Its Art and philosophy. Later on, post-retirement been Head of the Department of Buddhist and Tibetan Studies at Namgyal Institute of Buddhist and Tibetan Studies in Gangtok, Sikkim from 2019-2023. On his other activities he's been the Secretary at All India Harijan Sewak Sangh, Delhi as well as Senior representative and Regional Coordinator in United Religion of Initiative (URI) A global network initiative North Zone CC.



Asha Chaubey

Senior Principal Scientist and Head of Fermentation and Microbial Biotechnology Division, New Delhi, India.

Dr. Asha Chaubey is presently working as Senior Principal Scientist and Head of Fermentation and Microbial Biotechnology Division. She is working in the area of fermentation technology for exploration and exploitation of microorganisms for the production of bioactives and novel enzymes for more than 18 years. These include isolation and characterization of microorganisms from unexplored niches of North-Western Himalayas, Shivalik foothills and endophytes. The significant contributions include biotransformation of industrially important molecules, immobilization of enzymes for enantioselectivity improvement, production of industrially important biopharpaceuticals and published her work in best journals of the field. She obtained Ph.D. degree from LLRM Medical college, Meerut in collaboration with National Physical Laboratory in the field of biosensors for diagnostics. During the doctoral research; she has significantly contributed towards the development of biosensors for health care and generated good quality publications and patents. Presently, she has been actively involved in developing fermentation processes for production of biopharmaceuticals, nutraceuticals, therapeutic enzymes and enzymes/products for agriculture applications.



Charu Dogra Rawat

Professor in the Department of Zoology at Ramjas College, University of Delhi, Delhi, India.

She has been involved in teaching and research for more than 18 years. She is the recipient of the most prestigious national teacher's award given to teachers in higher education - the Indian National Science Academy (INSA) Teacher's award 2021. She works diligently for the improvement of undergraduate education by exploring, applying and propagating various pedagogical approaches and has been conducting several workshops (organized by Centre of Excellence in Science and Mathematics education (CoESME), IISER, Pune) on research-based pedagogical tools across different regions of India. She is also a part of the Delhi Effective Education & Pedagogy Cluster (DEEP-C) under Delhi Research Implementation & Innovation (DRIIV) set up by the office of the Principal Scientific Advisor to Govt. of India (https://driiv.iitd.ac.in). As biology subject expert in Consortium for Education Communication (CEC), UGC, she has delivered > 50 EDUSAT live lectures including topics in microbiology for their 24X7 education channel; the lectures are available online on their YouTube Channel. She regularly writes articles on digital education, virtual universities, NEP 2020 etc. for CEC Newsletter and IndiaBioscience (supported by DBT, Govt. of India). She has co-organized outreach innovation camps at Bani & Biar schools in District Hamirpur, Himachal Pradesh, India and is actively involved in propagating microbiology literacy by conducting rural/urban outreach programs. On research front, Prof. Rawat is actively engaged in molecular biology and genomics research yielding publications in high impact reputed national and international journals. Her area of research includes environmental remediation, toxicology, genetic engineering, and thermophiles. She has received research grants from Department of Biotechnology (DBT) and Science and Engineering Research Board (SERB), Department of Science and Technology (DST), Government of India. In 2019 she represented young scientist of University of Delhi in a 20-member delegation from India to visit Universities in China to develop collaboration in science and technology research between the two countries.



Punyasloke Bhadury

Professor of Biological Sciences at IISER Kolkata, India.

He works at the interfaces of earth system science and biology looking at microbial biocomplexity and carbon cycling, developing new technologies for sustainability and also studies aspects of antimicrobial therapeutics. He is an Editor of a number of SCI journals including Geoscience Letters, Lithosphere, PeerJ and iScience.



Anil Kumar Tripathi

Senior Professor at School of Biotechnology, Jawaharlal Nehru University, New Delhi, India.

Dr Anil Kumar Tripathi is a Senior Professor at School of Biotechnology. Till recently (February 2024) he was also Director, Institute of Science at Banaras Hindu University, Varanasi (since February 2019). Before that during 2014-2019, he served as Director of CSIR-CIMAP (Central Institute of Medicinal and Aromatic Plants) at Lucknow. He conceptualized and led the CSIR-Aroma Mission (which is the most notable success story of CSIR in recent times) in its formative years as Mission Director. Prof Tripathi obtained his M. Sc. and Ph. D degrees in Botany from Banaras Hindu University, published 95 peer-reviewed articles and supervised 22 doctoral dissertations. His researches focus on genetics, genetic engineering, systems biology and synthetic biology of a plant growth promoting bacterium. He is a Fellow of the Indian National Science Academy (INSA), Indian Academy of Science (IASc), National Academy of Sciences India (NASI), National Academy of Agricultural Sciences (NAAS) and Association of Microbiologists of India (AMI). He is also a recipient of the prestigious J C Bose National Fellowship, Fulbright-Nehru Fellowship and a number of other national awards and grants. He made academic visits to more than 25 countries and delivered lectures at a large number of national and international conferences. At BHU, he was instrumental in establishing a DST-supported state-of-art Sophisticated Analytical Technical Help Institute (SATHI) and a BIRAC-supported Bioincubator for Nurturing Entrepreneurship for Scaling Technologies (BioNEST). He is Coordinator of both SATHI-BHU and BioNEST- BHU since their creation.



Sanjay Kumar Gupta

Assistant Professor of Microbiology at Swami Shraddhanand College (SSN), Delhi, India.

He received his Ph.D. in the area of Microbiology from the University of Delhi. After a brief stint as a postdoctoral fellow at the University of Louisville, USA, BNITM, Hamburg, NII New Delhi and IVRI Bareilly, he was appointed as Assistant Professor in the Department of Biotechnology, Mahayogi Gorakhnath University, Gorakhpur.

His research interest includes diversity of microorganism of extreme environments, development of vaccine against blackleg disease and diagnostic kits for protozoan's disease in cattle. He is currently producing Cordyceps militaris fungus and studying its different pharmacological activity in cell line, formulating probiotics possesses the property combats the problems of hypertension, high blood pressure, high cholesterol level, hepatotoxicity, colorectal cancer and rheumatoid arthritis.



Saravanan Matheshwaran

Assistant Professor at the Indian Institute of Technology Kanpur, India.

Dr. Saravanan Matheshwaran is an accomplished Assistant Professor at the Indian Institute of Technology Kanpur, specializing in Biological Sciences and Bioengineering. He earned his PhD from the Indian Institute of Science, Bangalore, under Prof. V. Nagaraja's mentorship, receiving accolades such as the Sreenivasaya Medal for his exceptional thesis. Dr. Matheshwaran's postdoctoral journey included stints at the London Research Institute (EMBO Fellowship) and the European Molecular Biology Laboratory (EIPOD-Marie-Curie Fellowship), shaping his expertise in molecular biology. He has been awarded INSA Young Scientist Medal and DBT Innovative Young Biotechnologist Award for his remarkable contributions. His research has significantly advanced the understanding of microbial adaptation to stress and the dynamics of chromatin during DNA repair. Notably, his research group's discovery of potential LexA-inhibitors with antimutagenic properties stands out as a testament to his innovative work. Dr. Matheshwaran's impactful research is reflected in his extensive publication record, with over 35 articles in renowned journals, and the acquisition of several patents. His contributions have attracted substantial funding from prestigious organizations such as INSA, SERB, DBT, ICMR, DST, and MHRD, further highlighting the recognition and support his work has received within the scientific community.



Bhabatosh Das

Faculty in Translational Health Science and Technology Institute (THSTI) Faridabad, India.

Dr. Bhabatosh Das is a molecular microbiologist trained in (i) Indian Institute of Technology (IIT)-Kharagpur (2003) (ii) Indian Institute of Chemical Biology (IICB) Kolkata (2008) (iii) Institute of Integrative Biology of the Cell (I2BC) France (2011) and (iv) Osaka University (2017) Japan. At present he is the faculty in Translational Health Science and Technology Institute (THSTI) Faridabad, India. He has research experience in (i) microbial genomics (ii) metagenomics and (iii) genome engineering. Dr. Das has recently developed robust metagenomic DNA extraction methods and studied microbiome of Indian population in health and diseases. His research has led to the development of a novel genetic tool for functional evaluation of any hypothetical genes including antibiotic resistance and anti-inflammatory genes.

Research interests The main focus of Dr. Das's research is oriented to understand (i) The ecological principles of the microbial communities inhibiting in the human body and their role in health and diseases (ii) Vaginal microbiome of Indian women and its importance in birth outcomes and (iii) Role of human associated microbiota in the emergence and spread of multidrug resistant (MDR) bacterial pathogens.



Minakshi Grover

Principal Scientist, Microbiology at ICAR-Indian Agricultural Research Institute, New Delh, India.

Dr Grover is Ph. D. Botany with sp. in Microbiology, ICAR NET (1998). Her major research areas are Microbial Ecology, Plant-microbe interactions under Abiotic Stress conditions; PGPR, Biocontrol, Soil biological health. Dr Grover has handled 5 externally funded and 5 inhouse projects as Principal Investigator. She has been actively involved in teaching and MSc/ PhD research guidance as postgraduate faculty of Microbiology at IARI. Dr Grover has number of research publications in international and national journals.

Her major Scientific Contributions are as follows

- Development of mixed bacterial inoculum for drought (CRIDA MI-I) and heat (CRIDA MI-I) stress management in rainfed crops.
- PUSA-AIM Technology: An Azospirillum based formulation for moisture deficit and nutrient management in millets.
- Characterization of seed endophytes from maize and pearl millet for application in stressed agriculture.
- Characterization of rhizobacterial diversity of rainfed crops for abiotic stress tolerance.
- Identification of Bacillus subtilis RP24, antagonistic to ove 15 phyto-pathogenic fungi.
- Characterization of antifungal metabolite (iturin A) produced by B. subtilis RP24.
- Partial purification of antifungal metabolite from Bacillus subtilis strain RP24.
- More than 120 16SrDNA sequences submitted to NCBI GenBank. (NCBI database).



Durgesh Narain Singh

Scientific officer in BioNEST-BHU, Banaras, India.

Dr. Durgesh Narain Singh completed M. Sc (Microbiology) from Dr. R.M.L. Avadh University, Ayodhya, U.P., India in year 2005. He was awarded Chancellor gold medal for his outstanding performance in M. Sc (microbiology) exams. After passing M. Sc and qualifying National eligilibity test he joined Ph. D program in microbiology at the School of Biotechnology, Banaras Hindu University, Varanasi, U.P., India. He completed his doctoral thesis in the area of “microbiology and metagenomic of an Indian coalbed”, a pioneer work in India. Based on his Ph. D publications, he was invited to deliver a lecture in an international conference titled “Secondary Biogenic Coal Bed Natural Gas International Conference” organized by the School of Energy Resources, University of Wyoming, Laramie, USA. He has post-doctoral stints at CSIR-Central Institute of Medicinal and Aromatic Plants, Lucknow, U.P., India. He joined University College Dublin as a post-doctoral fellow, and after his selection as CSIR-Senior Research Associate under the Pool Scientists scheme (Council of Scientific and Industrial Research, India) he joined the Department of Zoology, University of Delhi, Delhi, India.

Currently, Dr. Singh is working as a Scientific officer in BioNEST-BHU, a bioincubation center where he is promoting innovation and entrepreneurship among BHU faculties. He has been able to mobilize more than 3.0 crore as a startup grant in BHU. His research includes employing “omic” (genomics, metagenomics, and proteomic) approaches to address the challenges in environment and agriculture. His research findings have been published in different peer-reviewed journals, and he is the recipient of many awards including Gold medal-2005, FEMS Young scientist meeting grant-2011, DST Travel grant-2012, and Young Scientist award-2019.



Rajeev Kaushik

Principal Scientist and Professor in Division of Microbiology at ICAR-IARI, New Delhi, India.

- Teaching experience: 26 years of teaching experience as faculty of Environmental sciences (1997-2005) and Microbiology (2010 – till date) at ICAR-IARI. Guided 3 M.Sc. and 8Ph.D. students.
- Funds generated: Generated total funding of 655.508 lakhs through different externally funded projects from ICAR-NAIP, ICAR-AMAAS, ICAR-NASF and DBT as Principal Investigator and total combined funding of Rs 7,120.793 lakhs as Consortium C-PI in ICAR-NAIP projects.
- Technology developed and commercialized: Developed and commercialized “Pusa SAMPOORN” Liquid biofertilizer for various field crops for providing N, P, and K
- Technology developed and in the process of commercialization:
- PUSA SANJEEVNI: Bacterial formulation for imparting resilience in various crops against heat and drought stress.
- PUSA BioGreen: Bacteria-Cyanobacteria consortium for reducing methane emission and growth promotion of flooded rice.
- Advanced research in Microbial Genomics: Carried out genome, metagenome and transcriptome sequencing projects on halophilic archaea, PSB, Psychrophilic bacteria, microbiome of desert monocots.

Extension activities:

- Developed three Climate Smart Villages under ICAR-NICRA project.
- Developed two self-help groups at Anta, Baran, Rajasthan under DBT funded project Biotech-KISAN Hub in Aspirational Districts.”
- Regular MGMG and Institute’s mandated extension activity

SPEAKERS

International Symposium of Ciliate Biology (ISCB)



Alan Warren

Scientific Associate, Natural History Museum, London, UK.

After graduating with a BSc in Microbiology in 1977, I joined the Natural History Museum (NHM), London, to undertake a PhD focused on the ecology and systematics of peritrich ciliates. In 1979, I became a member of staff in the Protozoa Research Group at the NHM. I was awarded my PhD in 1983. I continued to carry out research on the systematics and biodiversity of ciliates, initially focusing on freshwater forms but for the last 25 years of my career I focused on marine forms, mainly in collaboration with various research groups in China. For ca. 35 years, I also had curatorial responsibility for the NHM protozoa collection. I have been an editorial board member of several journals and held various positions on the committees of both Protistology-UK and the International Society of Protistologists. In addition, I am a former member of the Editorial Board of the World Register for Marine Species (WoRMS) with responsibility for the Ciliophora (ciliates). I have published ca. 380 articles in peer-reviewed journals, 23 book chapters and co-edited two books. I retired in 2021 but continue to pursue my research interests as a Scientific Associate of the NHM.



Rosaura Mayén Estrada

Professor, Protozoology Laboratory, Department of Comparative Biology, Faculty of Sciences, Universidad Nacional Autónoma de México (UNAM), Mexico

Full-time Professor at the UNAM, Mexico. Her main research area is taxonomy and ecology of peritrich ciliates; she has participated in several international conferences. She has publications in several journals and is an academic editor in some journals. She has published several manuals with a teaching focus. She has been invited for research stays at several Universities and Institutes. As a teacher she teaches classes on protists and in the area of Animal Biology. She has been a tutor for several students who currently work as researchers. She currently collaborates with researchers at several institutions.



Bettina Sonntag

Senior scientist, Head of working group "Ciliate ecology and taxonomy", Research Department for Limnology, Mondsee of the Leopold-Franzens- University Innsbruck

Her research group focuses on the ecology, diversity and taxonomy of ciliates mainly from lakes. To understand the autecology of ciliates and their bacterial and algal endosymbionts, we study these protists on an alpha- taxonomic level including morphological and molecular state-of-the-art methods. Presently She is a Senior scientist and Head of the research group 'Ciliate ecology and taxonomy', Research Department for Limnology, Mondsee, University of Innsbruck, Austria. Academic education: 2000 Ph.D. in Natural Sciences, University of Innsbruck, Austria; 1998 Diploma in Biology with a focus on Ecology and Limnology.

Recent and ongoing researchprojects
'Concert of Trumpets: Next Generation Taxonomy of Stentor', Jan 2024 – Jan 2028, Austrian Science Fund FWF
'NGTax – Next Generation Taxonomy: Ciliophora and their bacterial symbionts as a proof of concept' (PI Giulio Petroni, University of Pisa, Italy), EU-Horizon2020 Marie-Curie Actions – Research and Innovation Staff Exchange (RISE),Jul 2021- March2026
'Aquatic Symbiosis Genome Project', Subhub of Patrick Keeling (University of British Columbia, Canada), 'Ciliates as models for symbiosis: using genomic analyses of functionally diverse symbiotic associations with parallel origins to gain insights into basic evolutionary principles of symbiosis' Wellcome Sanger Institute and Gordon and Betty Moore Foundation, ongoing since Oct 2020
'Pan-European Lake Sampling – Microbial Eco-genomics' Czech Academy of Sciences, Biology Centre CAS, Budweis Czech Republic, PI Rohit Ghai, Michaela Salcher, Jan 2020 – Dec 2024
'Freshwater endosymbiotic algae and their ciliate hosts: morphology, phylogeny, ecology', Apr 2016 – Mar 2021, Austrian Science Fund FWF
'Co-occurrence networks in aquatic food webs: ciliates as models', Sep 2015 – Aug 2020, Austrian Science Fund FWF

Publications (peer-reviewed)
See www.ciliates.at for a full list
>45 publications in total



Valentina Serra

Researcher at the Biology Department of Pisa University

She carried out PhD at the Biology Department of Pisa University on biodiversity of Ciliates and their symbionts, from the Indian subcontinent. She contributed to the development of the "next generation taxonomy" (NGTax) workflow to achieve a comprehensive description of ciliates and their symbionts, incorporating traditional techniques, ultrastructural analyses, molecular and state of the art genomics through bioinformatics tools. She has been contributing to the field of ciliate biodiversity, systematic and symbiosis for more than ten years.



Elena Sabaneyeva

Associate Professor at the Department of Cytology and Histology, Faculty of Biology, Saint-Petersburg State University, Russian Federation.

For more than 30 years, she has been studying symbiotic associations between ciliates and other microorganisms. Her other research interests include nuclear dualism in ciliates and the role of the intranuclear actin in nuclear organization in protists. Elena Sabaneyeva possesses expertise in light, electron and confocal laser scanning microscopy, fluorescence in situ hybridization and immunocytochemistry. The results of her studies are published in “Protist”, “European Journal of Protistology”, “Protoplasma”, “Plos ONE”, "Scientific Reports", “Symbiosis”, “The ISME Journal”,“Nature Communications”. She gives a general course of lectures “Cell Biology” and specialized courses of lectures “Model Objects in Cell Biology" and "Special Issues of Cell Biology".

She was a Saint-Petersburg Unit coordinator in two projects supported by European Commission: 7FP IRSES projects “CIliates as NAtural Reservoir of potentially PATHOgenicBACTERia: an ecological, functional and evolutionary genomic investigation” (CINAR PATHOBACTER)and "CARbonBALAncing for nutrient control in wastewater treatment" (CARBALA).

Elena Sabaneyeva is on the editorial board of an international journal "Protistology".



Komal Kamra

Associate Professor (Retd.), SGTB Khalsa College, University of Delhi, Delhi

Dr Kamra, a University topper in her post graduation, earned her PhD in ciliate biology from University of Delhi. She has teaching experience of more than 44 years in SGTB Khalsa College and has been a visiting scientist with Dr J Martin, Cordoba, Spain and with Dr Alan Warren, Natural History Museum, London. She has successfully completed research projects funded by UGC, DST,DBT and University of Delhi. She has delivered several invited lectures in national and international meetings and has published 32 research articles in peer reviewed journals and chapters in 6 books. She also has a patent “Fluorescent Powder Compositions for Developing Latent Fingerprint”. Life Member of various societies in the field of microbiology, spinal cord injuries and epilepsy, she is actively involved in rehabilitation of people with spinal cord injury and epilepsy. She is recipient of National award for outstanding employee in 2004 conferred by Dr APJ Kalam, Late President of India. Her research interests span development biology of ciliates, ciliate diversity, and ecology and biomonitoring of water using ciliates. Her research collaborations include University of Camerino, Italy, International Research Coordination Network for Biodiversity of Ciliates funded by National Science Foundation (USA) and China National Science Foundation and with Dr Alan Warren, former SeniorScientist, Natural History Museum, London.

She has been associated with the RBPT program with IISER Pune right from its inception. Five students completed PhD and several undergraduate studentshave been trained under her supervision. She is presently associated with the Ciliate Biology Research Lab at Acharya Narendra Dev College, University of Delhi as Adjunct Scientist.



Nageswara Rao Amanchi

Assistant Professor in of Zoology at University College of Science, Osmania University, Hyderabad, Telangana, 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, bioremediation, ciliate biology and metagenomics. Two of his Research students have been awarded PhD degree and three are pursuing. 22 students have completed MSc dissertations under his supervision. He completed two research projects funded by UGC and DBT successfully and published 19 research papers in national and International repute journals, three book chapters/books on Biodiversity and Human Health, Environmental Toxicology. He has collaborations with other researchers in the disciplines of Environmental Sciences, genetics, microbiology and biotechnology. He is the instructor for both Undergraduate and Post-graduate programmes for the past 18 years besides research experience. The topics he teaches are Biology of Invertebrates and Vertebrates, Bio molecules, Environmental and Conservation Biology, Embryology, Molecular Genetics and Developmental Biology, Systems Biology, Principles of Toxicology, Environmental and Occupational Toxicology and Research Methodology. 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 the Journal of Ecotoxicology and environmental safety and others.



Gaytha A. Langlois

Chair of the Department of Science and Technology at Bryant, Smithfield, Rhode Island, USA.

Gaytha A. Langlois, PhD, is Professor Emerita in Environmental Policy at Bryant University, located in Rhode Island, USA, where her scholarly pursuits have included studies of microbial communities associated with coral reefs and oil-stressed ecosystems. Her research focuses on the microbial dynamics of ciliates in shallow coastal sediments and the diversity of epiphytic marine ciliates in rock pools, along with the ecological implications of ciliate/coral interactions following bleaching episodes. She has served as Membership Secretary and President of the International Society of Protistology (ISOP). Her courses and writings have addressed climate change impacts on Arctic tundra habitats, protection strategies for endangered Metasequoia redwoods in China, and the challenges of integrating innovative energy technology solutions.

Dr. Langlois served as Chair of the Department of Science and Technology at Bryant and co-developed the Global Environmental Studies program. She created the Center for Sustainable Business Practices and has been active in community service where she helped to craft municipal and statewide environmental policy in both governmental and NGO roles.



Alexey Potekhin

Professor at the Department of Microbiology, Faculty of Biology, St Petersburg State University, Saint Petersburg, Russia.

Prof. Dr. Alexey Potekhin, born in 1975, Saint Petersburg (ex Leningrad), USSR. Obtained his Ph. D. in Cell Biology (2002) in St Petersburg State University. Since 2007 – associate professor, since 2015 he worked as a full professor at the Department of Microbiology, Faculty of Biology, St Petersburg State University, Saint Petersburg, Russia. Since summer 2022 he is a senior researcher at the Department for Limnology, Mondsee, University of Innsbruck, Austria. His research focuses in ciliates, and his main interests are Paramecium genetics, epigenetics and speciation, and diverse symbioses between ciliates and bacteria.

Prof. Potekhin is an author of more than 50 publications in the peer-reviewed journals, including Nature, Nature Communications, ISME Journal, Genome Biology and Evolution, Microorganisms. He worked as an Invited Professor in Ecole NormaleSuperieure, Paris, France, at the University of Pisa, Italy, and at the National Autonomous University of Mexico. In last 10 years he was a principal investigator in a number of research grants, and his group participated in several European international network projects. His group collaborates with the groups from Ecole NormaleSuperieure, Paris, France; University of Pisa, Italy; University of Wuppertal, Germany.



Santosh Kumar

Senior scientist at the Zoological Survey of India, Kolkata. versity, Saint Petersburg, Russia.

His research mainly focuses on the taxonomy and ecology of ciliated protists. He obtained his Ph.D. from the University of Delhi, where he studied the diversity of ciliates from selected biotopes in India and the effects of heavy metals on certain ciliates, especially the recombinant cell lines of Tetrahymenathermophila. Additionally, he explored the community structure of ciliates from extreme habitats and their adaptation to high sulfur tolerance, photosensitivity, feeding behavior, and cytotoxic compounds. He was part of the Soil Mapping project in Italy, where he studied ciliated protozoa as bio-indicators of soil quality in agricultural fields under different farming practices. He also participated in the Korean Research Fellowship program, where he investigated ciliated protists as bio-indicators of water quality in industrial polluted sites and extreme habitats.His current research focuses on studying the diversity of ciliates and gastrotrichs from Protected areas (National parks and Sanctuaries) as well asRamsar wetlands of India;

the diversity of marine ciliates associated with healthy and diseased corals; developing technology for reducing bacterial contamination in rivers, ponds, and drains; and studying faunal diversity in the Ramsar Wetlands of India. Dr. Kumar has described over 20 novel ciliates from India, Australia, Jamaica, South Korea, and Italy, using standard methods such as morphology and molecular phylogeny employing ribosomal and mitochondrial genes. He has published numerous articles in reputable journals, holds a patent, and has contributed to over 25 presentations in national and international conferences, symposia, and workshops.



Jasmine.P

Senior Scientist in the Protozoology section of Zoological Survey of India, Kolkata, under Ministry of Environment and Forests, Govt. of India.

Jasmine's research interest focuseson testate amoebae, Marine zooplankton and tardigrade studies.She is particularly interested on the effect of climate change on Microbial diversity of India, especially marine, freshwater and soil protozoans. She is associated with the projectSeasonal dynamics of microzooplankton (ciliates) and its role in the pelagic food web of the northern coastal waters of Bay of Bengal. Her graduation and Post-graduation was at University of Kerala, India. Her career started as a doctoral researcher at National Institute of Oceanography in 2002, and joined the academic ranks as a Research Scientist in Centre for Marine Living Resources (CMLRE) under Ministry of Earth sciences in 2007. During her research in NIO & CMLRE, she was mainly involved in the research on environment and productivity patterns of the Northern Indian Ocean and the seasonal diversity of mesozooplankton community especially planktonic ostracods in the ArabianSea and Bay of Bengal.She was participated regularly in research cruisesand an onboard experience of more than 400days. She was also selected as one of the zooplankton specialists during the Pilot Expedition of Southern Ocean by National Centre for Antarctic and Ocean Research (NCAOR) India during 2004, and it was India'sfirst venture to Southern Oceanresearch. She served as a scientist in Biological Oceanography in the Marine Fisheries Research Centre, Ministry of Fisheries, Sultanate of Oman in 2009 to 2011. As a researcher her contribution towardsthe Microbial diversity of India and Ocean sciences has been accepted and published in the international and national peer reviewed journals. Recently 2017 to 2019, she was participated in the ArcticExpedition of India, 3 times, conducted by NCAOR, MoES. She is also involvedin the supervision of curatorial, care and maintenance of the Nationalzoological collections of Protozoa section, ZSI, Kolkata.

INVITED SPEAKER
ABSTRACTS



The power of microbes

Rino Rappuoli[1]

[1]Biotecnopolo, Siena, Italy

President of IUMS, the International Union of Microbiological Societies

Abstract

The recent Covid-19 pandemic has been a painful reminder that microbes, by causing infectious diseases, often changed the course of human history by killing more people than any war, by destroying flourishing economies and by causing the extinction of powerful civilizations. Fortunately, only 1400 of the 1 trillion of microbial species living on Earth are responsible of infectious diseases. The rest of microbes support every form of life on Earth and make the planet habitable. The International Union of Microbiological Societies (IUMS) is calling microbiologists to take advantage of the power of microbes to identify microbe-driven solutions that can contribute to achieve the Sustainable Development Goals (SDGs) of the United Nations. IUMS believes that many microbe- mediated, solutions can contribute to mitigate climate change. Microbes can reduce greenhouse gases by mitigating CO2, CH4, and N2O emissions. Microbes can produce biofuels, increase soil fertility and food production, increase clean water availability and contribute to the health of people by providing an healthy and diverse microbiome, and by producing medicines and vaccines to prevent pandemics and infectious diseases.

Production of new natural products by bridging regulatory functions

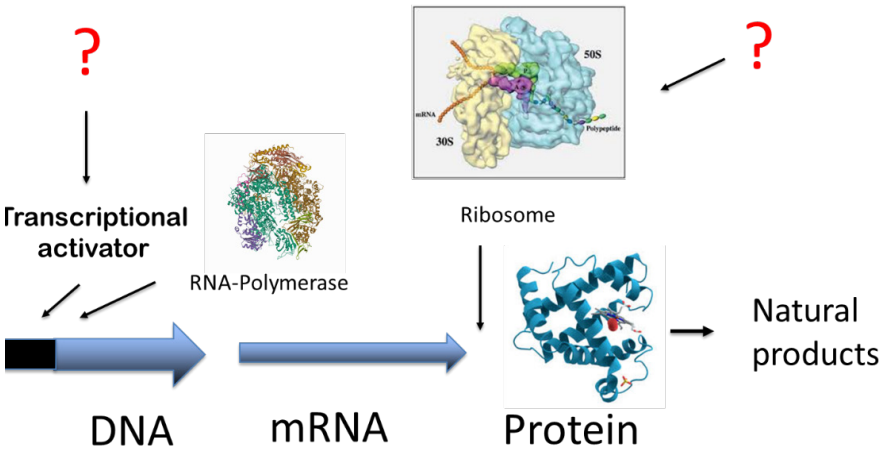
Andreas Bechthold[1]

[1]University of Freiburg, Germany

Abstract

Natural products play a crucial role in the development of drugs. Over the last forty years one third of all approved drugs are natural products or derivatives from them. Additionally, another third uses at least a pharmacophore of a natural product. The therapeutic areas do not only cover the widely known fields of antibiotics and cytostatics, but also anticoagulants, anti-hypertensive or anti-diabetic drugs and many more. Nevertheless, antibiotics are one of the most prominent fields for natural products. Increasing antibiotic resistance in the upcoming years is leading to an urgent need for the development of new antibiotics. The World Health Organization stated the antibiotic resistance crisis to be a “global public health concern”. Also, the Center for Disease Control and Prevention and the European Medicines Agency are substantially concerned about the course in the last decades.

Streptomyces are the largest source of natural products among microorganisms. Unfortunately, most of natural product biosynthetic gene clusters in the genome of these Streptomyces are not activated under lab conditions. In my talk I will present examples showing how our research on regulatory genes paved the way to activate gene clusters and to generate novel compounds.



Exploring the ocean multiverse with *Tara* Oceans

Chris Bowler[1]

[1]Ecology and Evolutionary Biology Section, Institut de Biologie de l'Ecole normale supérieure (IBENS), Paris, FRANCE

Abstract

The ocean is the largest ecosystem on Earth and yet we know very little about it. This is particularly true for the plankton that drift within, even though they form the base of marine food webs and are key players in Earth's biogeochemical cycles (Bowler et al. Nature Microbiol., 2022). Ocean plankton are at least as important for the Earth system as the forests on land, but most of them are invisible to the naked eye and thus are largely uncharacterized. To increase our understanding of this underexplored world, a multidisciplinary consortium, Tara Oceans, was formed around the 36m research schooner Tara, which sampled plankton at more than 210 sites and multiple depth layers in all the major oceanic regions during expeditions from 2009-2013 (Karsenti et al. Plos Biol., 2011). This talk will summarize the foundational resources from the project, which collectively represent the largest DNA sequencing effort for the oceans (see Science special issue May 22, 2015 and Cell, Nov 14, 2019), and analyses that illustrate several aspects of the Tara Oceans' eco-systems biology approach to address microbial contributions to ecological and evolutionary processes. The project provides unique resources for several scientific disciplines that are foundational for mapping ocean biodiversity of a wide range of organisms that are rarely studied together, exploring their interactions, and integrating biology into our physico-chemical understanding of the ocean, as well as for identifying new organisms and genes of biotechnological interest. These resources, and the scientific innovations emerging to understand them, are furthermore critical towards developing baseline ecological context and predictive power needed to track the impact of climate change on the ocean.

Novel insights into the oxidative catabolism of (+)-pinoresinol by *Pseudomonas* sp. strain SG-MS2: Pathways, enzymes, and biochemical implications

Gunjan Pandey*

*Senior Research Scientist, Environment CSIRO, Australia

Abstract

This talk presents research on the microbial degradation of (+)-pinoresinol, a plant defense compound and significant lignan found in the human diet, focusing on the oxidative catabolism by *Pseudomonas* sp. strain SG-MS2. Unlike previously characterized bacteria that employ reductive transformation, SG-MS2 utilizes an oxidative strategy to mineralise (+)-pinoresinol, a process initiated by a novel flavoprotein from the vanillyl alcohol oxidase/p-cresol methyl hydroxylase (VAO/PCMH) enzyme family. This enzyme, crucially supported by a cytochrome component, hydroxylates (+)-pinoresinol at the benzylic carbon, a step pivotal for the subsequent metabolic breakdown involving a series of unique biochemical transformations. Through a combination of comparative genomics, proteomics, and enzyme assays, we elucidated a gene cluster encoding for this enzymatic pathway, highlighting its efficiency in not just degrading pinoresinol but also in funneling the breakdown products into valuable biochemicals such as vanillin, vanillic acid, protocatechuate, and 2-methoxyhydroquinone. Our findings not only shed light on a novel biochemical route of lignan degradation but also open new avenues for the biotechnological exploitation of lignin-derived compounds. The implications of this work extend beyond environmental microbiology to encompass potential health benefits, given the association of lignan metabolites with reduced risks of cancer and cardiovascular diseases. This research underscores the versatility of microbial metabolism in lignin valorization and the potential for developing new strategies for the biosynthesis of industrially and pharmacologically relevant compounds.

Multi-Element Isotope Enantiomer Fractionation and molecular biological concepts to track transformation of persistent organic contaminants in soils and plants

Xiao Liu[1,2] & Hans H. Richnow[2,3]

[1]Institut Terre et Environnement de Strasbourg (ITES), Université de Strasbourg/EOST/ ENGEES, CNRS UMR 7063, F-67084 Strasbourg, France

[2]Department of Technical Biogeochemistry, Helmholtz Centre for Environmental Research-UFZ, Permoserstraße 15, 04318 Leipzig, Germany.

[3]Isodetect GmbH, Deutscher Platz 5b, 04103 Leipzig, Germany

*presenter: Hans H. Richnow

Abstract

We explore the options to tack the transformation of persistent organic pollutants (POPs) in soil and plants using stable isotope and enantiomer fractionation concepts. Hexachlorocyclohexane isomers (HCHs) were selected as representative model compounds for POPs to characterize uptake and degradation processes from source via rhizosphere and into plants. Through a series of field and laboratory experiments, we aim to explore the potential of combining isotope and enantiomer concepts to comprehensively investigate the transformation of HCH in soil-plant systems. In parallel molecular biology was used to characterize soil and plant microbiome.

The enantiomer and isotope fractionation of α-HCH ($\delta^{13}C$ and $\delta^{37}Cl$) allow characterizing the transformation of α-HCHs in soils by soil bacteria. The analysis of $\delta^{13}C$ and $\delta^{37}Cl$ of HCHs in plants demonstrate the potential transformation of HCHs facilitated by plant enzymes and endophytes.

The fluctuation in $\delta^{13}C$ and $\delta^{37}Cl$ values of α-HCH in trees over several years' growth periods suggests the involvement of distinct transformation mechanisms at different stages. Likewise, the shift in the enantiomer fraction (−) indicates that preferential transformation of enantiomers varies across different growth periods. Moreover, the detailed tree ring study further indicated that the transformation of α-HCH differs among the different tree growth periods, especially in the middle section.

Concurrently, we investigated the microbiome capable of degrading HCH in both soils and plants using molecular biological tools. Our findings suggest that the soil microbiome has the potential to inoculate the plant microbiome, thereby facilitating the transformation of HCHs in plants. This observation is further supported by the isotope study for β-HCH. The transformation of POPs, such as HCH, in soil-plant systems appears to be a widespread phenomenon, as indicated by the examination of multi-element isotope patterns in trees from a field study.

For this presentation we summarized our recent work on stable isotopes and enantiomer fractionation and discuss the perspectives for future work.

Understanding interactions in soil microbial communities for the prospect of bioremediation

Jan Roelef van der Meer[1]

[1]Department of Fundamental Microbiology, University of Lausanne

Abstract

Soil microbiota are among the most taxa-diverse communities we know, yet we know surprisingly little how they form and maintain. In this talk I will give an overview of our recent efforts to measure interactions between soil microbial taxa, how they shape the development of soil microbiomes, and what we could do to redirect and potentially restore damaged soil communities.

Microbes at the interface of human and environmental health

Jana Jass[1]

[1]Örebro University, Sweden

Abstract

All organisms are colonized by microbes at birth and subsequently form a symbiotic relationship. The most diverse and dense microbiota is found in the gut of humans and animals and there is increasing evidence that it has propound influence on our health and wellbeing. Gut microbiota has multiple functions; it facilitates digestion and supplies nutrients and vitamins, primes our immune system, induces maturation, drives evolution, protects us from pathogens, metabolizes incoming substances such as xenobiotics and more recently is believed to affect our mental state. The microbiota forms an interface between the intestinal lumen and external environment forming a barrier that is believed contribute to our resilience to microbial and chemical challenges. The *Caenorhabditis elegans* nematode is a good model to study the combined effects of microbiota and environmental toxins on the host. Studies using this nematode have shown that altering the gut microbiota influences lifespan and nematode metabolism. Different gut microbiota also altered host responses to xenobiotics such as global contaminants, arsenic and per/polyfluoroalkyl substances (PFAS). The balance between opportunistic pathogens and beneficial / non-pathogenic microbes influences longevity. Although the presence of opportunistic pathogens may not always alter *C. elegans* lifespan under normal conditions, they become more sensitive to toxic substances. By understanding how gut microbiota influences our resilience to environmental toxins may lead to novel interventions to sustain health in an increasingly contaminated environment.

In the era of antibiotic resistance, understanding the mechanisms through which microbial communities adapt and survive antibiotic challenges is paramount. This study dissects the survival strategies of microbes within the microbiomes of preterm infants under antibiotic exposure, leveraging an innovative combination of metagenomics, metaresistomics, metareplicomics, and causal inference methodologies. The research illuminates the complex dynamics of microbial communities, examining the microbiome's social network, replication rates (metareplicome), and antibiotic resistance profiles (metaresistome) alongside Bayesian networks for causality analysis. Findings reveal bacterial taxa exhibit varied responses to antibiotic exposure, ranging from continued replication to total succumbing. This study elucidates the intricate interplay between microbial community members by utilizing the MeRRCI (Metagenome, metaResistome, and metaReplicome for Causal Inferencing) pipeline. It identifies crucial causal relationships, such as cross-resistance to unrelated antibiotics and the impact of maternal antibiotics and milk on microbial dynamics. This work significantly advances our understanding of microbial ecology and antibiotic resistance, offering new perspectives on managing and predicting the consequences of antibiotic use in vulnerable populations, such as preterm infants.

The microbiologist's special duty of care for the wellbeing of humanity and the planet

[1]Kenneth Timmis and [2]John E. Hallsworth

[1]Technical University of Braunschweig, Germany
[2]Institute for Global Food Security, School of Biological Sciences, Queen's University Belfast, 19 Chlorine Gardens, Belfast, BT9 5DL, UK

Abstract

Microbes are special

Microbes are the dominant life form on Earth, collectively constituting a global biochemical reactor carrying out an unimaginable number of diverse reactions that directly or indirectly sustain and regulate all life in the biosphere, and drive planetary processes and evolution. These reactions determine to a significant extent the wellbeing of the planet and its other biological inhabitants, and are at the root of many processes that currently affect humanity, both positively and negatively. They are also the basis of a multitude of biotechnological applications that provide products and services crucial to human survival, development, wellbeing, culture and other endeavours. This makes the discipline of microbiology rather special.

This is the *Age of Microbial Technology*

Whereas the era of modern science has been driven by the *Age of Physics* and the *Age of Chemistry*, much of the 20th Century has been the *Age of Microbiology*, characterised by spectacular advances in understanding obtained by the use of microbes, including the elucidation of mechanisms underlying much biochemistry, genetics, the pathogenesis of infectious agents, ecology and food webs, biosphere matter transformations and the resulting energy flows, and applications based upon this knowledge, such as the discovery and production of a wealth of pharmaceutical products, including vaccines, that save millions of lives each year, and much more. Applications resulting from basic research on microbes are not only increasing in number and importance, but also in their societal significance (witness the global-scale deployment of polymerase chain reaction-based SARS-CoV-2 diagnostics, and vaccines, during the recent COVID-19 pandemic). Microbial processes are central to the *Bioeconomy*, *Green Deal* and other current bioknowledge-centric socio-economic endeavours. The 21st Century is the beginning of the *Age of Microbial Technology*[1].

Microbiology is special and microbiologists have a *special duty of care*

Among the sciences, therefore, microbiology is special, which means that microbiologists are special: they collectively have knowledge, expertise and technologies that have the potential to make a wide range of transformational changes benefitting humanity and the biosphere. This is not to imply that microbiologists are inherently gifted people *per se*: it is simply that our education has provided *manna* – knowledge about powerful but invisible agents of change. We see things others do not see, namely microbes that offer solutions/mitigation strategies to problems and crises, and that provide us with the opportunity to discover, develop and deploy microbial processes of immense importance for the wellbeing of humanity and the planet. This vision constitutes a gift that brings with it a special duty of care: *the microbiologist's global civic responsibility.*

Walking the walk, not just talking the talk

Many of the problems facing communities, nations, humanity *in toto*, and the planet itself can be either solved or mitigated by microbial processes and interventions[2,3]. Examples include,

but are not limited to, sustainability (https://sdgs.un.org/2030agenda; https://ami-journals.onlinelibrary.wiley.com/toc/17517915/2017/10/5), improving food security at various stages in the supply and consumption chain[4], and combatting climate change and global warming[5].

Microbiologists know how to do these things, either by modulating microbial activities in nature, or by harnessing specific activities in controlled environments, and there are many laudable efforts that are ongoing worldwide. But the reality is that humankind is not doing enough, and what we are doing is not being done fast enough, so global crises are not being solved. On the contrary, some are worsening[6,7] (https://news.un.org/en/story/2023/07/1138777). A quantum increase in efforts to tip the balance is urgently need, especially efforts to harness the power of microbes[8]. The microbiology community must rise to the occasion and confront the immense challenges facing humanity!

Effective use of microbial technologies to benefit humanity and solve problems and crises also requires political will, stakeholder acceptance and public engagement. This in turn will require a much greater societal knowledge and understanding of the benefits and dangers of microbial activities and their impact on the biosphere and planet[9,10]. The International Microbiology Literacy Initiative (IMiLI) aims to satisfy this need by creating a curriculum in societally-relevant microbiology and the teaching resources required for this. And here the microbiology community is stepping up and generously consecrating its time and energy to provide *pro bono* a huge and comprehensive set of teaching resources appropriate for teaching and self-learning at all levels[11]. This is the *Age of Microbial Technology*: microbiologists are now centre stage and have a special duty of care for humanity and the planet, but also a special responsibility to engage and educate the public in aspects of microbiology relevant to human and planetary health.

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Ammonia Oxidizing Microorganisms in Agricultural Soil Ecosystems

Kosala Sirisena[1]

[1]*Department of Environmental Technology, Faculty of Technology, University of Colombo, Sri Lanka*

Abstract

Nitrification, once believed to be a two-step process performed by two phylogenetically distinct groups of microorganisms; oxidation of ammonia to nitrite by ammonia-oxidizing bacteria (AOB) followed by oxidation of nitrite to nitrate by nitrite-oxidizing bacteria (NOB). However this historical view has changed in recent years, with the revelation of ammonia-oxidizing archaea (AOA), followed by the discovery of bacteria capable of entirely oxidizing ammonia to nitrate (COMAMMOX) in 2015. These ammonia-oxidizing microorganisms, collectively referred to as ammonia oxidizers, play a crucial role in the terrestrial nitrogen cycle, by governing the rate-limiting step of nitrification: the oxidation of ammonia to nitrite which is rapidly oxidised to nitrate. Nitrate can be a substrate for microbes and a nutrient for plant growth, while concurrently causing adverse environmental impacts such as nitrate leaching and emissions of a potent greenhouse gas, nitrous oxide (N_2O). One of the largest agricultural N_2O contributors is the intensively grazed pasture system, where the main source of nitrogen deposition is urine and dung from livestock. Urea which is the principal nitrogen component of urine (comprising 60%–95%), undergoes rapid conversion to ammonium in soil, subsequently progressing through nitrification to form nitrate. However, a small fraction of nitrate can be assimilated into biomass and the remaining nitrogen is a potential source of N_2O production and/or nitrate leaching. Therefore, it is crucial gain understanding of factors influencing the activity of ammonia oxidisers as this knowledge is fundamentally important for understanding and management of the nitrogen cycle. The growth and activity of these ammonia oxidisers are shaped by both biotic and abiotic factors within their habitats. The aim of this presentation is to discuss the attempts that have been made to decipher the influence of biotic and abiotic factors that influence the abundance and activity of ammonia oxidizing microorganisms in agricultural soil ecosystems.

Emerging Pollutants in Urban Aquatic Environments: Microbes to the Rescue

Max M. Häggblom[1]

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Abstract

Microbial degradation is one of the key factors that determine the ultimate fate of pollutant chemicals in the environment. Over the past decades pharmaceuticals and personal care products (PPCPs) as well as microplastics have emerged as a major group of environmental contaminants in watersheds and estuarine ecosystems around the world, but their long-term fate is poorly understood. PPCPs include a diverse array of thousands of chemical substances, which are primarily used either to prevent or treat human and animal disease or to improve the quality of life. PPCPs are biologically active and can thus pose adverse effects to aquatic biota, while microplastics and plastic debris provide a new "hotspot" for colonization by bacterial communities. Our aim is to elucidate the diverse catabolic activities of microbes mediating biodegradation of organic pollutants compounds and to understand the microbial processes that control their fate in watersheds. We also aim to understand the influence of urbanization and pollutant exposure on the community structures and functional capabilities of microplastic-associated biofilms. Some PPCPs are biodegraded to various degrees in river and estuarine sediments by native microorganisms, but depending on the dominant redox condition of the sediments, some PPCP compounds are recalcitrant in the natural environment. Different microplastics select for distinct bacterial biofilm communities which may have ecological implications on aquatic ecosystems with the increasing concentration of microplastics in the aquatic environment. Identification of the microorganisms responsible for the biodegradation activity can help us better understand degradation processes in the field and determine biomarkers for these processes. Natural microbial communities can play a key role in improving water and sediment quality through the process of biodegradation, which offers an approach towards eventual detoxification and complete degradation of these persistent organic pollutants.

Deciphering Microbial Dynamics in Preterm Infants: An Integrative Omics Approach to Antibiotic Resistance and Replication

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Abstract

In the era of antibiotic resistance, understanding the mechanisms through which microbial communities adapt and survive antibiotic challenges is paramount. This study dissects the survival strategies of microbes within the microbiomes of preterm infants under antibiotic exposure, leveraging an innovative combination of metagenomics, metaresistomics, metareplicomics, and causal inference methodologies. The research illuminates the complex dynamics of microbial communities, examining the microbiome's social network, replication rates (metareplicome), and antibiotic resistance profiles (metaresistome) alongside Bayesian networks for causality analysis. Findings reveal bacterial taxa exhibit varied responses to antibiotic exposure, ranging from continued replication to total succumbing. This study elucidates the intricate interplay between microbial community members by utilizing the MeRRCI (Metagenome, metaResistome, and metaReplicome for Causal Inferencing) pipeline. It identifies crucial causal relationships, such as cross-resistance to unrelated antibiotics and the impact of maternal antibiotics and milk on microbial dynamics. This work significantly advances our understanding of microbial ecology and antibiotic resistance, offering new perspectives on managing and predicting

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

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Abstract

As argued previously, there is a pressing need for society to become more microbiology-literate, not least to connect the roles played by microbes to the decisions we face (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). It also considers some lessons learned from recent visits to the University of Essex of hundreds of schoolchildren aged 9 to 11 years.

The African Microbiome Project: Insights from studying the gut microbiomes of South Africans

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Abstract

Microbiome studies have led to unprecedented increases in sequence data, resulting in novel insights on the diversity and function of microbial communities. Despite the increase, comparatively little is known regarding African microbiomes. Bibliometric analyses suggest that studies on African microbiomes constitute less than 5% of global outputs. Given the fact that these microbiomes are known to be more complex and diverse and may harbour novel microbiota with yet uncharacterized functional attributes, we urgently need to elucidate the phylogenetic diversity and ecology of African ecosystems. In this presentation, I will provide an overview of the current insights regarding African microbiomes and propose a mechanism for increasing studies on the continent. As an example, I will discuss our studies on urban and rural South Africans. These studies have revealed that rural populations harbour comparatively complex microbiomes compared with those from urban areas. Functional analysis suggests that markers linked to antimicrobial resistance genes are present at higher abundances in individuals from urban regions. Taken together, the results suggest that consistent with studies from other regions, a transition from urban to rural localities may have profound effects on the health of Africans.

Potential pathogenic bacteria in drinking water of Nepal

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Abstract

The existence of Himalayan glaciers, lakes, rivers along with plenty of groundwater are main sources of drinking water in Nepal. Rising population and urbanization with unmanaged solid waste and untreated wastewater have polluted surface and groundwater sources and consequently deteriorated the water quality. However, aligning the commitments to achieve UN sustainable development goals (SDGs), Nepal has developed national drinking water quality standards and sound institutional and legal framework. Our recent culture and genomic based studies have revealed that different urban drinking water sources are alarmingly contaminated with potential enteric pathogenic bacteria. We found that water isolates are resistant with associated genes to common therapeutic antibiotics. We assume this signifies a potential public health risk for the outbreak of waterborne epidemics in Nepal. We highlight the urgent need for continuous microbial surveillance of drinking water and research on innovative interventions to combat the microbial burden in water.

Keywords: Sustainable Development Goals; Water Quality; Research

Novel Antibacterial Strategies: Cheating Vs Killing Bacterial Pathogens

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Abstract

Bacteria are the most competent and versatile organisms among all living beings. They adapt to changing environments in a very agile manner. In nature, their contributions to human welfare are manifested through their role in agriculture, marine, and environmental bioremediation. Bacteria develop symbiotic and pathogenic relationships with plants, animals, and human beings. Pathogenic relationships are diseased conditions harmful to the host organism. The discovery of antibiotics almost a century ago was expected to be the most effective life-saving drugs ever discovered. However, bacteria developed resistance to almost all types of antibiotics. Bacteria-causing infectious diseases adopt biofilms to protect themselves from antibacterial agents and associated stress conditions. It has thus forced researchers to look for alternatives to counter the emergence and persistence of drug resistance. Biofilm formation is regulated by different signaling mechanisms, such as cyclic dinucleotide, small non-coding RNAs, and quorum sensing (QS). Here, c-di-GMP acts as a global messenger responsible for bacterial adhesion, production of extracellular matrix, and their transition from the planktonic to biofilm stage. QS, a cell density-dependent phenomenon regulates the expression of genes related to stability of the biofilm, virulence, and acquisition of nutrients. In this brief talk, information will be shared on mechanisms by which bacteria will not be killed (as is the case with antibiotics) but will be "cheated" to prevent them from expressing genes for biofilm formation. This new strategy will help to curtail the emergence of drug-resistant bacteria and develop drug molecules for treating pathogenic bacteria (https://doi.org/10.1016/j.ecoenv.2023.115389; https://doi.org/10.1016/j.biotechadv.2018.11.006; https://doi.org/10.1016/j.biotechadv.2012.10.004).

Two codes of prokaryotic nomenclature: how do they become one?

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Abstract

Codes of nomenclature enable biologists to create unambiguous and well defined names and are crucial for efficient communication about organisms. The Code of Nomenclature of Prokaryotes Described from Sequence Data (informally the SeqCode) is a new code of nomenclature in which genome sequences are the nomenclatural types for the names of prokaryotic species [Hedlund et al. 2022, Whitman et al. 2022]. While generally similar to the International Code of Nomenclature of Prokaryotes (ICNP) in structure and rules of priority, it does not require deposition of type strains in international culture collections. Thus, it allows for the formation of permanent names for uncultured prokaryotes whose complete or nearly complete genome sequences have been obtained from environmental DNA as metagenome-assembled genomes [MAGs] or single-cell amplified genomes [SAGs]. Fastidious prokaryotes that cannot be deposited in culture collections due to their growth requirements, resistance to isolation, or poor preservation as well as those that cannot be deposited in culture collections for legal reasons but whose genome sequences are known can also be named in this system. The start date of the SeqCode was January 1, 2022, and the online Registry (https://seqco.de/) was created to ensure valid publication of names. The SeqCode recognizes all names validly published under the ICNP prior to 2022. After that date, names validly published under the SeqCode compete with ICNP names for priority. To avoid creation of synonyms, ie. different names for the same taxon, the ICNP should be amended to recognize names formed under the SeqCode. This change in the ICNP will ensure that species and other taxa will have only one name, either from the SeqCode or ICNP, and enable efficient communication between scientists from diverse disciplines.

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Circulation of antibiotic resistance in water environment of Kathmandu, Nepal

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Abstract

Environmental antibiotic resistome is pool of antibiotic resistant bacteria and their determinant genes including mobile genetic elements. The resistome pose significant risk of transmission of antibiotic resistance in community and clinical settings. The monitoring the circulation of antibiotic resistant bacteria carrying resistance genes and mobile genetic elements wastewater and discharged environment is important public health strategy to mitigate global burden of antibiotic resistance. In this talk, we present the occurrence and circulation of Extended-Spectrum β-Lactamase (ESBL) and carbapenemase producing bacteria, associated genes including the integrons and insertion sequences in wastewater samples from hospital, pharmaceutical industries, municipal sewage and a receiving river in Kathmandu, Nepal. We report high frequency ESBL and Carbapenemase producing phenotype and genotype of *E. coli* and *Klebsiella* spp in hospital and municipal wastewaters and receiving rivers, indicating antibiotic resistance in river was impacted by these sources. We assume that municipal sewage and hospital wastewater are key reservoir of antibiotic resistome whereby dissemination to surface water and groundwater and drinking water. This implies a need for monitoring and control strategies to prevent the circulation of resistance in the environment and its potential consequences on human health.

Innovative NextGen discovery approaches for Simpler, Safer, Shorter drug regimens for tuberculosis

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Abstract

In 2022, TB was number 1 infectious diseases killer in the world, killing more than 1.6 million people. Multi or extreme-drug resistance (MDR/XDR) tuberculosis poses big public health challenge globally as Tx success rates that are usually low (~60%).

Our discovery of Bedaquiline (BDQ) brought a paradigm shifts in treatment MDR/XDR TB patients in about 170 countries and till date more than 0.8 million doses have been shipped worldwide. BDQ is recognized by WHO as part of their essential medicines listing both for adult as well as paediatric TB patients.

However, we urgently need a next wave of innovative TB drugs that can further reduce treatment duration to <3 months. The aim is to have new TB drug regimen that has reduced toxicities like myelosuppression, peripheral neuropathy, renal and cardiotoxicities associated with some of the currently used drugs. We also aim to simplify TB treatment landscape which still requires >800 pills per treatment course. We are capitalising on recent technological in pharmaceutical drug development, including using AI/ML tools, and our deep understanding of energy metabolism pathways that TB bacterium uses to survive in host cells.

Soil microbiomes to improve health outcomes for soil, plant and human.

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Abstract

Soil microbiomes provide key ecosystem functions including primary productivity, climate regulation and nutrient cycling[1-3]. Similarly, plant-associated microbiomes, which are mainly recruited selected from soils, play critical role in the provision of vital host functions including nutrient absorption, provisions of key phytohormones, metabolites, and resilience against biotic (e.g. pathogens and pests) and abiotic (e.g. drought, heatwave) distrubances[4,5]. Soil microbiomes also play direct role in plant and human health via reducing exposure to pathogens, supressing antibiotic resistance gene transfer, and degrading harmful chemicals pollutants from the environments[6,7]. This presentation will provide overview, empirical data and mapping in direct evidence for 1. linkage between soil microbial diversity and ecosystem functions at local to global scales[1-3], 2. current and future global distribution of pathogens[4], and 3. critical role soil microbial diversity in supressing pathogens. The presentation will argue that effective conservation policies of microbial diversity is integral to improve health outcomes for ecosystem, human and plant[7,8].

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Global Metagenomic Biodiscovery to Fuel Biotechnology

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Abstract

Many of humanity's greatest assets, from life-saving therapeutics to novel materials to enzymes enabling green industrial chemistry, come from nature. However, we have only explored a tiny fraction - less than 0.00001% - of the estimated trillion species that inhabit our planet. By developing Access and Benefit Sharing partnerships around the world, Basecamp Research is building an ethical supply chain to explore undiscovered microbial genetic diversity.

Basecamp Research is combining high quality global metagenomic sequencing to build the largest knowledge graph of biodiversity, which forms the foundation of the next generation of deep learning models in biology. Our rapidly growing knowledge graph currently covers over 6 billion relationships including full environmental metadata, with 5 times greater protein sequence diversity than that seen in existing public data. This dataset not only lets us discover more proteins of commercial relevance, but the more representative sequence diversity also offers a proven data advantage for more performant biodesign AI tools, from protein structural predictions to sequence generation. By activating a global network of labs exploring local biodiversity through metagenomic sequencing, and sharing benefits back for any commercialization, Basecamp Research is working to simultaneously accelerate our ability to learn from nature and to incentivize its conservation.

Foodomics a frontier to translate traditional fermented foods into functional foods of multifarious health benefits

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Abstract

The richness and diversity of ethnic fermented food products are chiefly observed in many Himalayan States. Traditional fermented food products are potential sources of a wide range of biologically active molecules, including peptides that can provide better health benefits to consumers. Fermentation by individual starter cultures (at strain level) results in unique food products by a series of enzymatic hydrolysis, leading to the production of a diversity of bioactive molecules and peptides responsible for specific health benefits. The major fermented food products consumed in the Himalayan region are produced using soybean, Yak and cow milk, fish and meat products. In our study, multi-omics approaches were applied for the characterization of microbial diversity and peptidome of fermented soybean products (Kinema, and soybean cheese products) and fermented milk products (Yak and cow milk), including *chhurpi*. Many bioactive peptides were identified using a combination of mass spectroscopy and computational analysis, followed by validation of selected peptides on their synthesis. The peptides identified in these foods are possibly involved in diverse functionalities, including antioxidant, antihypertensive, antidiabetic, and immunomodulatory activity. Further, several multi-functional peptides were identified in some of the protein-rich food products, highlighting the multi-functional potential of the fermented foods produced from milk as well as soybean. Fermented food products consumed at higher altitude regions can be explored to produce functional foods with better health, providing nutrition security.

Keywords : Fermented foods, bioactive peptides, health benefits, functional foods, nutrition security.

Cells as Drugs : The Future Medicine

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Abstract

In last century modern medicine based on small molecules and biologics has improved the life expectance of humans considerably. However, the effectiveness of small molecules and biologics to heal the human suffering is limiting either due to development of drug resistance or evolution of new pathogens. With many more pandemics in comparison to that experienced in 20th century has diverted the attention of medical treatment to kill the pathogen concept to heal the body. More and more attention being paid to make the whole human system more robust to fight the pathogens than using different mode of treatments. The concept of prevention is better than cure is becoming more prevalent option for medical treatment. Cells in body act as therapeutic intervention in many cases. The living cells because they sense, move and act can be a combination of drug, device and diagnostic tool. The current trend is to use the power of living cells and use them as drug for treatment. This concept of treatment is called advance therapeutic medicinal products (ATMP) and essentially involves treatment of the body at the level of gene, cell and tissue. These are essentially the gene therapy, cell therapy and tissue engineering currently used as treatment option. Even if the field is new, US FDA has approved more than 30 products as ATMP in the recent years. More interestingly many live microorganism are increasingly being used for many medical interventions. Live microorganisms such as Salmonella, Clostridium, Bifidobacterium and many mores are used as therapeutic bacteria for cancer therapy. Live cells as drug and therapy have its challenges and advantages but opens new avenues for disease treatments.

Carbon Source Utilization Ability is Crucial for the Rhizocompetence of a Plant Growth Promoting Rhizobacterium, *Azospirillum brasilense*

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Abstract

Bacteria of the Genus *Azospirillum* inhabit roots of a wide variety of C3 and C4 plants and promote their growth by producing phytohormones and fixing atmospheric nitrogen. Their ability to successful colonization of plant roots depends on their ability to efficiently utilize carbon compounds present in the root exudates of their host plants. *Azospirillum brasilense* is one of the most successful plant growth promoting rhizobacteria which has been used as a bioinoculant to promote growth of different crop plants. It is able to efficiently utilize dicarboxylates present in the root exudates of C4 plants. Inactivation of the genes encoding dicarboxylate transporters, DctP and DctA in *A. brasilense* led to a drastic decline in its ability to grow on dicarboxylates, and to colonize and promote growth of a C4 plant, *Eleusine coracana*. Since *A. brasilense* fails to utilize glucose it is known to be a poor colonizer of rice roots as roots of rice seedlings exude profuse amount of glucose. We identified the genes involved in glucose utilization in *Azospirillum lipoferum* and transferred them to *A. brasilense* to enable it to utilize and grow on glucose. Engineering glucose utilization ability in *A. brasilense* led to an increase in its ability to colonize rice seedlings and promote rice growth. *A. brasilense* was not known to utilize ethanol. We have shown that it can co-metabolize ethanol in presence of fructose and glycerol to reduce ethanol toxicity to plants under anaerobic situations. Fructose is able to induce a large number of proteins in *A. brasilense* which include a fructose phosphotransferase system (PTS) and a Type 6 Secretion System (T6SS). We have shown that *A. brasilense* is able to inhibit growth of *E. coli, Agrobacterium tumefaciens* and *A. lipoferum* in a contact-dependent manner in the presence of fructose. But, when the *tssFG* genes involved in the biogenesis of T6SS were inactivated, it lost the ability to inhibit growth of *E. coli* and *A. tumefaciens* indicating that its ability to utilize fructose induces biogenesis of T6SS, which is able to kill other competing bacteria in the rhizosphere to make it one of the most successful colonizer of the plant rhizospheres.

Towards understanding the anti-cancer role of gut metabolite indoxyl sulfate on colon cancer cells

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Abstract

There are number of reports about anti-cancer activity of indole derivatives and some of them such as Vinblastine have been used in clinic evaluations. In this study, we investigated the role of indoxyl sulfate (IS), an indole derivative, for its selective anti-cancer activity on colon cancer cells. Whether indoxyl sulfate has any harmful effect on normal colonic cells has also been studied. IS treatment on HCT-116 and HT-29 human epithelial adenocarcinoma cell lines led decrease in cell proliferation efficiency, cell viability and ATP content and showed 10% increase in cell apoptosis in comparison to control. Indoxyl sulfate also caused cell cycle to cease at G2/M phase. During animal study, balb/c mice were treated with 100mM of indoxyl sulfate to check colonic inflammation, if any, by IS administration and level of inflammatory cytokines IL-17A, IL-1β and TNF-α were studied. The change in the level of inflammatory cytokines after IS treatment was found statistically insignificant, hence IS was found not causing inflammation. No significant change in the length of intestine and spleen was noted after IS treatment. In conclusion, we found IS has selective deleterious and anticancer effect on colon cancer cells and does not cause harm to normal colonic cells.

Microbial Polysaccharide-Based Oral Thin Films for Nutraceutical Delivery: A Case Study of Pullulan

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Abstract

In recent years, the development of innovative delivery systems for nutraceuticals has gained significant attention, aiming to enhance their bioavailability, stability, and therapeutic efficacy. Oral thin films (OTFs) are such innovative dosage forms which provide several advantages such as ease of administration, rapid disintegration, fast absorption, rapid onset of action, bypass first-pass hepatic metabolism, accurate dosing, enhanced stability, portability, discreetness, dose flexibility and most importantly consumer acceptance. The physicochemical properties of the oral thin films are the crucial parameter for development of high quality film. In this regard, microbial polysaccharides, with their unique physicochemical properties, have emerged as promising film forming materials/polymers for such delivery platforms. Pullulan, a water-soluble exopolysaccharide produced by *Aureobasidium pullulans*, possesses remarkable film-forming properties and offers unique properties such as biocompatibility, biodegradability, and mucoadhesiveness, making it an ideal candidate for oral thin film development for nutraceutical delivery. In this talk, I will provide insight on the implication of pullulan for the development of oral thin films for nutraceutical delivery.

Decoding the virulence strategies of *Rhizoctonia solani* AG1-IA to engineer rice for tolerance to sheath blight disease

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Abstract

Sheath blight disease of rice caused by the fungal pathogen *R. solani* AG1-IA remains a big threat to rice production worldwide. A limited genetic variation in rice for tolerance to this pathogen and little success in understanding how it defeats host defense are major reasons behind it. In this study, we attempted to decode the virulence spectrum of *R. solani* AG1-IA in rice using time-course transcriptome analysis and functional genomics tools. Several stage-specific, as well as commonly expressed genes, were identified. Notably, the shikimate pathway emerged as an important pathway and was implicated in the virulence of *R. solani* AG1-IA. Inhibition of the shikimate pathway by glyphosate, a known inhibitor of 5-enolpyruvylshikimate-3-phosphate (EPSP) synthase, reduced the vegetative growth of *R. solani* AG1-IA and several other phytopathogens. Our results were complemented by *in vitro* inhibition studies of RsEPSP synthase using a recombinantly expressed protein. Comparative sequence analysis of RsEPSP synthase with plants and known major phytopathogens revealed a distinct region in RsEPSP synthase. Using *Nicothaiana benthamiana* as a model system and stable rice transgenic lines, we established that by targeting this distinct region by host-induced gene silencing (HIGS), the growth and virulence of *R. solani* AG1-IA are compromised. The study lays a foundation for a deeper understanding of the identified virulence genes and establishes the shikimate pathway as a central target to control phytopathogens.

Cold deserts of NW Himalayas as untapped resource of bioactive metabolites

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Abstract

Cold deserts of North Western range of Himalayas are bestowed with vast hidden microbial diversity. These include, extremophiles as well as mesophiles from soil, hot springs and salt lakes situated in various locations of the region. The diversity of the group of microbes including rare actinobacteria and rare species of *Streptomyces* genus have numerous untapped molecules that possess unique properties and bioactive applications. My research group has been involved in bioprospecting these unexplored niches for production of bioactives and enzymes. The proposed presentation will focus on some of the recent research outcomes of the group on diverse microbial species and their therapeutic potential, including antimicrobial, anticancer and antiviral activities. Therefore, some aspects on the fermentation process development for these isolates will also be discussed during the presentation.

Key words: NW Himalayas; cold deserts; bioactives; bioprospecting; extremophiles

Emerging Trends and Opportunities in Microbial Entrepreneurship

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Abstract

Entrepreneurship has a vital role in driving innovation and converting scientific discoveries into practical real-world applications in the dynamic field of microbiological sciences. This talk delves into the fascinating world of microbiological entrepreneurship, showcasing new developments and a plethora of unrealized opportunities. Using microorganisms for a variety of purposes, from environmental sustainability to agriculture and healthcare, is known as microbial entrepreneurship. It is critical that we understand the existing situation and identify the developing trends that will shape the future of microbial entrepreneurship as we navigate this always changing field. The field of microbiology has made significant strides, as seen by startups in several industries reaching noteworthy benchmarks. Driven by the unique qualities of microbes, entrepreneurs are developing novel treatments and establishing sustainable methods in agriculture. Driven by the unique qualities of microorganisms, entrepreneurs are developing novel treatments and leading the way in sustainable agricultural methods. This changing environment highlights the importance of microbes in solving pressing problems and encouraging creative thinking.

Wastewater Epidemiology and its relevance in AMR

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Abstract

The importance of wastewater-based epidemiological monitoring was established with the early detection method for the SARS-CoV-2 virus. Monitoring sewage had yielded a large picture of the spread if infection. This methodology was successfully extended to monitoring antimicrobial resistance in the environment. Sewage is an important hot-spot for the occurrence of pathogenic bacteria including AMR and hence regular monitoring of such niches is likely to give answers to resistance trends, emerging threats and mitigation clues.

It is reported that developing countries may be at a greater risk of AMR related health burdens as per the World Health Organisation's (WHO's) Global Antimicrobial Surveillance System (GLASS) report. Untreated wastewater could be one of the major factors here. CSIR-NEERI's study has carried out surveillance of sewage-carrying drains across 47 cities in India and demonstrated the presence of ARBs against 7 classes of antibiotics, namely, β-Lactams, Chloramphenicol, Glycopeptides, Macrolides, Tetracycline, Third Generation Cephalosporin, and Quinolones. An Antibiotic Resistance Index (ARI) was calculated and results demonstrated that the highest ARI was observed in Delhi and Mumbai, ranging from 0.81-0.92 in Delhi and 0.49-0.56 in Mumbai.

Artificial Intelligence: Role in Biomolecule Identification

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Abstract

Artificial Intellizommonly used to analyze patterns in biological data and helps computers discover patterns, allowing them to make intelligent decisions when new data is presented.

One of the fascinating fields where machine learning has been used successfully is the classification of the biomolecules. Biomolecules including peptides and nucleic acids are essential components of living organisms, carrying critical information. Taking cues from the vast amounts of the biological data, we have successfully implemented machine learning models to distinguish one subset of biomolecules from another. AI algorithms to successfully process complex information and build high performance prediction models. In addition, ML has also made inroads in assigning biomolecules with specific properties and has also been instrumental in studying correlations among them. AI in Biomolecule Identification has proven to have a promising role in clinical research and therapeutics.

Genomics for genome decoding and functional-enabled genome editing to identify novel antibiotic potentiators against MDR bacterial pathogens

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Abstract

Microbes display incredible genome plasticity and house thousands of novel functional potentoncy and functional activities that directly or indirectly modulate drug efficacy, human physiology, and the growth and viability of other microbes living in the same environment. Decoding the whole genome sequences of commensal and pathogenic microbes helped researchers to identify genes that may encode ribosomal or non-ribosomal derived therapeutic peptides. Subsequent genetic engineering of the reference microbe with the resistance functions helps us to develop genetically defined specific antibiotic resistant bacterial strain for novel hit identifications. Molecules that inhibit function of antibiotic resistance associated enzymes for substrate hydrolysis or chemical modifications increase the efficacy of existing drugs against resistant pathogens. Our work lays the foundation for the development of antibiotic potentiators for clinically important antibiotics.

Assessing the impact of Microbiology Literacy Outreach Camps involving a blend of activities

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Abstract

To reach out to the learners at remote areas of Hamirpur district, Himachal Pradesh (HP), India, an outreach program on Microbiology Literacy is being organised since 2016. Bani School Innovation Camp (BaSIC) as it is called was conceptualised by Prof. Rup Lal, a renowned microbiologist from India. BaSIC attempts to unleash the power of youth by innovation and inclusion. In the year 2023, BaSIC V was organised at the Government Senior Secondary School (GSSS), Bani, Hamirpur, HP, India on 13th February, 2023. Along with BioSCOPE II (Biar Initiative – A School Outreach Program for Enrichment) was also conducted at GSSS, Biar Village, Hamirpur, HP, India. The programs were organised under the aegis of many national such as Indian National Science Academy (INSA), Indian Network for Soil contamination Research (INSCR) and Association of Microbiologists of India (AMI) and international organizations, such as International Microbiology Literacy Initiative (IMiLI), Federation of European Microbiological Societies (FEMS) and International Society for Microbial Ecology (ISME) in association with academic and industrial partners. In BaSIC V and BioSCOPE II, teaching modules included a blend of activities ranging from dissemination of textual information in conventional chalk-board method to hands-on activities using local materials and DIY experiments to role play. To assess the immediate gain-in-knowledge, students were made to take pre-tests (before the modules) and post-tests (after the modules). An analysis of these tests would be presented. By what is perceived by the behaviour of the learners and as disclosed by them verbally, the outreach programs have been very advantageous for them by making them aware of the basic microbiology that can help them to make informed choices for better living. The formal pre/post tests made this evident and will be shared and discussed.

Novel Strategies of drug Development for Enhanced Antimicrobial Efficacy in Neisseria gonorrhoeae

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Abstract

Neisseria gonorrhoeae (Ng) poses a significant public health challenge due to its increasing resistance to antibiotics, necessitating the exploration of novel therapeutic strategies. Here, we present a computational drug discovery approach aimed at identifying potential inhibitors targeting glutamate racemase (Ng-MurI), a crucial enzyme involved in peptidoglycan biosynthesis. We constructed a three-dimensional model of Ng-MurI through homology modelling and validated its quality. Subsequently, molecular docking studies facilitated the identification of the protein's binding site, and a structure-based pharmacophore model was developed using interactions of a control ligand. Employing this pharmacophore model, high-throughput virtual screening of the ZINC library was carried out to identify novel Ng-MurI inhibitors. The top five compounds were shortlisted based on their optimum docking scores and the criteria they have passed like ADMET and Lipinski's filter. Further optimization of the model was achieved through molecular dynamics (MD) simulations, confirming the stability of protein-ligand complexes over a 100 ns time frame. Validation studies ascertained that ZINC000014657962 (Lead 3) is one of the best ligands which exhibited good docking energy scores, and showed maximum stability and binding energy during simulation studies. In parallel, diverse families of phytochemicals were screened *in silico* for their binding affinity with NG-MurI protein. Esculetin, one of the shortlisted compounds, was evaluated for its functional, structural, and anti-bacterial activity. Treatment with esculetin resulted in growth inhibition, cell wall damage, and altered permeability as revealed by fluorescence and electron microscopy. Furthermore, esculetin inhibited the racemization activity of recombinant, purified NG-MurI protein. Overall, our study provides valuable insights into the design and development of novel Ng-MurI inhibitors through computational approaches. Additionally, the promising activity of esculetin underscores its potential as a therapeutic agent against antibiotic-resistant NG infections, offering a viable avenue for future drug development efforts.

Keywords: *Neisseria gonorrhoeae*, Molecular Docking, Esculetin, virtual screening.

Evidence for high-risk pollutants and emerging microbial contaminants at two major bathing ghats of the river Ganga using high-resolution accurate mass spectrometry and metagenomics

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Abstract

An efficient wastewater treatment plant is critical to limit the transmission of emerging pollutants (EPs) and emerging microbial contaminants (EMCs) in the river ecosystem. Detecting the emerging EPs of global concern in aquatic environments is challenging due to complex sample preparation methods. In Varanasi (India), the river Ganga holds immense significance as a holy river but is consistently polluted with municipal (MWW) and hospital wastewater (HWW). We developed an efficient method for untargeted detection of EPs in the water samples using High-resolution accurate mass spectrometry and identified 577 and 670 chemicals (or chemical components) in the water samples from two major bathing ghats, Assi Ghat (AG) and Dashashwamedh Ghat (DG), respectively. The presence of EPs of different categories *viz* chemicals from research labs, diagnostic labs, lifestyle and industrial chemicals, flavor and food additives, and toxins Different categories of EPs indicated the unsafe disposal of MWW and HWW. EPs are linked to AMR, and shotgun metagenomic analysis depicted the presence of plasmid-borne β-lactamases, aminoglycoside transferases, antibiotic resistance genes (ARGs), and ARGs associated with transposons. This suggests the risk of AMR transmission through horizontal gene transfer. Further, detection of human pathogens *Arcobacter*, *Polynucleobacter*, *Pseudomonas*, *Klebsiella*, *Aeromonas*, *Acinetobacter*, *Vibrio*, *Campylobacter*, and *mcr*-3 gene conferring resistance to colistin, the last resort of antibiotics confirmed the presence of EMCs. Subsequent genome reconstruction studies also confirmed the incidence of EMCs. This study demonstrates poor wastewater management in Varanasi, a traditional holy city, and underlines an urgent need for an efficient wastewater treatment plant to safeguard river Ganga.

Key Words: River Ganga; Municipal and hospital wastewater, Emerging pollutants; Antimicrobial resistance; High-resolution accurate mass spectrometry; Un-cultivable pathogens

Emerging Infectious Diseases – Role of Ecology and Technology

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Abstract

The world is witnessing an increasing frequency of emerging infectious diseases in the last two decades. Though the use of antibiotics, vaccination and improvements in sanitation has resulted in a significant reduction in human mortalities due to microbial infections in the later half of the 20th century, the situation is fast changing. Emergence of diseases such as severe acute respiratory syndrome (SARS), mad cow disease, reemergence of dangerous strains of bird flu virus and more frequent food borne infections with multi drug resistant pathogenic bacteria are questioning our ability to successfully defend ourselves against these organisms. An understanding about biodiversity (especially that of tropical region), ecology and changing technologies are required to understand this phenomenon in a holistic manner. Centralized food processing/ production facilities and increased movement of food and feedstuff as well as international travel in a globalized world are found to trigger emergence of such infections diseases. Massive infrastructure projects through pristine environments and activities like illegal wild life trafficking are exposing humans to hithrerto unknown infectious agents. Natural phenomena such as bird migrations are also contributing significantly to the emergence of infectious diseases. Huge population density, poor infrastructure facilities and close proximity between humans and animals in South East Asia put the people from this region particularly at risk. The proposed lecture aims to discuss the issue in an integrated manner.

Key Words: Emerging Diseases, pathogens, ecology, globalization

Microbial Literacy: A viewpoint of Microbial Literacy by a society member

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Abstract

As a member of society and not from the biological sciences I was unaware of the importance of microorganisms in maintaining human health, protection of the environment and global peace. After attending few microbiology sessions, it is evident that this is very important information and aspect of literacy among society and I believe if microbial literacy is spread all over the country especially to the common society members and children, it can help the nation and communities all over the world to bring peace and have healthy society.

Study of Genomic Variations of *Staphylococcus Aureus*: A Host Specific Analysis

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Abstract

Staphylococcus aureus is a versatile opportunistic bacterial pathogen, widely known for infecting its hosts through direct contact with the infected person's wounds or cuts. Infection becomes severe with the spread of bacteria to distant tissues and organs via. bloodstream. From past few decades, sharp increase in the rate of mortality and morbidity has been observed in *S. aureus* patients. It has been listed among a zoonotic pathogen and the development of high drug resistance has even enhanced the rate of worldwide deaths per year. To perform a host specific analysis, we include 95 complete genomes of *S. aureus* strains which have been reported to infect different host organisms. This includes Human, Macaca, Camel, Cattle and Swine. Phylogenomic analysis on pairwise average nucleotide identity has shown a clear demarcation of Macaca strains compared to the other four hosts, where Macaca strains clustered separately and other hosts showed mosaic pattern of clustering. The core-pan analysis further revealed the genetic attributes critical for staphylococcus infection such as biofilm formation, quorum sensing and secondary metabolites biosynthesis such as Staphyloferrin A and Staphyloferrin B. These genomic signatures further help in improving our understanding in mode of action of *Staphyloccocus* infection and its zoonotic status.

Risk assessment of foodborne antimicrobial resistance

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Abstract

Antimicrobial resistance is considered to be causing a "silent" pandemic. Considerable morbidity and mortality due to microorganisms resistant to all available antimicrobials has been reported from several countries all over the globe. Antimicrobial resistance evolves naturally, but the use of antimicrobial agents in producing food animals, aquaculture and in hospitals leads to selection and proliferation of resistant organisms. Further, genetic determinants of antimicrobial resistance are often associated with mobile genetic elements like plasmids and transposons and can be transferred across bacterial genera and species; between environmental bacteria and zoonotic pathogens. Thus resistance can be transferred between human pathogens, animal pathogens and environmental organisms. Due to use of antimicrobial agents in agriculture and animal production, microorganisms resistant to antimicrobials may be associated with food. To understand the risk to human health due to microorganisms resistant to antimicrobials, it is important to perform risk assessment. This presentation provides an overview of guidelines for performing risk assessment of foodborne antimicrobial resistance elaborated by the FAO/ WHO Codex Alimentarius Commission. Such risk assessment would facilitate adopting risk management measures based on the risk associated with plant and animal derived foods.

A Molecular View of Biofilms formation by Plant Growth Promoting Bacteria Isolated from Arid regions of Rajasthan and their potential role in Tripartite "Plant-Microbe Interactions"

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Abstract

Desertification and aridification have emerged as one of the major environmental challenges. According to recent estimates, arid or semi-arid regions cover ~27% of global terrestrial regions. These regions are characterized by extremes of topographical and climatic conditions that induce a very strong biotic and abiotic stress. Therefore, plant growth and survival within these regions are rather challenging. Plant-growth promoting bacteria (PGPB) isolated and characterized from these regions are projected to mitigate the hazards of both biotic and abiotic stress. Previously, we had carried out isolation and characterization of several PGPBs from arid and semi- arid regions of Rajasthan. These strains are bestowed with multifaceted plant growth promotion characteristics including ACC-deaminase activity and biofilm formation. Interestingly, PGPB strains with the capability of forming biofilm are found to mitigate the harmful effects of simulated biotic stress and allow the plant growth. However, the putative mechanism for plant growth-promotion by biofilm forming PGPBs remained unexplored. To address the same, we generated deletion mutants in different components of the molecular cascade of biofilm formation in Bacillus sp. strain. It was observed that deletion of proteins essential for biofilm formation (viz., homologs of ΔBsTasA, ΔBsBslA and ΔBsSinI) were significantly deficient in seed colonization, seed germination, radical growth promotion and seedling growth when subjected to bacterial infection with Pseudomonas syringae in comparison to control groups. These observations put forward the molecular view for a vital role of biofilms formation in plant growth promotion by inhibition of bacterial pathogens by PGPBs from arid and semi-arid regions.

Phylogenomics-based reclassifications in the genus *Psychrobacter*

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Abstract

The taxonomic status of 43 *Psychrobacter* species was examined based upon the genome sequences of their type strains. Three groups of type strains were found to be conspecific, *Psychrobacter salsus* Shivaji et al. and *Psychrobacter submarinus* Romanenko et al.; *Psychrobacter oceani* Matsuyama et al. and *Psychrobacter pacificensis* Maruyama et al.; and *Psychrobacter proteolyticus* Denner et al., *Psychrobacter marincola* Romanenko et al. and *Psychrobacter adeliensis* Shivaji et al. For all three groups, the average nucleotide identity (ANI) and digital DNA–DNA hybridization (dDDH) values are > 97.69% and > 80.2%, respectively. This conclusion is supported by similarities in morphology, growth properties, and fatty acid compositions. Based on this evidence, we propose the reclassification of *Psychrobacter salsus* Shivaji et al. as a later heterotypic synonym of *Psychrobacter submarinus* Romanenko et al.; *Psychrobacter oceani* Matsuyama et al. as a later heterotypic synonym of *Psychrobacter pacificensis* Maruyama et al., and *Psychrobacter marincola* Romanenko et al. and *Psychrobacter adeliensis* Shivaji et al. as later heterotypic synonyms of *Psychrobacter proteolyticus* Denner et al.

BIRAC- Catalyzing the Biotech Innovation Ecosystem in India

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Abstract

According to the India Bioeconomy Report 2023 by ABLE, India's bioeconomy crossed USD 137 billion in December 2022, registering a growth of 29% compared to the previous year. The bioeconomy contributes over 3.5% to the overall economy, positioning the biotech sector as a key contributor to the country's growth. The Biotechnology Industry Research Assistance Council (BIRAC), a not-for-profit, Section 8, Public Sector Enterprise under the Department of Biotechnology, Government of India, has been spearheading the growth of the biotech innovation ecosystem as a central enabler. Over the last 12 years, BIRAC has supported innovations in varied areas of biotechnology and has worked aggressively on building new pathways for entrepreneurial journeys through various focused initiatives, including funding, incubation, mentoring, and global networking. The Major schemes of BIRAC include (i) BioNEST (Bio-incubators Nurturing Entrepreneurship for Scaling Technologies) and E-YUVA (Empowering Youth for Undertaking Value Added) for creating a strong incubation network. (ii) BIG (Biotechnology Ignition Grant) as the largest early-stage funding for startups and entrepreneurs (iii) BIPP (Biotechnology Industry Partnership Programme) and SBIRI (Small Business Innovation Research Initiative) for mid-late validation support for Startups, SMEs & large companies (iv) PACE (Promoting Academic Research Conversion to Enterprise) for academic entrepreneurship. (v) SPARSH (Social Innovation programme for Products Affordable & Relevant to Societal Health). BIRAC also provides equity funding through three of its schemes, namely, SEED (Sustainable Entrepreneurship and Enterprise Development), LEAP (Launching Entrepreneurial Driven Affordable Products), and the Fund of Funds, AcE (Accelerating Entrepreneurs) Fund. Each scheme supports a specific stage of development to facilitate the forward movement of the product or technology across the development chain. BIRAC's Grand Challenges India (GCI) programme, in collaboration with the Bill & Melinda Gates Foundation, and the National Bio-Pharma Mission (NBM), in collaboration with the World Bank, are two major international co-funding partnerships. The mission of GCI is to foster innovation and research to develop affordable and sustainable solutions to improve health and well-being in India and around the world. The National Bio-Pharma Mission is an industry-academia collaborative mission for "accelerating discovery research to early development for biopharmaceuticals. BIRAC schemes and programmes have helped create a network of 95 incubation and pre-incubation centers across the country, supported over 4000 beneficiaries, and enabled the development of over 800 biotech products that have reached the market. BIRAC (including mission programmes) has invested close to INR 4000 crore over the last 12 years and mobilised over INR 2600 crore from Industry and other partners. BIRAC-supported startups have raised investments of over INR 5500 crore from private investors,

providing a testimony to the potential that many of these startups hold for the future. BIRAC's new initiative, Regulatory Affairs and Policy Advocacy (RAPA), aims at strengthening the regulatory and policy milieu of India. The "Ask Me Anything" platform "FIRST HUB" is the first of its kind single-window facilitation platform to address the queries of startups, entrepreneurs, researchers, academicians, incubation centers, SMEs, etc. Till now, more than 800 queries have been addressed. BIRAC's in-house IP & Technology Management group provides support to startups, institutes, academia, and SMEs on various aspects of IP & Technology Management, which include Patent Searches (Freedom-To-Operate, Patent landscape, Patentability search), facilitation of patent drafting & filing, Technology evaluation, and commercialisation. India's success in the COVID vaccine segment has been globally recognised and has made India proud. BIRAC played a significant role in implementing various COVID initiatives along with the Department of Biotechnology. Four indigenously developed COVID vaccines, namely, ZyCoV-D (World's 1st and country's indigenously developed DNA Vaccine), CORBEVAX™ (protein subunit vaccine), GEMCOVAC™ 19 (mRNA based vaccine), and iNCOVACC (intranasal COVID-19 Vaccine), have been validated through BIRAC support.

Saffron microbe interaction: questions that beg answer

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Abstract

Bacillus sp. strain D5 (Bar D5) is a native PGP bacterium isolated from the saffron corm. Its efficacy has been evaluated first in pot trials and then in in field at Pulwama i.e traditional area and few non-traditional saffron cultivations sites of Jammu and Kashmir. Among all the trails in non-traditional areas, best results were obtained from various locations of Poonch District. At all the places, Bar D5 increased the morphological parameters such as root length, root number, shoot length, leaf length and weight of daughter corms, number of flowers and yield of spice. The most interesting observation was that it decreased the shoot number and number of daughter corms but increases the size of the daughter corm compared to unprimed corms. The size of the saffron corm has direct relation to the flowering and overall yield of saffron. Another interesting fact was that the corms were inoculated by priming only once in the first year and the trails continued for minimum of the three years as saffron propagates vegetatively and is a perennial crop like ginger. However the yield of saffron increase around 2 fold in all the three years, whereas as expected the load of Bar D5 decreased from 85 to 50 to 20% in the rhizosphere from 1st ,2nd and 3rd years respectively. The other important observation was the absence of contractile roots in Bar D5 primed corms at most of the locations; however, in unprimed corms contractile roots were present. Further the NPK concentration in the soil of treated corm went up and load of the Fusarium went down. These results have lead to more questions that beg answers

1. How does D5 inoculation lead to decrease in the number of shoots, and number of daughter corm selectively as number of all other saffron organs is increased,
2. How does D5 achieve the constant plant growth promotion in saffron for three years , without added inoculation, even when its load decreases,
3. Is it a keystone species, that effects the microbiome rather than direct interaction with the saffron corm or does both.

Fermented Foods as Medicine

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Abstract

Traditionally and historically, the Asian food habits do not require additional medicines or supplementary drugs. The people believe on their foods having therapeutic values and eaten for prevention of illness. Ancestors have innovated the ethno-microbiological knowledge of utilization of beneficial microorganisms present in eco-systems for production of perishable bio-resources to obtain the organoleptically and culturally acceptable ethnic fermented food. The novelty of application of metagenomics and metabolomics is the validation of science-based evidences on domestication of beneficial microbial communities, their functionalities, health-promoting benefits and disease-combating mechanisms. Many untargeted metabolites including bio-peptides, immunomodulators, vitamins, etc, which are considered as the primary health-promoters to the consumers have been detected in some Asian fermented foods. Some Asian fermented foods have been scientifically studied and proved to have several health-promoting benefits to the consumers. However, health-claims of Asian fermented foods (except few Japanese and Korean) based on human clinical trials are yet to be conducted to authenticate their therapeutic values. Application of metagenomics and multi-omics integrated approaches including metagenome-assembled genomes (MAGs) may validate the traditional fermented foods as “Foods as Medicine”.

Treat-after-too: Strategies for treatment of wastewater generated from cancer hospitals

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Abstract

Globally, wastewater treatment plants of cancer hospitals are lacking to remove antineoplastic agents reaching through cancer patients urine except few countries like Sweden, Switzerland. In the current scenario antineoplastic agents are not removed from wastewater and finally reached to water bodies which are harmful for aquatic/human life. Beside this, the increasing rate of cancer patients all over the World has become a global fact during the last two decades. Keeping in the view, an integrated approach developed for removal of antineoplastic agents like cyclophosphamide, 5-flurouracil, etoposide, paclitaxel etc.

Biodegradation of plastics and plasticizers by diverse bacteria: Genomic insights into the metabolic pathways

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Abstract

We explored diverse plastic and plasticiser biodegradation bacteria by combining culture-based experiments with whole genome sequencing strategies. This approach provided novel insights to the metabolic capability, organization and pathway of key biodegradative genes and enzymes which helps in unravelling the metabolic versatility of the isolated bacteria. In fact the comprehensive analysis of the contaminated soil at the municipal dump sites revealed the presence of wide varieties of plastic and plasticizers contaminants. A *Dietzia kunjamensis* IITR165 able to metabolize plastics and plasticizers including dibutyl phthalate (DBP), dimethyl phthalate (DMP), terephthalate (TPA), and polyethylene terephthalate (PET) indicated that it is a robust organism possessing activities on wide substrates. Sequencing revealed a complete genome (3.53 Mb) comprising a circular chromosome of 3,477,711 bp and a plasmid of 58,850 bp with 70.6% GC content and genes for plastic metabolism spread on both in chromosome and plasmid. Similarly, a *Brucella intermedia* IITR130 was isolated from a contaminated lake ecosystem found efficiently biodegrading PET. Considerable changes in the surface morphology of the PET sheet were found as holes, pits, and cracks on incubation with strain IITR130, as revealed by scanning electron microscopy (SEM). Monomethyl terephthalate (MMT) and terephthalic acid (TPA) were identified by gas chromatography-mass spectrometry (GC-MS) analysis as PET degradation metabolites. Interestingly, a multiple hydrocarbon biodegrading *Achrombacter xylosoxidans* IITR150 screened from a crude oil contaminated soil also found to have multiple plastic biodegradation genes and plethora of other biodegradation genes indicating the nature of the bacterium. As a remediation strategy, the insights obtained on biodegradation of plasticizers and polyaromatic hydrocarbons and also the insight from genome analysis aiding the understanding of the bacteria present in contaminated soils will be presented.

Understanding the fungal-mediated arsenic bio-transformation/ detoxification and its utilisation for reducing arsenic in crops

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Abstract

The biogeochemical cycle of the elements is primarily influenced by biotic and abiotic factors. Biotic factors play a crucial role in the movement of the elements into abiotic components and its reversal into biotic components. In the present scenario, arsenic exposure through the food chain is an emerging environmental problem associated with accumulation of the As in the edible parts of crop . Unique rhizospheric microbial interaction influences arsenic (As) detoxification/mobilisation into crop plants and its level of toxicity and burden. Free-living rhizospheric fungus, isolated from arsenic-contaminated plant rhizosphere, has the ability to transform arsenic into nano- and micro-sized arsenic particles with reduced toxicity to soil-dwelling bacteria, fungi, plants and slime mould. These As particles showed poor absorption and mobilisation in plants. However, a plant-interacting fungus, *Serendipita indica*, isolated from a plant growing in metal-contaminated soil, shows a diverse ability of arsenic transformation and reduces bioavailability by three different mechanisms viz. bio-transformation of the toxic arsenic into insoluble particulate matter on their cell wall and accumulate in the cell vacuole and spores. During association with the plant root, the fungus immobilises arsenic in the root while a small fraction of it translocated to shoots and grains/fruits of colonised plants. Further, a broad host range and a comprehensive metabolic profile of the endophytic fungus make it suitable for reduced arsenic accumulation in crops grown in highly arsenic-contaminated agricultural fields.

Role of Viral Omics in searching drug and vaccine targets

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Abstract

The need to comprehend the intricate dynamics among viruses, their animal hosts, and human communities has been prompted by the ongoing proliferation of zoonotic viral illnesses. Riboviruses, categorized within the kingdom Orthornavirae, play a significant role in numerous widespread human ailments, often leading to epidemics and pandemics. Among the riboviruses fall Flaviviruses and Coronaviruses. The present work the multiomics approach on these two groups of viruses to effectively work on prevention and cure i.e. to look for drug as well as vaccine candidates. Flaviviruses and Coronaviruses are included within the riboviruses. The current study employs a multiomics approach to address these virus groups, aiming to efficiently investigate prevention and treatment strategies, including the search for potential drug and vaccine candidates.

The work revolves around looking for valuable phytocompounds that are safe to use by docking and MD simulation study. For vaccine, the conserved segments were explored to find conserved epitopes and conserved CpG islands. Hence, a multiomics approach is indispensable for thorough understanding and analysis of viruses.

Bacterial biostimulants: Prospects in Millets cultivation

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Abstract

The bacterial biostimulants exert a variety of plant growth promoting mechanisms including enhanced nutrient availability for plant uptake, improved germination and root proliferation through secreting phytohormones, and increased resistance/ tolerance to biotic and abiotic stresses. Millets are major crops in the semi-arid and arid regions of Asia and Africa, owing to their ability to resist dry, hot climate of these regions conditions and produce better yields as compared to the major cereal crops. Use of bioinoculants including *Azospirillum*, *Bacillus*, *Acetobacter*, *Pseudomonas* sp. has been demonstrated to enhance the plant growth and productivity in different millet crops. The bacteria belonging to genus *Azospirillum* form associative associations with the roots of host plant and exert their positive effects by modulating root traits through the production of phytohormones, extensive colonization through biofilm formation, increasing the nutrient use efficiency through biological nitrogen fixation and/or, nutrient acquisition through production of siderophores and/or EPS. In addition, they also give competition to the phytopathogens through extensive colonization and releasing inhibitory metabolites or nutrient. The case study on *Azospirillum*-Pearl millet interactions under nitrogen limited and moisture deficit conditions indicate the potential of biostimulatory bacteria in the nutrient limited and stressed agriculture. The indigenous germplasm of PGP *Azospirillum* spp. strains isolated from pearl millet rhizosphere significantly improved the root traits, plant growth and physiological status under moisture deficit conditions indicating their successful establishment and positive interaction with the host plant. A carrier based formulation (Pusa AIM) has been developed for rainfed millet crops. Additionally, the PGP strains can be harnessed for the biostimulatory metabolites for the development of next generation biostimulatory formulations. Also, there is lot of scope to use endophytic microbiome and synergistic microbial interactions to develop designer microbial communities for enhancing the nutrient use efficiency and modulating stress responses in the millets in a sustainable way.

Nanotechnology: The Tiny Revolution with Big Impacts in Science

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Abstract

Nanotechnology is emerging as a transformative field with profound implications across diverse sectors, underscoring its paramount importance in today's world. At the nanoscale, materials exhibit unique properties and behaviors, enabling unprecedented breakthroughs in science, technology, and medicine. This abstract highlights the significance of the upcoming field of nanotechnology. Nanotechnology promises groundbreaking advances in materials science. Nanostructured materials possess exceptional strength, conductivity, and reactivity, revolutionizing industries like electronics, aerospace, and energy storage. Such innovations hold the potential to enhance product performance, reduce resource consumption, and mitigate environmental impacts. Furthermore, nanotechnology's influence extends to the environmental sector, offering novel solutions for clean energy production, pollution remediation, and sustainable agriculture. Nanomaterials enable efficient catalysts, solar cells, and water purification systems, addressing global challenges like climate change and resource scarcity. In conclusion, the importance of nanotechnology lies in its transformative potential to reshape industries, enhance human health, and address critical environmental issues. Harnessing the power of the nanoscale is not only essential for technological progress but also holds the key to solving some of the most pressing challenges of our time. One of the most popularly used nanoparticle is silver nanoparticle. Silver nanoparticles (AgNPs) have been used in various medicinal and commercial products because of their exceptional anti-microbial and anti-odor properties. Further, the talk also focusses on research involved with the synthesis of AgNPs from aqueous-leaf-extract of *Mentha piperita* and its effecton one of the most important neurological enzymes i.e. acetylcholinesterase (AChE) to predict its neurotoxicity.

Crafting a Winning Innovative Grant Application

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Abstract

In this session, participants will delve into the art and science of developing grant proposals that captivate funders and secure support for innovative projects. We will explore the essential elements of a compelling grant application, from crafting a compelling narrative to highlighting the unique value proposition of your project. Through practical insights and real-world examples, attendees will gain a deeper understanding of how to identify funding opportunities, tailor proposals to meet funder expectations, and effectively communicate the transformative impact of their initiatives. By the end of the session, participants will be empowered with the knowledge and strategies needed to craft winning grant applications that bring their innovative ideas to life.

अभाव से समाधान तक:

Microbial magic for sustainable industry and environment

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Abstract

Imagination is more important than knowledge. For knowledge is limited to all we know and understand. While imagination embraces the entire world and all there ever will be to know and understand. By doing science in a creative way we can take science from classroom to laboratory to society.

In modern cities majority of the sewage water is treated in sewage treatment plants (STP) but even after treatment it is mainly disposed of in natural water recourses. However tertiary treated sewage water (TT Water) can be used for number of alternate purposes such as irrigation, construction, service stations, recreational purposes like replenishment of lakes etc. However there are problems associated with the use of treated water for these purposes such as

- Improper treatment and irregular monitoring of the efficiency of STP'S
- Presence of excess nutrients such as phosphates and nitrates which lead to eutrophication
- Growth of sulphate reducing bacteria (SRB) which lead to foul smell.

By working in collaboration with Department of Environment Chandigarh all these problems were addressed.

For one year STP's of Chandigarh were monitored regularly and it was concluded that it is not the type of technology it is management of the STP's which determines the quality of treated water, with given recommendations quality of treated water was improved.

To explore the possibility of using TT water for the management of Sukhna Lake Chandigarh quality of TT water was compared with water of Sukhna Lake. It was found to be fit in all aspects except excess of nutrients. An inherent technology was standardized using denitrifying and phosphate solubilizing bacteria; which completely removed these nutrients from TT water. **Chandigarh administration has taken a note of the work and exploring the use of sewage water with this process for saving the Sukhna lake Chandigarh**.

TT water is being used for irrigation in Chandigarh but the foul smell in it is the major problem. a process was standardized reduce the growth of SRB's by aeration and addition of acceptable chemicals which led to the complete removal of smell form TT water. **Municipal Corporation has taken up the process and is going to apply it for solving the problem of foul smell**.

Therefore microbial process can be used to convert waste water into asset and solving various problems related to society at large.

Furthermore, we are standardizing the application of novel enzymes for biobleaching of pulp, bioremediation of industrial effluents, and dehairing animal skin, among other uses. Pilot-scale trials are being conducted in collaboration with various industries.

Unveiling Gene Co-optive evolution of LysR type transcription regulators across strains of Mycobacterial

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Abstract

Mycobacterial species are adept at surviving diverse environments, from soil to the hostile intracellular conditions within animal hosts, necessitating rapid metabolic adaptations. Environmental cues are sensed by membrane-bound sensors, triggering metabolic shifts via regulator-mediated pathways and post-translational modifications. Signal-dependent transcriptional regulators are vital for perceiving these cues and orchestrating adaptive responses. LysR-type transcriptional regulators (LTTRs), ubiquitous across life kingdoms, vary in abundance among bacterial genera and mycobacterial species. To probe LTTRs' evolutionary role in pathogenicity, we conducted a phylogenetic analysis of LTTRs from non-pathogenic (NP), opportunistic (OP), and fully pathogenic (TP) mycobacteria. TP LTTRs clustered distinctly from NP and OP counterparts, with reduced TP LTTR frequency per genome megabase compared to NP and OP. Furthermore, protein-protein interaction analysis revealed increased LTTR interactions correlating with higher pathogenicity. These findings imply an expanded LTTR regulon during TP mycobacteria evolution, underscoring LTTRs' significance in shaping pathogenic phenotypes.

Key Words: Functional convergence; Interactomics; LysR-type transcriptional regulator; Mycobacterium; Phylogenetic analysis.

Anaerobic growth and drug susceptibility of versatile fungal pathogen *Scedosporium apiospermum*

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Abstract

Although severe cases of invasive mycoses of different hypoxic and anoxic body parts have been reported, growth and drug susceptibility of fungal pathogens under anaerobic conditions remains understudied. The current study evaluated anaerobic growth potential and drug susceptibility of environmental *Scedosporium apiospermum* isolates under aerobic and anaerobic conditions. All tested strains showed equivalent growth and higher sensitivity to tested antifungal drugs under anaerobic conditions with lower MIC as compared to aerobic conditions. Antifungal azoles were effective against isolates under both aerobic and anaerobic conditions. Most strains were resistant to antifungal echinocandins and polyenes under aerobic conditions but exhibited sensitivity under anaerobic conditions. This study provides evidence that resistance of *S. apiospermum* to antifungal drugs varies with oxygen concentration and availability and suggests re-evaluating clinical breakpoints for antifungal compounds to treat invasive fungal infections more effectively.

Exploring Microalgal Potential

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Abstract

Microalgae the potential feedstock for commercial production of carotenoids, are currently the most sustainable natural source of production of wide variety of carotenoids including astaxanthin, β-carotene, lutein, lycopene, canthaxanthin and zeaxanthin. These remarkable microorganisms are found in different taxonomic groups and hold immense promise for addressing global challenges ranging from environmental sustainability to human health. Hence, these microalgal carotenoids are in huge demand in food, pharmaceutical, nutraceuticals, and cosmetic industries, along with its emerging application in the biofuel sector. To obtain desired carotenoids with higher productivity, genetic modification by inactivation or over expression of endogenous genes as well as for expressing a wide array of recombinant enzymes from other species are being used. In recent times, with the advent of the new genome sequencing techniques, there is an overabundance of the genomic data of interest. However, most of these protein coding genes have not been characterized. In this study we have done a comprehensive survey of genes and enzymes associated with the less studied methylerythritol 4-phosphate/1-deoxy-d-xylulose 5-phosphate pathway as well as the carotenoid biosynthetic pathway in microalgae through bioinformatics and comparative genomics approach. The genes/enzymes were subsequently analyzed across 22 microalgae species of lineages in order to study the evolutional divergence in terms of sequence-structure properties. Enzymes playing a vital role in carotene, lutein, zeaxanthin, violaxanthin, canthaxanthin, and astaxanthin were unraveled. Of these, many were hypothetical proteins and putative functions to these hypothetical proteins were successfully assigned through comprehensive investigations of the protein family, motifs, intrinsic physicochemical features, subcellular localization, pathway analysis, etc. Furthermore, these enzymes were categorized into major classes as per the conserved domain and gene ontology. Functional signature sequences were also identified which were observed conserved across microalgal genomes. The detailed functional information about individual vital enzymes will certainly help to design genetically modified algal strains with enhanced carotenoid contents.

Key Words: Bio-manufacturing, Microalgae, Carotenoids, Bioinformatics, Enzymes

Exploring the microbial ecology of deep continental subsurface underneath the Deccan Traps, India

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Abstract

Deep subsurface microbiome presents within the hot, oligotrophic igneous crust, thousands of meters below earth surface represents a hidden, enigmatic realm of our biosphere. Recent deep life related explorations across the continents though identified presence of prokaryotic microorganisms surviving close to the 'limits of life', details of their identity and metabolism remain largely unknown. Exploration of life within such unexplored environments has strong implications on the understanding of evolution, adaptation and limits of life, and even in search for life beyond our planet. Scientific deep drilling, considered to be the major window (except the mines and deep caves) to sample deep continental subsurface has enabled us to explore microbial life within the 65 million years old Deccan Traps and underneath the Archean granitic basement. A combination of omics tools is used to decipher the microbial ecology, community assemblages, ecological processes governing those communities and their metabolic functions. Along with whole metagenome shot-gun sequencing of rock microbiome, specialized cultivation approaches, metabolomic and metagenomic analysis enabled us to devise nutrient medium to reactivate the extremophilic microbial populations and their metabolic characterization. Presence of active bacterial communities is observed upto a depth of 3000 meter below surface with an in-situ temperature of nearly 75 ˚C. Co-occurrence of autotrophic and organotrophic taxa with abundance of poly-extremotrophic Actinobacteria and an endemic community linked with H_2 and CH_4 are noted. Abilities to utilize inorganic carbon and electron donors, fermentation, acetogenesis and sulfate reduction are identified to be the major metabolic processes driving this deep biosphere. The study highlighted ubiquity and adaptability of prokaryotic microorganisms within the hot, energy starved crystalline crust and throw light on their metabolic property, biogeochemical significance and potential for applications in environmental, biotechnological and astrobiological research.

Keywords : Astrobiology, Biotechnology, Biogeochemistry, Deep life, Deccan Traps, Extremotolerance, Rock Microbiome

iIL13Pred : Improved Prediction of IL-13-inducing Peptides through Effective Feature Selection Method and Machine Learning Classifiers

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Abstract

IL-13 is a pleiotropic cytokine that is secreted by T-Helper 2 (Th-2) cells, basophils, mast cells, eosinophils, and natural killer cells. Similar to IL-4, this cytokine plays role in Th-2-mediated immunity that includes responses to allergic reactions and parasitic infections. IL13 is associated with several infectious and non-infectious diseases. For instance, it is found to be an important mediator in airway inflammation seen in asthma and reactive airway diseases. Elevated levels of IL-13 were observed in mice following *Chlamydia muridarum* infections. It was further observed that IL-13 knock-out mice suffered from less disease severity, inflammation and bacterial load as compared to the wild-type mice infected with *Chlamydia muridarum*. Interestingly, elevated levels of IL-13 and IL-18 were also reported in patients with severe Dengue Hemorrhagic Fever suggesting that these cytokines play a critical role in the shift from Th1 to Th2 responses among them. Another study reported that exogenous treatment of IL-13, IL-6, and IFN-g led to exacerbating pulmonary abnormality of enterovirus-infected mice. Additionally, levels of IL-13 have been recently correlated with the severity of COVID-19 thereby prompting us to investigate the molecules having the potential to induce this cytokine.

We obtained the experimentally validated IL-13 inducing peptides and used pfeature algorithm to compute features constituting the positive and negative dataset. Feature selection was performed using mRMR algorithm and highly distinguishing features were obtained. These features were then used to test seven machine learning classifiers, including Decision Tree, Gaussian Naïve Bayes, k-Nearest Neighbour, Logistic Regression, Support Vector Machine, Random Forest, and eXtreme Gradient Boosting, to effectively classify IL-13 inducing peptides.

Extensive benchmarking experiments suggest that our prediction tool (iIL13Pred) could provide improved performance metrics in terms of sensitivity, specificity, accuracy, the area under the receiver operating characteristics (AUCROC) and Matthews correlation coefficient (MCC) as compared to the existing method (IL13Pred) on the validation dataset and an external dataset comprising of experimentally validated IL-13 inducing peptides. A user-friendly web server (www.soodlab.com/iil13pred) is also designed to facilitate rapid screening of IL-13-inducing peptides.

Pseudomonas bharatica CSV86^T: an ideal host for metabolic engineering and bioremediation

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Abstract

Pseudomonas bharatica CSV86^T, a novel Indian soil isolate, preferentially degrades wide range of aromatics like naphthalene, benzoate, benzyl alcohol and phenylpropanoids over simple carbon sources like glucose and glycerol, making it unique amongst *Pseudomonas* spp. The strain exhibits advantageous eco-physiological traits like indole acetic acid production, siderophore production, alginate synthesis, assimilatory nitrate reduction and organic sulphur metabolism, which enhances its survivability. Further, availability of whole-genome sequence, well-characterised growth conditions and lack of plasmid make it an ideal metabolic engineering host. Strain CSV86^T was engineered for Carbaryl degradation *via* salicylate-catechol route by expression of Carbaryl hydrolase (CH) and 1-naphthol 2-hydroxylase (1NH) under the P*nah* promoter. *In-silico* analyses and carbon source-dependent expression of McbT (encoded by *mcb*T, Carbaryl degradation upper operon) from *Pseudomonas* sp. C5pp suggested it to be an outer membrane protein. The expression of McbT in addition to CH and 1NH enhanced the degradation efficiency, affirming its involvement in Carbaryl uptake. Additionally, presence of Tmd+Sp at the N-terminus of CH resulted in the periplasmic localisation of Carbaryl degradation enzymes in the engineered strain, providing insights into an efficient compartmentalisation strategy to optimise degradation. The enzyme activity, whole-cell oxygen uptake, biotransformation, protein analyses and quantitative PCR results suggest that the engineered strain preferentially utilised Carbaryl over glucose with localisation of enzymes in the periplasm. The plasmid-encoded degradation property was found to be stable for 75-90 generations even in the absence of selection pressure. These results indicate that *P. bharatica* CSV86^T is a potential host for the metabolic engineering of aromatic degradation pathways.

Microbial bioremediation using bio-computational approaches-perspectives and challenges

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Abstract

The various bio-computational approaches are gaining immense interest among researchers towards innovative insights for the understanding of microbial assisted bioremediation. These techniques have incredible potential for the understanding the role of metabolic pathways, protein transporters and their mechanisms for efficient bioremediation of environmental pollutants. Nevertheless, there is lots of field scale limitations and challenges due to several environmental factors. In the present study, we have used various bio-computational tools towards identifying the novel genes and also their possible role in the metabolic pathways. Our ongoing study also trying to understand the use of syncom (synthetic microbial consortium) and idea of microbe's co-cultivation for bioremediation of hazardous heavy metals residues in soil. We have successfully explored the role of the bacterial isolates i.e. *Bacillus cereus* BPS-9 and *Ochrobactrum ciceri* BPS-26 in the Lead bioaccumulation along with understanding of its metabolic pathway. Our study deciphered the role of genes encoding heavy metal resistant proteins and transporters for the efflux of heavy metals in *Bacillus cereus* BPS-9. In addition, we have also explored the comparative heavy metal bioaccumulation potential of *Ochrobactrum intermedium* BPS-20 and *Ochrobactrum ciceri* BPS-26. Such approaches, if combined with metabolic engineering may be quite crucial for achieving effectual microbe assisted bioaccumulation of heavy metals.

Exploring microbial biocomplexity in coastal ocean: the importance of time series

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Abstract

Coastal oceans are home to unique functional microbial communities, offer key ecosystem level services and contribute towards blue economy. Coastal oceans which are influenced by flow of carbon pool originating from the land along with continuous freshwater flow are home to microbial communities with functional complexities. Ecological time series offer a unique approach to understand intricacies in terms of structure and functions of microbial communities in coastal ocean. Sundarbans Biological Observatory Time Series (SBOTS), a unique time series running in the Sundarbans mangrove of the coastal Bay of Bengal for more than a decade, has provided intricacies of the microbial community dynamics and their role in shaping carbon cycling. The functional microbiome signatures of SBOTS and wider Sundarbans have shown the ecosystem level responses of increasing anthropogenic pressors in a changing climate. From the ongoing learnings garnered from SBOTS, new approaches to microbiome assisted sustainable technologies are being developed to tackle issues of pollution and also towards ecological restoration using nature-based solutions.

Unraveling the Microbial Fabric of Manikaran: A SeqCode-Based Approach to Identify Metabolic Activities in the Hot Spring Ecosystem

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Abstract

Nestled amidst the majestic Himalayas, Manikaran is a geological marvel renowned for its boiling springs. Beyond the alluring landscapes, however, lies a hidden world teeming with microbial life, thriving in extreme temperatures. However, this incredible realm could not be previously accessed due to the unavailability of the majority of prokaryotic phyla as pure cultures (>70%), they do not satisfy the requirements for naming as per the International Code of Nomenclature of Prokaryotes (ICNP). To tackle this challenge, a novel concept called SeqCode has been introduced in 2022. SeqCode is a code of nomenclature that utilizes genome sequences as the foundation for assigning names to prokaryotes. It allows for the valid publication of names for prokaryotes based on isolate genome, metagenome-assembled genomes, or single-amplified genome sequences. The functioning of the SeqCode is facilitated by the SeqCode Registry, a registration portal that establishes links between names, nomenclatural types, and metadata. This code establishes a framework for reproducible and objective nomenclature for all prokaryotes, regardless of their cultivability, and promotes effective communication across various microbiological disciplines. Furthermore, the SeqCode incorporates provisions for the revision and updating of names as new data becomes available. The development of the SeqCode marks a significant advancement in the study of uncultivated prokaryotes. Through the implementation of a standardized system that utilizes genetic information to name and categorize microorganisms, the SeqCode is expected to greatly improve the understanding of these microorganisms, their impact on the environment, and their influence on Earth's functioning. As the announcement of SeqCode took place only in 2022, its code (SeqCode v1.0) is still undergoing continuous updates and refinements with the active involvement of scientific communities. Although new, the SeqCode registry has already identified and cataloged 9167 names from 3396 publications, including 192 validly published names in 43 lists. In this study, we aim to employ the SeqCode pipeline as the fundamental basis for analyzing our Metagenomic sample derived from various locations in the Hot Water Spring at Manikaran, Himachal Pradesh, India.

Key Words: SeqCode, Taxonomy, Uncultured Prokaryotes, ICNP, MAGs



Microbes as revitalizing options in protected cultivation

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Abstract

Microorganisms underpin a majority of the activities related to the biogeochemical cycling of nutrients, playing significant roles in the health and productivities of agricultural crops. Among them, cyanobacteria occupy a unique niche as their diversity in space, time, ecologies and their physiological and biochemical repertoire makes them ideal candidates in agriculture Our investigations undertaken at the ICAR-Indian Agricultural Research Institute, New Delhi, India, over the last ten years led to the development of novel consortia of bacterial-cyanobacterial Isolates from the rhizosphere and edaphic habitats, as inoculants, for various crops, in diverse crops - rice, wheat, maize, cotton, chickpea, flowers and vegetables, using compost: vermiculite as carrier.

Protected cultivation is gaining significance as an important of horticulture, including growing *out of season* or exotic crops. Systematic evaluation of these '*microbials*' under controlled, greenhouse and field conditions, amendment of cyanobacteria to soil-less potting media revealed their promise for providing better aeration, aggregation and nutrient availability, thereby invigorating nursery-raised vegetable and flower crops. Laboratory-developed biofilms using cyanobacterium *Anabaena* sp. as a matrix and agriculturally beneficial bacteria and fungi further increased their proficiency in relation to better colonisation, residence times, metabolic activity in the rhizosphere and roots, as well as moisture-deficit habitats. Culture-based as well as the cultivation-independent methods of DGGE, SEM, and PLFA supported their colonisation and growth.

The unique feature of our formulations is the multifarious modes of application- as seed dressing or seedling dip or dry flakes which can be mixed in soil before sowing/transplanting or as foliar sprays or soil drenches; and being native to rhizosphere, these cyanobacteria establish well in this niche. The characteristic modulation of eubacterial, archaeal and cyanobacterial communities of the host plants, both in the phyllosphere and rhizosphere by microbial inoculation was illustrated using phospholipid fatty acids (PLFA) analyses, PCR-denaturing gradient gel electrophoresis (DGGE) profiling of soil metagenomes, qPCR analyses of microbial abundances and functional genes related to nitrogen fixation and indole acetic acid production. This favourably influenced nutrient uptake and growth promotion, fruit yield was significantly higher by 20-30% and quality of fruits in terms of higher lycopene and other quality attributes, as well as flower quality over control. Our investigation provides environmentally friendly options as a biological and sustainable alternative to chemicals, and highlights their promise as a supplement in protected cultivation.

Microbes and climate change: Significance of Methane Utilizing Bacteria in Agriculture

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Abstract

Climate change is posing extensive adverse consequences and losses for both ecosystems and human populations worldwide. Within this complex web of environmental challenges, microbes play a crucial role in elemental cycles, particularly those of carbon, nitrogen, and phosphorous. They serve as primary producers and consumers of greenhouse gases such as carbon dioxide, methane, and nitrous oxide, thereby significantly influencing the Earth's climate. Microorganisms, acting as both sources and sinks of methane, a potent greenhouse gas, play a pivotal role in driving climate change. Consequently, microbial research assumes critical importance in understanding and mitigating the trajectory of global warming and its cascading impacts on agriculture and the environment. One promising avenue of research involves investigating the microbial communities inhabiting the rhizosphere and phyllosphere of plants, particularly those growing in natural (e.g., mangroves) and artificial wetlands (e.g., flooded agricultural ecosystems). These environments harbor methane-utilizing bacteria that can oxidize methane at its source, thus reducing its net flux into the atmosphere. Traditionally, microorganisms have been utilized as biofertilizers to enhance plant growth. However, recent research has highlighted their potential to mitigate greenhouse gas emissions, especially in flooded agricultural ecosystems. Efforts have been directed towards developing multifunctional microbial inoculants capable of both methane oxidation and promoting plant growth. Research in this field has primarily focused on understanding the taxonomic diversity of methanotrophic bacteria and the environmental factors governing methane utilization in wetland ecosystems. Additionally, there has been a growing interest in exploring combinations of taxonomic groups commonly found in rice paddies and those traditionally used as biofertilizers, with the aim of developing effective strategies for methane mitigation and sustainable agriculture. In summary, microbial research offers promising avenues for addressing the challenges posed by climate change, particularly in the context of reducing greenhouse gas emissions from agricultural ecosystems. By harnessing the potential of microorganisms to mitigate methane fluxes and promote plant growth, we can contribute towards building a more resilient and sustainable future for our planet.

Assessment of Microbial Indoor Air Quality in Microenvironment for Health Risks

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Abstract

Indoor air quality(IAQ) is one of the most significant variables affecting people's health and well-being. Air pollution in indoor microenvironments has a considerably worse impact on health than outdoor air pollution. IAQ deterioration is primarily caused by airborne pollutants, including pollen, allergens, SO_2, particulate matter(PM), carbon monoxide, N_2O, radon, and polycyclic aromatic hydrocarbons(PAHs). Human health is greatly impacted by IAQ since most individuals spend 80–90% of their time indoors. The adverse air quality in indoor spaces may be caused by a higher concentration of airborne microorganisms in microenvironments, which closely relates to adverse impacts on the respiratory system and overall health, such as sick building syndromes, especially in regions within proximity to industrial zones. The microorganisms known as bioaerosols are sourced from organic dust, animals, humans, and various other products and can contribute to allergies, infectious diseases, skin problems, immunomodulatory responses, Chronic Obstructive Pulmonary disorders(COPD), like laryngitis, asthma, bronchitis, etc. The most common fungal genera found in indoor microenvironments are Alternaria, Aspergillus, and Penicillium, and the most common bacterial genera are Streptobacillus, Micrococcus, and Staphylococcus. Higher respirable fungal proportions may produce different health impacts by penetrating deeper into the lungs. The fungal component of airborne microorganisms is responsible for Conjunctivitis, Aspergillosis, rhinitis, UTI, etc. Hospitals, offices, and residential spaces are important indoor microenvironments for the dissemination and transmission of bioaerosols. Since microbes can adapt to various environmental conditions, their concentrations in different sub-areas of the same microenvironment can vary significantly. The abundance and composition of microorganisms in indoor microenvironments vary seasonally as well as with climatic variables including temperature, relative humidity, and air exchange rate. Considering environmental challenges and public health concerns, there is a pressing need for a comprehensive understanding of microbial indoor air quality and associated health risks across diverse microenvironments.

Key Words: Indoor air quality, Microenvironments, Airborne microorganisms, Public health

Vitamin D_2 enrichment of captive cultivated Shiitake mushroom for the production of value-added products

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Abstract

Shiitake [*Lentinula edodes* (Berk.)] mushrooms are rich in nutrients and have a significant ergosterol content that can be converted into vitamin D_2 through UV light exposure. In this study, we investigated the cultivation and nutritional properties of shiitake mushrooms, focusing on substrate variations, and vitamin D_2 enrichment. Firstly, seven hardwood and two softwood substrates were collected from Indian Himalaya, and investigated for shiitake production, compositional changes, nutritive value, ergosterol content and its conversion to vitamin D_2. The findings demonstrated significant variations in shiitake production among the substrates ($p<0.05$), with hardwood species, particularly *Populus ciliata* substrate (341±6.5 g/kg), and *Mangifera indica* (MI) (234±7.4 g/kg), exhibiting higher yields compared to softwood substrates. Additionally, optimization studies on ergosterol conversion to vitamin D_2 indicated that 30 KJ m^{-2} of UV-B exposure significantly enhanced the vitamin D_2 content (99.8±2.6 µg/g). Further, UV-irradiated shiitake soup formulation (32024±20 IU D_2/20g sachet) was formulated and were determined to ensure their safety for consumption. Stability studies of shiitake soup indicated minimal vitamin D_2 loss upon boiling for three minutes (31703±152.8 IU/20g). Further, to determine the bioavailability of vitamin D_2 shiitake soup in healthy humans deficient in serum 25-hydroxyvitamin D (25OHD), fifty-three patients were randomized to three treatments viz., 1. irradiated shiitake soup (n=18), 2. vitamin D_2 supplement (n=18), and 3. placebo shiitake soup (n=17) for five weeks. After four consecutive weeks, vitamin D_2 shiitake soup alleviated 25OHD from 30±8.3 nmol/L (baseline) to 49.1±21.7 nmol/L. Similarly, in the supplement arm, 25OHD also increased (31.1±7.2 to 44.8±20.5 nmol/L), but there was no improvement in the placebo group (28.3±6.8 to 29.1±11.5 nmol/L). The optimized vitamin D_2 shiitake soup demonstrated effectiveness in improving serum 25OHD and offers a potential solution for the population affected with vitamin D deficiency.

Key Words: *Lentinula edodes*, Vitamin D_2, Ergosterol, Indian Himalaya, 25-hydroxyvitamin D

Future Prospects of Microalgae in Agriculture and Food Security

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Abstract

Food security is a concept that is used to think systemically about how and why malnutrition arises, and what can be done to address and prevent it. Conflicts, economic shocks, climatic shift and roaring fertilizer prices causing unprecedented food crisis. In this context, microalgae are attracting more and more attention as future food sources because of a strong carbon sequestration ability and high photosynthetic efficiency thus, playing an important role in the new food supply system and world carbon neutrality process in the future. Microalgae-based foods are already evident as opportunities for food research and development and consumed as SCP in the form of supplements and other innovative products, including chocolates and beverages. The optimization of processes and knowledge of cultivation steps and their reagents are crucial for quality control. Our lab has already designed photobioreactor and mass cultivated the microalgae including cyanobacteria for food, bioactive molecules, and biofuel purposes. A eukaryotic wall-less halotolerant microalga, *Dunaliella salina* and its ability to maintain lower intracellular Na^+ even at higher salinity is a source of novel genes for crop improvement. It is interesting as it grows in hypersaline conditions with 10% carotenoid. Therefore, membrane transporters and carotenoid biosynthesising genes are candidate gene(s) to improve the crop plants to make them salt tolerant as well as carotenoid enriched. As Se is a requirement in biomedicine, Se-enriched *D. salina* biomass may be used as food and feed supplement after evaluating the toxicity assay. *Arthrospira platensis*, a cyanobacterium is a well-established dietary supplement. The metabolic profiling of *A. platensis* is not well documented to date. An attempt to optimize biomass production *vis-a-vis* whole metabolites in varying salt concentrations revealed that the significant metabolites belonged to chemical classes such as benzene and substituted derivatives, carboxylic acids and derivatives, fatty acyls, and organonitrogen compounds. However, such a study would pave the way to plan mass cultivation of *A. platensis* in a specific culture condition to be used biotechnologically for food supplement.

Microbial Literacy Initiative for Viksit Bharat through IMiLI: Healthy Society, Environmental Protection and Global Peace

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Abstract

Microbiology and microbial literacy in society especially teaching this subject at the school level has become very important for maintaining better human health, environmental protection, and for global peace. This has become very important in India where a lot more activities are already underway to achieve the target of Viksit Bharat by 2047. We in India are propagating microbial literacy among society members and school children through the International Microbial Literacy Initiative - South Asian Centre (IMiLI-SAC) in New Delhi. We will present briefly the overview of the activities that are underway to achieve this target to create microbial literate society.

Amycolatopsis mediterranei: A Powerhouse for the generation of rifamycin B analogues Effective Against MDR Strains of *Mycobacterium tuberculosis*

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Abstract

Amycolatopsis mediterranei an actinobacterium produces rifamycin B and semi-synthetic derivatives of rifamycin B are in use for curing tuberculosis caused by *Mycobacterium tuberculosis*. The first semi-synthetic derivative of rifamycin B called rifampicin was introduced for curing tuberculosis in 1968. Since then there appears to be no effective drug except bedaquiline to tackle the problem of MDR strains of Mycobacteria. We have developed methods to manipulate the rifamycin polyketide synthase gene cluster in *A. mediterranei* that can now be used to generate rifamycin B analogues. These analogues can be starting material to produce semi-synthetic derivatives that could be more effective against MDR strains of *Mycobacterium tuberculosis*. Our efforts that resulted in the genetic manipulation of *A. mediterranei* to produce a variety of compounds by combinatorial biosynthesis approaches will be presented.

Soil Metaproteome: A comparative analysis of wheat rhizosphere metaproteome grown in saline and non-saline soils

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Abstract

Metaproteomics is a powerful tool for obtaining data on all proteins recovered directly from environmental samples at a given time. It provides a direct evidence of structural and functional diversity among microbiota present in niches and significant insights into microbial activity together with metabolomics. Since rhizosphere microbiome plays important role in plant growth and development, the present study is conducted to optimize the metaproteomic extraction protocol from maize rhizosphere and analyse functionality of microbial communities. The present study was conducted to characterize functional metabolic changes in the rhizosphere microbiota of wheat grown under saline and non-saline soils using comparative metaproteomics. In total 1538 and 891 proteins were obtained from wheat rhizosphere from saline and non-saline soils, respectively. The proteins DNA-directed RNA polymerase subunit beta' (48.43%) followed by LeucinetRNA ligase (4.45%) and translocase subunit SecA (2.69%) were relatively most abundantly present in salt stressed wheat rhizosphere metaproteome. Induced accumulation of proteins related to proline and spermidine biosynthesis was found in saline wheat rhizosphere. Inositol transporter involved in the osmotic balance and HSP90A, a key player to response regulator in stress were present in saline rhizosphere but were absent in non-saline conditions. Among 1410 proteins unique for saline soil, those linked predominantly with the pathways were sphingolipid, phosphinate and phenazine metabolism. The data is available in ProteomeXchange with the identifier PXD015387. The present study extends knowledge about the rhizosphere community functions utilizing a metaproteomic approach in wheat growing under saline conditions and can help in characterizing key proteins that may lead to physiological adaptations of the plants under saline environment.

Marine algae biorefinery

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Abstract

Algae are the most diverse photosynthetic organisms. Algae biomasses contain polysaccharides, lipids, pigments, protein, and amino acids and thus carry immense potential for production of value-added biomolecules in a refinery approach. Algae can be grown in fresh water, marine water as well as in wastewater in mixotrophic growth mode. Among all, growing algae in sea water has several advantages, as it does not require potable water for cultivation and does not compete with terrestrial crops.

Marine algae can grow and utilize sea water effectively to produce biomass by sequestering atmospheric CO_2. One of the crucial aspects for growing marine algae is isolation of select algae and its adaptation for outdoor cultivation in large scale with high biomass productivity. Marine algae biomass is a rich source of bioactive compounds and thus gaining global attention to raise this biomass for production of biofuel and biochemical in a biorefinery approach. major cost for algae-based bioproduct is associated with their downstream recovery from the biomass. To make these processes economically viable, there is a need to develop end-to-end low-cost technologies for recovery of oil, sugar and pigments, and process scale up without compromising product yield/ recovery.

This presentation will focus on TERI leads on demonstration of bioprocesses for large scale outdoor algae cultivation and use of algae biomass (fresh water and marine algae biomass) as feed stock production of next generation biofuel (bioethanol, biohydrogen) along with value added, biochemical.

Targeting Mycobacterial "SOS" Response- a strategy to toggle Antimicrobial Resistance (AMR)

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Abstract

The "SOS" response is an essential systematic mechanism against DNA damage in bacteria. It is indispensable for its regulatory role in maintaining genome integrity and in gaining fitness advantage by developing useful mutations to tolerate genotoxic stress, leading to the development of antimicrobial resistance. LexA and RecA are the key players regulating the global network of stress-responsive and damage-repair genes involved in this pathway. In an era of expanding drug resistance, targeting such non-traditional yet non-compromising pathways can provide useful answers in tackling global health hazards such as Tuberculosis (TB). The potential of targeting the "SOS" response is gathering increasing support to strengthen therapeutic efficacy. RecA inhibitors have been reported from chemical screening assays conducted in *E.coli* and *Mycobacterium tuberculosis* (Mtb), the latter being the causative agent of TB. However, RecA bears homologs not only across prokaryotic but also eukaryotic organisms, posing a challenge for specific action. Consequently, a shift in gears has taken place with scientists switching to the other master regulator, LexA, which does not possess any eukaryotic counterpart. An academic-industry partnership successfully delivered the first-of-its-kind inhibitors targeting *E.coli* LexA autoproteolysis. Such efforts have not yet been extended to Mtb and addressing this gap forms a major objective of our study. Here, we report potential inhibitors of Mtb LexA. We have elucidated the kinetic parameters of interaction and generated a homology model to obtain an idea of possible drug-binding sites in Mtb LexA. Our studies involve characterizing such compounds with the broader aim of improving the existing arsenal of anti-TB therapeutics. Characterizing such inhibitors of Mtb LexA autoproteolysis can be effective in stalling "SOS" induced mutagenesis and AMR in mycobacteria.

Tiny But Mighty: Microbes & Sustainable Development

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Abstract

In the past few decades, we have realized how the human dominance and exploitation of nature has resulted in serious damage to our planet in terms of waste production and also depletion of natural resources. The sustainability of the environment is on the verge of collapsing unless we re-new our ways and shift to greener options. It is astonishing to know that more than 700 million people, or 10 per cent of the world population, still live in extreme poverty today, struggling to fulfil the most basic needs like health, education, and access to water and sanitation, to name a few. Nearly 690 million people are hungry, or 8.9 percent of the world population. If recent trends continue, the number of people affected by hunger would surpass 840 million by 2030. These are just a few numbers which has raised a concern. Should the global population reach 9.6 billion by 2050, the equivalent of almost three planets would be required to provide the natural resources needed to sustain current lifestyles. Foreseeing this United Nations expressed its intervention with a hope of creating a sustainable tomorrow. In Jan 2016, 193 countries worldwide agreed to 17 Global Goals with 169 targets for a sustainable development of the world by 2030. As said, big changes start small. Microbes behold the route to sustainability which in simpler words means the *"capacity to continue into distant future"*. Since ages, these tiny beings have influenced our day-to-day life from health to food, climate change to bioremediation, bio-fuels to improvement of water quality and even discovery of new drugs and sustainable food production.

Translating Virus-Host interaction data into antiviral modalities

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Abstract

Viral pathogens are formidable foes of humanity. The COVID-19 pandemic has been a stark reminder of this fact. Although substantial progress has been made in developing vaccines, there remains a scarcity of antiviral drugs, which are also susceptible to rapid resistance from target viruses. Exploring and analyzing extensive virus-host interaction multi-omics data can illuminate novel antiviral targets. Our team has created advanced algorithms for big data analysis of virus-host interactions, enabling the identification of clinically approved agents that can be repurposed as antivirals. Successfully applying this approach, we have identified potential candidates for SARS-CoV-2, Influenzas, and Flaviviruses.

In silico bio-prospecting and chemoinformatics screening of potential lead molecules against multi-drug resistant WHO priority pathogens

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Abstract

Multidrug-resistant *Acinetobacter baumannii* (MDRAb) and *Pseudomonas aeruginosa* (MDRPa) were declared by WHO (2019) as priority-I and II pathogens, respectively. *In silico* bioprospecting has become the latest tool in pharmaceutical biotechnology and chemoinformatics screening of potential lead molecules has profound applications in developing drug candidates against several drug resistance pathogens. The study focused on screening novel phytoleads as potential binders against prospective targets of MDRAb and MDRPa by *in silico* bioprospecting and chemoinformatic approaches. Based on the functional role, γ-carboxymuconolactone decarboxylase (CMD) was prioritized as the target of MDRAb and its three-dimensional (3D) structure was computationally modeled. A focused natural compound library was constructed and subjected to computational screening, molecular docking, and molecular dynamic simulation. The present study showed that Hirsutine present in *Uncaria rhynchophylla* and Thymoquinone present in *Nigella sativa*

were qualified for drug likeliness, pharmacokinetic, and toxicity features and demonstrated significant effectual binding to CMD when compared with the binding of co-crystallized inhibitor and CMD (control). The docked complexes of Hirsutine and Thymoquinone, and CMD were stabilized by the binding energies of -8. 30 and -8. 46 kcal/mol respectively. Molecular dynamics studies showed that the ligand-protein complexes were stable throughout the simulation. The binding free energies of the complexes by MMGBSA were estimated to be -42.08157745 kcal/mol and -36.58618242 kcal/mol for Hirsutine and Thymoquinone respectively when compared with the calculated binding free energy of the control (-28.75032666 kcal/mol). Similarly, Rotiorinol present in *Chaetomium cupreum* and Celastrol

present in *Celastrus paniculatus* and showed better binding with GacA and RhlR of the potential target of MDRPa, respectively, when compared to the binding of Meropenem and its target. MD simulation studies showed that and RhlR-Rotiorinol and GacA-Celastrol complexes demonstrated conformational stability throughout the simulation. The present study suggested that phytotherapeutics screened by *in silico* bioprospecting are probably used as effectual binders against the prioritized molecular targets of MDRAb and MDRPa.

Key Words: Multidrug-resistant *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, *In silico* bioprospecting, Chemoinformatics screening, molecular docking, molecular dynamic simulation

Two success stories of environmental microbial technology: Improving productivity of shifting cultivation and treating AMD in small-scale coalmines

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Abstract

Shifting cultivation, and Acid Mine Drainage (AMD) from small-scale coalmines are the two most important environmental problems of north-eastern India. Although AMD treatment technologies do exist across the world including India, small scale coal miners cannot afford the cost of such technologies and therefore, untreated AMD with pH up to 1 flow unabated from the mine dumps and mines to surface water bodies, crop fields and forests causing serious environmental and health hazards. Similarly, maintaining the productivity of shifting cultivation plots beyond the second year of cropping has been an age-old problem worldwide in shifting cultivation areas. A research team at North-Eastern Hill University, Shillong led by the author, screened and isolated both aerobic and anaerobic microbes from AMD channels, and developed a low-cost hybrid technology taking both passive and active approaches. The technology could successfully enhance the pH of AMD from ~1 to 6. The microbial isolates from shifting cultivation fallows targeting for Phosphorus solubilizers and Nitrogen fixers were screened and the most efficient strains were used for formulation of biofertilizers to retain the soil fertility year after year so that the cultivators need not shift from the plot due to loss of soil fertility and clear a new forest patch. The technologies are being deployed successfully in large-scale projects, and individual small-scale mine owners of Jaintia Hills of Meghalaya.

Microbes and enzymes for sustainable production of high value products

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Abstract

Microbes have been recognized as potential organisms for providing solutions in diverse areas like food, agriculture, health and environment for the sustainable development. Towards this, some work has been conducted by using microbes and their enzymes in our laboratory. Also, biotechnology, synthetic biology and bioprocessing approaches have been used for efficient use of microbes and enzymes for sustainable production of valuable compounds. An efficient and economic process has been developed for the production of bacterial cellulose from isolated strain of *Acetobacter pasteurianus* RSV-4 bacterium. In order to globally understand the genetic structure and mechanism of cellulose production, a draft genome sequence of *Acetobacter pasteurianus* RSV-4 was performed. Microbial enzymes have been used for rare sugars productions. Nanoflowers of L-arabinose isomerase was developed as a stable and recyclable nanobiocatalyst for equilibrium level conversion of D-galactose to a rare low-calories sugar D-tagatose. Similarly, immobilized L-ribose isomerase was used for the sustained synthesis of a rare sugar D-talose. Further, a metal-based micro-composite of L-arabinose isomerase and L-ribose isomerase was also developed for the sustainable synthesis of L-ribose and D-talose. Xylanase and mannanase from microorganisms have been documented for prebiotic oligosachharides production from agrobiomass. Efficient processes have been developed by using microbes for the production of ethanol and acetic acid from the secondary biomass. We have identified and characterized a lytic polysaccharide monooxygenase (LPMO) for oxidative cleavage of lignin. Hence, such LPMO could be an attractive biocatalyst for use in enzymatic cocktails for lignin valorization. Hence, these some of the examples where microbes and/or enzymes have been explored for their potential in the production of valuable compounds in sustainable manner.

Cyanobacteria: A sustainable resource for food and organic agriculture

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Abstract

Cyanobacteria or blue green algae (BGA) are considered as primary producers and a potential source of several metabolites with applications in food, feed, biofuel, agriculture, environment management, therapeutic and nutraceuticals. The bioactive molecules from cyanobacteria are considered as safe dietary supplements for long-term physiological health benefits, boosting the immunity, decreasing the cardiovascular disease risk, cancers and diabetes and promoting a better quality of life. They possess antioxidant, antimicrobial, antitumor and immunomodulatory characteristics making them a suitable option for nutraceutical, pharmacological and biomedical application. In many cases there is utilization of whole biomass or certain valuable constituents are extracted including metabolites and enzymes. They are a promising alternative to animal sources for vegan consumers and offer healthier, natural and sustainable products to bio-fortify food, to boost immunity and to satisfy the nutritional deficiencies of many foods and feeds in an economic way. New trend of research is inclined towards development of bioactive fortified functional food items consumed popularly like doughnuts, pasta, salad dressing, mayonnaises and gelled-desserts etc. Enrichment with different cyanobacteria particularly *Spirulina/ Arthrospira* etc. results in enhancement of protein and functional properties of fortified foods along with increase in the total phenolic content and antioxidant capacity with good consumer acceptance at correct formulation proportion. Cyanobacteria-based ω-3 fatty acids can be used to provide the daily dietary recommendation for basal nutritional needs especially for pregnant women and people with health complications.

The agricultural importance lies in the capacity of these organisms to fix atmospheric nitrogen, liberation of growth promoting substances, solubilising phosphates, addition of organic matter and improving soil health. Cyanobacteria (BGA) are considered as an important biofertilizer for rice because rice field conditions are conducive for growth and multiplication of these organisms thereby contributing handsomely to essential crop nutrients like N and P and sustaining crop productivity. In addition, BGA benefit crop plants by also producing various growth-promoting substances, improve the physico-chemical properties of the soil by enriching them with carbon, nitrogen and available phosphorus. Use of cyanobacteria biofertilizer in integrated nutrient management and organic farming is now a recommended practice. No doubt, their unique ability and metabolic diversity and their economic viability for large scale production has made cyanobacteria an important feedstock for a number of applications to benefit humans and other higher organisms.

Herbicidal influence on soil biochemical parameters and microbial community in tropical rice agroecosystem

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Abstract

The application of herbicides is a widespread practice in intensive agriculture. However, herbicide residue accumulation in the ecosystem may affect important soil health determinants. Extensive use of chemicals like herbicides in rice and other fields to manage weeds is expected to have a lasting influence on the soil environment. Considering this rationale, we aimed to decipher the effects of herbicides, Pendimethalin and Pretilachlor, applied at 0.5 and 0.6 kg ha 1, respectively on the rhizosphere microbial community and soil characteristics in the tropical rice field, managed under zero tillage cultivation. The quantity of herbicide residues declined gradually since application up to 60 days thereafter it reached the non-detectable level. Most of the soil variables *viz*., microbial biomass, soil enzymes etc., exhibited slight reduction in the treated soils compared to the control. A gradual decline was observed in Mineral-N, MBC, MBN and enzyme activities. Quantitative polymerase chain reaction results showed maximal microbial abundance of bacteria, fungi and archaea at mid-flowering stage of rice crop. The 16 rRNA and ITS region targeted amplicons high throughput sequencing microbial metagenomic approach revealed total of 94, 1353, and 510 species for archaea, bacteria and fungi, respectively. The metabarcoding of core microbiota revealed that the archaea comprised of *Nitrososphaera, Nitrosocosmicus,* and *Methanosarcina*. In the bacterial core microbiome, *Neobacillus, Nitrospira, Thaurea,* and *Microvigra* were found as the predominant taxa. *Fusarium, Clonostachys, Nigrospora, Mortierella, Chaetomium,* etc., were found in core fungal microbiome. Overall, the study exhibited that the recommended dose of herbicides found to be detrimental to the microbial dynamics, though a negative relation between residues and soil variables was observed that might alter the microbial diversity. The outcomes offer a comprehensive understanding of how herbicides affect the microbial community in zero tillage rice soil, thus has a critical imputation for eco-friendly and sustainable rice agriculture. Further, the long-term studies will be helpful in elucidating the role of identified microbial groups in sustaining the soil fertility and crop productivity.

Attributes of Infectious Diseases: A cholera paradigm

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Abstract

More than 20 million people die from infectious diseases, in which bacterial infections contribute 7.7 million deaths. Viral and bacterial pathogens mostly instigate high rate of morbidity and mortality both in developed and developing countries. In this talk, the acute diarrheal disease cholera has been applied as a model to illustrate several integrated components, which are more or less pertinent to other infectious diseases. Historically, cholera has caused seven pandemics with two biotypes of *Vibrio cholerae* O1 serogroup. In 2022 alone, 44 countries reported more than 7,72,000 cholera cases with 2349 deaths. With the retreat of classical biotype of *V. cholerae* during late 1960s, the El Tor biotype predominating as 7th cholera pandemic. Emergence of the O139 was thought to be the 8th pandemic, but this serogroup lost its hold and mysteriously disappeared. Whole genome sequence of *V. cholerae* strains indicated three waves of cholera since 1960 with specific single nucleotide polymorphism (SNP), cholera toxin (CT) and antimicrobial resistance (AMR) encoding genes. The loss of CT and AMR encoding genes was thought to be the reason for the revocation of O139 serogroup from the cholera scenario. Conventional methods have inadequacies in addressing the complexity of infectious disease. This talk consolidates the importance of viable but non-culturable *V. cholerae*, the role of point-of-care testing for outbreak investigations and the usefulness of cholera vaccines**.** There is an inherent relationship between climate change and health outcomes. This global phenomenon has several consequences, including increase of outbreaks contributed by El Niño effect. One health approach is considered as an important strategy in understanding the interrelation of environment, animals and humans, which has the potential to transform our understanding, and mitigate the impact of infectious diseases. Nuanced understanding is needed among researchers, health professionals and policymakers to make effective strategies to safeguard the human health.

Coevolutionary Dynamics of Microbes, Climate Change and AMR

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Abstract

Bacteriophages (phages) are estimated to be the most abundant biological entity and are crucial in checking bacterial populations and maintaining bacterial diversity through coevolutionary interactions. In natural ecosystems like oceans, phages are estimated to destroy half the bacterial population every forty-eight hours, highlighting their role in nutrient cycling and climate regulation. As climate change progresses, the effects of warming on microbial communities and their impact on human, animal, and plant health are becoming more apparent. Permafrost thawing will likely lead to the re-emergence of ancient microbes, which could cause new infections.

In the face of the global antibiotic resistance crisis, predatory phages are fast emerging as promising alternatives to antibiotics. Hence, understanding how microbes evolve and respond to changing environments, including antibiotic treatments, is crucial. Microbes' ability to regulate their responses to environmental changes is critical for their survival. Still, exposure to extreme environments can lead to the loss of this regulation, contributing to the evolution of antibiotic resistance in pathogens. Hence, studying phage biology and its applications is paramount both for environmental and clinical studies, offering potential solutions to combat climate change and the antibiotic resistance crisis.

In my talk, I will explain the coevolutionary dynamics of phage-host and how climate change drives antimicrobial resistance (AMR). I will also give a brief account of my laboratory's focus on exploring the antibacterial potential of phages and encoded lytic enzymes against E.coli and tubercular & non-tubercular mycobacteria and their biofilms, which protect pathogens from the host immune system and also confers resistance to antibiotics. Building a bank of well-characterized, novel bacteriophages is a valuable asset and a promising source of therapeutic phage and enzymes to feed the antibacterial pipeline.

Scale-up production of thermostable DNA polymerase and protease from *Thermus parvatiensis*

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Abstract

Microbes living in extreme environments like hot water springs have a great biotechnological potential. They produce thermostable enzymes with industrial applications. We are working on an Indian extremophile viz. *Thermus parvatiensis* isolated from Manikaran hotspring that grows at an optimum temperature of 70° C. The DNA polymerase of this isolate is novel and was cloned in a heterologous host. It has shown promising results in laboratory-scale testing with comparable results to the commercially available Taq polymerase. The global market size for DNA polymerase reached USD 132.6 million in 2022, with a projected compound annual growth rate (CAGR) of 1.30% from 2023 to 2030.In addition to this, *T. parvatiensis* also produces an extracellular serine protease that is stable at 70° C. The gene sequence of this enzyme has been identified from the genome and will be cloned in *E. coli* for mass production. The worldwide protease market, with a value of $3,454.3 million in 2020, is anticipated to achieve $5,762.7 million by 2030. It is pertinent to mention that currently, India imports 70% of these enzymes used in the industry. Presently, our focus is directed towards the scale-up of fermentative production of thermostable DNA polymerase and protease by the recombinant heterologous hosts. The results related to the same will be presented.

Decoding the Dynamics of Insect-Plant Interactions: Are microbes on the driver's seat?

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Abstract

During herbivory, insects identify their host plant through specific chemical cues, triggering diverse chemical and morphological defence responses in plants to resist these attacks. However, this seemingly bi-directional insect-plant interaction involves numerous complex factors influencing the performance and fitness of both participants. Microbiota, competitors, predators, and parasitoids further contribute to this ecological interplay, either obligately or facultatively.

Insect endosymbionts play a pivotal role in this association by influencing various metabolic processes such as host sensory perception, nutritional provisioning and reproduction. This symbiosis dictates the survival and fitness of the insect on the plant, concurrently facilitating the circumvention of plant defenses through metabolite detoxification. Simultaneously, plant-associated microbes enhance induced systemic plant resistance by reinforcing chemical and morphological defense mechanisms.

These intricate interactions form a complex web of relationships extending beyond the immediate insect-plant interaction, impacting higher trophic levels and ecosystem dynamics. The insect-plant interaction unfolds as a scientifically intriguing and multi-dimensional phenomenon, with microbial participants serving as integral contributors to the ecological narrative, providing a comprehensive understanding of the natural environment.

Ectomycorrhizae:A Boon for Himalayan Environmental Management using Biotechnological Approaches

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Abstract

Ectomycorrhizal fungi also known as ectomycorrhizae (ECM) are symbiotic association of fungi with the feeder roots of higher plants in which both the partners are mutually benefited and indeed the association appears to be significant for the existence of both the partners. The mycorrhizae, due to their key position in the soil-plant interface, are important to consider in the study of the ecosystem. It is known that mycorrhizal fungi affect plant performance through the benefits they confer on their hosts. It is likely that mycorrhiza-mediated processes influence plant nutrition, plant competition and the nutrient cycle in the soil. ECM can alter the chemistry of mycorrhizosphere by increasing the rate of weathering of soil minerals and supply the released nutrients to the plant. It also benefits the host indirectly by influencing important ecosystem properties such as soil structure. The diversity of ECM fungi is likely to contribute to the resilience of forest ecosystems to changing environmental factors, such as pollution and global climate change. In addition, N fixing bacteria appear too associated with specific types of ECM. Some plant growth promoting rhizobacteria stimulate tree growth only in the presence of mycorrhiza. Hence, an urgent consideration for harnessing this natural source of biofertilizer for growth, improvement of natural tree species is requisite. Most previous mycorrhizal research is focused on interactions between plant fungi; its role in the development of the community ecosystem, although important, remains poorly understood. As the fungal diversity of local region is poorly known in India as well as in the Himalayan region, it is essential to document this important wealth of our state and also to find out the ways to conserve and strengthen our important tree species by utilizing this important component of the nature. Uttarakhand state is very rich in tree biodiversity however Ectomycorrhizal fungal diversity and its possible impact on tree diversity in the Himalayan region have not been well studied.These fungi are very important for the growth and development of higher tree species. Ectomycorrhizal diversity through effective plant growth would affect tree species composition , ecosystem functioning and ultimately the whole environment. In Uttarakhand, Oak forests are very important as they retain water and are essential for conservation of natural water resources. The major problem these days in the state is replacement of oak forests with pine forests which is very alarming for natural water resources. With this broad prospective this work had been designed to study the improvement in the growth, performance and fitness of important himalayan tree species in presence of specific ectomycorrhizal species. . As these fungi are very important for the growth and development of higher tree species, it is essential to document the outcome of the tree species of kumaun Himalayan occurring together in forests with the change in associated

ectomycorrhizal fungal species. The study of diversity of ectomycorrhizal fungi at community or local level to develop management plans and to understand the pattern of diversity in relation to environmental changes are also important for finding ways to conserve it. This study on the comparative symbiotic efficiencies of two ectomycorrhizal fungi viz., *Amanita hemibapha* and *Russula vesca* assessed in association with oak (*Q. leucotrichophora*) and pine (*P. roxburghii*) seedlings indicated that the fungal species seem to have a marked influence on competitive outcome of the seedlings, their growth and health status. This work will help us to trace out the new ectomycorrhizal species which will be more beneficial to a particular tree species and will help in conservation of important forest types of Central Himalayas as well as natural resources. It will also provide a platform in development of a technology package which is relevant for nursery rising of these important tree species.

Key Words: Ectomycorrhizae; *Amanita ;Russulla;*Oak(*Quercus Sp.);*Pine*(Pinus sp.).*

Unveiling the Rich Microbial Diversity: Understanding Pathogenic Associations and Antimicrobial Resistance Profiling in the Najafgarh Drain Ecosystem

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Abstract

The Najafgarh drain is a major contributor to the pollution of the Yamuna River, accounting for 40% of the total pollution load. Thus, it is imperative to conduct an investigation into the microbial diversity, metabolic functional capacity, and prevalence of antibiotic resistance genes (ARGs) within the Najafgarh drain. Furthermore, assessing the water quality and its correlation with the proliferation of microorganisms in the drain is of paramount importance. Our results reveal a significant deterioration in water quality, with physico-chemical parameters such as biochemical oxygen demand (BOD), chemical oxygen demand (COD), dissolved oxygen (DO), and total suspended solids (TSS) exceeding both national and global permissible standards, ranging from 125-140, 400-460, 0-0.2, 25-140.4 mg/l, respectively. Additionally, next-generation sequencing (NGS) analysis identified various genera including Thauera, Arcobacter, Pseudomonas, Geobacter, Dechloromonas, Tolumonas, Sulfurospirullum, Desulfovibrio,

Aeromonas, Bacteroides, Prevotella, Cloacibacterium, Bifidobacterium, Clostridium, along with 864 ARGs in the wastewater from the Najafgarh drain. Notably, pathogenic species identified in this dataset pose severe threats to both faunal and human health. Furthermore, Pearson's correlation analysis demonstrated that environmental variables, particularly total dissolved solids (TDS) and chemical oxygen demand (COD), significantly influence the microbial community structure within this heavily polluted drain. Consequently, the combination of poor water quality, the presence of a diverse microbial community, pathogenic markers, and ARGs within the Najafgarh drain suggests its potential role in disseminating disease-causing pathogens to household and drinking water supplies in the near future.

Protein Modifications: Orchestrating the proteome to run the life

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Abstract

Post-translational modifications of proteins play a decisive role in modulating many cellular pathways to maintain the microenvironment of the cell in almost all forms of life. Proteins are modified in a variety of ways including addition of charge, cleavage, addition of different polar and nonpolar groups etc. Most post-translational modifications occur after protein synthesis, however, some of the modifications occur while protein is being synthesized. The most common modification, phosphorylation, is regulated by protein kinases and phosphatases. Protein phosphorylation regulates many cellular processes such as energy generation, cell division and protein-protein interactions by reversible phosphorylation across all forms of life. Similarly, many proteins and enzymes are activated by cleavage. Gene transcription is a very well-known process regulated by acetylation and deacetylation. Using bacterial pathogens such as *Mycobacterium tuberculosis* and *Bacillus anthracis*, as model systems, we have shown that protein phosphorylation is also associated with survival and virulence of the pathogen. Many protein kinases and phosphatases are essential for survival of *M. tuberculosis*. In view of their importance in both virulence and survival, protein kinases and phosphatases constitute an important group of proteins for developing inhibitors to control the disease.

Microbiome dysbiosis as tools for metabolic disorder prediction

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Abstract

Microbiome-based predictions, diagnosis, and therapies represent a groundbreaking frontier in the realm of metabolic disorders, ushering in a new era of personalized medicine. The human microbiome, an intricate ecosystem of trillions of microorganisms residing in the gastrointestinal tract, plays a pivotal role in regulating metabolic processes. Recent advances in microbiome research have unveiled its significant influence on host metabolism, energy extraction, and immune function.

Predictive analytics harness the power of microbiome data to identify individuals at risk of developing metabolic disorders. Through comprehensive analysis of microbial composition and functional pathways, researchers can discern patterns associated with conditions like obesity, diabetes, and cardiovascular diseases. Early detection allows for targeted interventions, potentially preventing the progression of these disorders.

Diagnosis of metabolic disorders is evolving with microbiome-based tools providing nuanced insights. Integrating metagenomic sequencing and advanced bioinformatics, it is possible to pinpoint microbial signatures indicative of specific metabolic imbalances. This not only enhances diagnostic accuracy but also facilitates the development of tailored therapeutic strategies.

However considering the microbiome variation due to biogeography and diet not only the gut microbial composition of Indian population is different from West and East but there is tremendous variation within India too. This necessitates population specific studies on large cohorts leading to population specific tools and therapies. The talk will discuss studies on diabetes, cardiovascular and neurological disorders that are being conducted.

Functional Roles of Ciliates in Oiled Environments – Best Practices for Bridging Datasets

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Abstract

Emphasis on the functional roles of protists has been a dominant theme in recent microbial ecology studies. These assessments of ecological function have added a critical component to our understanding of microbial biodiversity and have focused our attention on the role of protists in microbial community dynamics, including the involvement of ciliates in food chains and biochemical cycles. Oiled habitats (harbors, marinas, oil spills underwater leaks or pumping operations, for example) are intriguing environments for ciliate researchers. Organics are increased (enhancing the growth of bacterial populations), pH and dissolved oxygen are reduced, and exposure of organisms to chemical toxicity is more likely. Specific ciliates acclimated to this set of ecological factors appear to be resilient, even thriving, while other protists and metazoans decline or disappear. The functional role of the ciliates has clearly changed.

The likelihood of climate-induced warmer water temperatures, coupled with a slow reversal of fossil fuel extraction, transport, and utilization, could make matters worse. Alternatively, a better understanding of these complex dynamics might result in the development of tools for intervention and recovery of presently contaminated waters, thus adding potential food production capacity. As we struggle to better understand the complex microbial ecology in oiled habitats, what types of data do we already have? Which research approaches might best serve our need for further clarification of the role of ciliates in altered environments?

Testate Amoeba: A Friend or Foe to the Soil ecosystem

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Abstract

Testate amoeba or testaceans are a group of eukaryotic, free-living protists in which the cytoplasm is enclosed within an external shell. They are widely distributed from tropical to polar regions. They form an important microfaunal component of aquatic, semi-aquatic and soil communities and play an imperative role in the biogeochemical cycles and energy flow of aquatic and terrestrial ecosystems. The shells of testate amoebae are relatively resistant to decay and are generally well preserved in the soils, lake sediments and peatlands. Therefore, testate amoebae can be used to record past changes in environment and are increasingly used as a biotic proxy of climate and environmental changes and as biological indicators of water quality and pollution. Globally, lakes and reservoirs ecosystems are integral parts of ecological processes, global warming is rapidly changing their function and sustainability. The ecological models developed based on the testate amoebae suggested that freshwater testate amoebae could contribute to a better understanding of the ecological integrity and its vulnerability in inland aquatic environments. Therefore, testate amoebae can be used to record past changes in environment and they are increasingly used as a biotic proxy of climate and environmental changes. They have shells of different compositions, shapes and sizes and are sensitive to ecological parameters like pH, humidity, temperature, etc. The relatively stable characteristics of shelled amoeba makes them a suitable companion for ecological studies. Therefore, we analyse remarkable contributions of testate amoeba and determine it as a suitable tool for research in scientific world.

Key words: Testate Amoeba, Ecological indicator, Pollution, Nutrient cycling, Paleo reconstruction

Next Generation Taxonomy of a novel predatory ciliate of the genus *Lacrymaria* (Alveolata, Ciliophora)

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Abstract

Predation occurs at every possible order of magnitude, even at micrometric ones and among unicellular organisms. *Lacrymaria* is one of the most known and representative predator among protists and also one of the first genera of ciliates ever described (Müller, 1786; Bory De St. Vincent, 1824). It is rarely cultivated due to being a highly specialized predator of other ciliates. Here we describe a new *Lacrymaria* species, named *Lacrymaria venatrix* sp. nov., recovered from freshwater in a Tuscan wetland, with the combination of methods following the new Next Generation Taxonomy (NGTax) workflow (Serra *et al*., 2020), which includes traditional morphological and morphometric analyses, ultrastructure, 18S rDNA-based phylogeny, symbiont's screening and mitochondrial genome sequencing. *Lacrymaria venatrix* sp. nov. shows a combination of morphological features that does not exactly correspond to any currently established species of either genus; in addition, 18S rDNA-based molecular phylogeny places it on a separate branch outside previously sequenced species, as well as suggesting that neither genus *Lacrymaria* nor *Phialina* as currently defined is monophyletic. Not by chance, during their taxonomic history these two genera were repeatedly merged and separated again from each other under different morphological criteria, and it might therefore be appropriate to combine the two genera into one once again. Accordingly to the NGTax workflow we also provide data on the mitochondrial genome of *Lacrymaria venatrix* sp. nov., which has been sequenced, assembled and annotated resulting in a single linear molecule of 62,315 bp. It's genome content includes 46 ORFs (open reading frames), of which 18 of known function, three tRNAs and two rRNAs. The use of such a multidisciplinary approach to describe unicellular eukaryotes helps to prevent species misidentification, consequent problems in systematics and favour a more comprehensive understanding of the organism itself and of the true biodiversity of an ecosystem.

The magnitude of marine species diversity, with emphasis on the protists

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Abstract

The question of how many marine species exist is important because it provides a metric for how much we do and do not know about life in the oceans. The World Register of Marine Species (WoRMS) is an open-access online database created by an editorial board that currently comprises 319 taxonomists from over 150 institutions in 35 countries. The first goal of WoRMS has been the compilation of a list of all taxonomically accepted marine species, commonly used synonyms, and key literature sources. In 2012, a subset of the WoRMS editorial board used this baseline dataset to estimate how many more species, partitioned among all major eukaryotic groups, may be discovered. It was concluded that between one-third and two-thirds of marine species may be undescribed, and previous estimates of there being well over one million marine species appear highly unlikely. In this talk I will give an overview of the main findings, with emphasis on protists in general and ciliates in particular.

Exploring Pesticide Toxicity: Comprehensive Insights from Paramecium Studies as a Model Organism

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Abstract

Pesticides are extensively used to enhance agricultural yields, particularly in countries like India, where land constraints and high population growth necessitate intensified farming. However, their widespread application poses significant risks to ecosystems and human health. This review paper consolidates the current understanding of pesticide pollution and its impacts on non target organism like *Paramecium*. Pesticides, including insecticides, fungicides, herbicides, and others, exhibit varied toxic effects on non-target organisms, highlighting the need for comprehensive toxicity studies. *Paramecium* species, sensitive to chemical pollutants, serve as valuable bioindicator in environmental toxicology studies due to their responsiveness. Pesticide stress induces irregularities in ciliary beating and locomotor behavior, ultimately leading to deformity and cell death. These changes also vary with pesticide concentration and time, with lower concentrations affect movement pattern and higher concentrations lead to deformities and cell death. The exposure time correlates with increased mortality rates, highlighting the importance of time-dependent observations. Furthermore, biochemical assays reveal how *Paramecium* adapts to oxidative stress through up-regulating antioxidant defenses. Population and growth studies provide insights into the inhibitory effects of pesticides on proliferation, with significant implications for ecosystem health. Recent research has focused on the toxicological effects of pesticides on different species of *Paramecium*, uncovering sub-lethal effects and behavioral changes. For instance, acephate, an organophosphate pesticide, was found to induce concentration-dependent alterations in *Paramecium caudatum*, resulting in irregular blistering of cell membranes and cell lysis. Amidophosphonates (AP1, AP2, and AP3) exhibited less cytotoxicity compared to chlorpyriphos ethyl on *Paramecium tetraurelia*. Amistar Xtra, a fungicide, affected the growth and generation time of *Paramecium tetraurelia*. Moreover, insecticides such as diflubenzuron, flucycloxuron, bifenazate, and monocrotophos showed cytotoxic effects on *Paramecium* sp., resulting in changes in behavior, morphology, and respiratory metabolism. Notably, carbamate pesticides, such as aldicarb, carbaryl, and mexacarbate, exhibited acute toxicity by inhibiting oxygen uptake in *Paramecium multimicronucleatum*. Hay infusion medium, a commonly used non-axenic medium, prepared by boiling hay, provide a nutrient rich substrate for *Paramecium caudatum*. Additionally, monoxenic cultures supplemented with boiled okra in hay infusion medium foster the proliferation of *Paramecium caudatum*. An innovative method involves inclined agar supplemented with Enterobacter aerogenes and Minalba® mineral water provides a novel approach to culture *Paramecium caudatum*. Baked lettuce powder infusion bacterized by *Klebsiella pneumonia* and rice straw medium offer additional options for *Paramecium tetraurelia* culture. Various culture media, including hay, lettuce, wheat plant, cucumber rind, potato rind, yeast, and peanut, are utilized for different strains of *Paramecium tetraurelia*. Precise media selection is essential for maintaining *Paramecium* cultures and conducting accurate experimental assessments. In conclusion, bioassay studies offer a comprehensive understanding of the adverse effects of pesticides on *Paramecium* species, underscoring the urgency of implementing effective regulatory measures to mitigate environmental harm.

Key words: *Paramecium* species, Culture media, Pesticide pollution, Comprehensive toxicity studies, Ecosystem health risks.

Ciliates involved in science communication

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Abstract

Ciliates are key organisms found in any aquatic ecosystem. Without using a microscope, most of them remain invisible to the public. To raise awareness for the hidden ciliate and protist diversity, various science communication approaches have already been developed. In the talk, some ideas how particularly ciliates can be presented and curiosity of pupils and laypeople be attracted. Exemplarily, the aquatic protist diversity and how the significance of single species up to communities can be introduced to the public will be shown. By training citizen scientists on how to recognize protists, where they live, in which habitats they can be found, what they look like and why they are important, a general awareness for them can be raised. Exemplarily, model ciliates such as stentors can be presented to the public as perfect role models because they are relatively large, colorful and they host many other microbes as endosymbionts.

Protein glycosylation and susceptibility to infection with endosymbiotic microorganisms in ciliates

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Abstract

Ciliates often get involved in symbiotic relationships with other microorganisms - bacteria, archaeans, algae, yeasts, or microsporidia. Nevertheless, there are apparent differences in the ability of ciliate genera, species or strains to engage in symbiosis. While strains of *Paramecium* or *Euplotes* isolated from nature often harbor endosymbiotic microorganisms, *Tetrahymena* or *Stylonychia* have never been reported to carry any of them. Furthermore, cryptic (closely related) species of *Paramecium aurelia* complex demonstrate different susceptibility to infection with the microsporidian *Globosporidium paramecii,* and various strains of *Paramecium caudatum* are known to differ in their capacity to form symbioses with *Holospora* bacteria. The causes of these differences are still obscure. Glycosylation status of the ciliate surface proteins at the moment preceding the encounter of the host and the potential endosymbiont might be one of them. Using fluorescently labeled WGA lectin (wheat germ agglutinin), specific for terminal N-acetyl-D- glucosamine and N-acetylneuraminic acid residues, we demonstrated the presence of glycoconjugants with these terminal residues on the surface of *P. caudatum* cells. Experimental infections of this strain with *Holospora undulata* bacteria were carried in the presence of enzymes specifically removing these terminal sugars (N-acetyl glucosaminidase and neuraminidase) from the ciliate glycoconjugates. The presence of terminal N-acetyl-D-glucosamines on the paramecium glycoconjugates proved to be a prerequisite for phagocytic function of the ciliate, whereas the presence of terminal N-acetylneuraminic acid residues appeared to be mandatory for the uptake of *H. undulata.* In another set of experiments, we assessed the glycosylation status of proteins in four strains belonging to *Paramecium aurelia* complex (*P. primaurelia*, *P. pentaurelia*, *P. biaurelia*, and *P. triaurelia*) using lectin blotting after SDS-PAGE electrophoresis. The glycosylation pattern revealed with WGA differed in these strains: *P. biaurelia* and *P. triaurelia* strains resistant to infection with *G. paramecii* possessed more proteins with terminal N-acetyl-D-glucosamines than *P. primaurelia* and *P. pentaurelia* strains susceptible to infection. Proteins with glycans carrying terminal mannose residues proved to be less common in all four strains of *Paramecium aurelia* species complex, as shown with lectin blotting using Con A specific to mannose. Protein glycosylation status of the potential host appears to play an important dual role in the early steps of the establishment of intracellular symbiosis in ciliates: depending on the mechanism of the infection it either promotes the uptake of the future endosymbiont (the case of *P. caudatum/ H. undulata*), or protects the ciliate from the infection (*P. aurelia*/*G. paramecii*).

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Integrative taxonomy and hidden diversity of *Paramecium*

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Abstract

Ciliates are a remarkable group of organisms where numerous morphological species, cryptic species and genetic species may exist in each genus. The overview on one of the best studied ciliates, *Paramecium*, as a model for species concept will be provided. In last twenty years many *Paramecium* morphological species have been re-described or discovered, also by my group. We follow the principles of integrative taxonomy, applying thorough morphological examinations on big sets of strains, performing multi-loci molecular phylogenetic analysis, and, when possible, testing reproductive barriers among the related groups of strains. The combination of morphological and physiological studies, molecular phylogenetics and genomics allows to unravel continuously *Paramecium* diversity and to shed light on speciation mechanisms. In my talk I will provide an overview of the state-of-the-art in the systematics of *Paramecium*.

My Tryst with Ciliates

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Abstract

The present paper deals with my journey with ciliated protists as tools in teaching and research. Using these unicellular eukaryotic organisms for cytochemical staining at the UG level was just the beginning. As I began looking deeper into ciliates during my research, I meandered into aging of ciliates, DNA damage and repair, ciliate taxonomy and nomenclature, developmental biology especially using cortical morphogenesis and gene sequences, exploration of new species including those from challenging environments using classical and molecular methods, changes in ciliate fauna with environmental factors, ciliates as bio-indicators of pollution, effects of metals on the ciliates, internal pathways for proteins in the ciliate cytoplasm and many more. As I delve into each of these, some important findings shall be shared to entice young minds to share my love for ciliated protists.

Epistylis species as symbionts of crustaceans: some notes about the current knowledge and world distribution

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Abstract

Epistylis is a genus with more than 185 described morphospecies as free-living species as well as attached to several animal and plant species. We present some data from this genus, which play a role as symbionts. About 93 *Epistylis* species including varieties and forms have been recorded as symbionts in crustaceans such as cladoceran, copepods, decapods, and isopods as the most common hosts. Almost 40 countries have at least one ciliate species recorded as a crustacean symbiont. Some species have been recorded only once in a host, and several species establish a kind of symbiosis with more than 15 hosts. Based on these data, we conclude the need to follow this kind of research. Acknowledgments: To DGAPA-PASPA, UNAM for the support to RME for a short stay in UFJF, Brazil.

Preliminary studies on ciliates associated with corals of Gulf of Mannar Marine National Park, India

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Abstract

Ciliates, a diverse array of single-celled organisms, have garnered attention in coral disease research due to their roles in coral health and disease dynamics. This study delves into the significance of ciliates in coral diseases, emphasizing their potential as indicators and contributors to the decline in coral health. Coral reefs, crucial ecosystems supporting marine biodiversity, are under unprecedented threats, including disease outbreaks linked to environmental stressors. Although often overlooked in coral disease research, ciliates have been found associated with various coral diseases globally. Their presence and abundance in diseased coral tissues suggest potential involvement in disease pathogenesis and progression. Ciliates exhibit a range of interactions with coral hosts, from commensalism to parasitism, with certain species causing tissue necrosis and lesions. Their capacity to colonize coral surfaces and infiltrate host tissues underscores their significant role in coral disease dynamics. The present study conducted in the Gulf of Mannar Marine National Park (GoM MNP) over a period of four years (2019 – 2023) revealed the presence of over 55 ciliate species associated with both live and diseased corals. The data indicates the presence of 22 ciliates known to cause diseases in corals worldwide. Moreover, this study expands the list of ciliates associated with coral diseases globally and suggests that the corals of GoM MNP may be at a higher risk than previously considered. Next-generation sequencing (NGS) data on the bacterial communities associated with corals indicated the presence of over 450 bacterial species. Understanding the interactions between ciliates and corals is crucial for effective coral disease management and conservation strategies. Targeted monitoring of ciliate populations in coral reefs can facilitate early detection and response efforts to mitigate disease outbreaks. Furthermore, incorporating ciliates into coral health assessments can improve our ability to evaluate ecosystem resilience and predict the future of coral reefs amidst ongoing environmental changes. In conclusion, ciliates play significant roles in coral disease ecology, influencing the health and resilience of coral reef ecosystems. Continued research on ciliate-coral interactions is vital for advancing our understanding of coral disease dynamics and guiding conservation efforts aimed at preserving these invaluable marine habitats.

Oral Presentation

ABSTRACTS



Cancer Dynamics and Role of Human Microbiome in its Regulation.

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Abstract

The human microbiome mainly comprises the symbiotic microbial cells and the genes expressed by them in the human body, principally in the gut bacteria. It has received greater prominence recently because of its significant impact on human wellness and disease. Studies have demonstrated the vitality of these diverse microorganisms for functions like immunity, metabolism, digestion, and the synthesis of vital vitamins and metabolites. Human microbes are constantly spreading onto or through touched surfaces as a result of the dynamic relationship among the human microbiota and the environment. This interaction affects the growth, development, and physiology of the host. In the last few years, many studies have shown the influence of the microbiome in initiating and progressing various diseases, including cancer. Moreover, the metabolites of these microbes can also be used to treat many diseases and may provide a therapeutic scope. In any diseased condition, the microbiome constitution in the body gets changed or altered, a term known as “dysbiosis”. The dysbiosis of the oral microbiome causes cancers of the oral cavity, colon and pancreas. Similarly, gynaecological and urological cancers are caused by dysbiosis of pelvic organs. For the detection of the microbiome, we can analyze the microbial DNA and RNA in the blood samples which can be differentiated from the healthy counterparts. Computational tools like QIIME have been established to analyze high-throughput sequencing data, determine microbiota patterns and identify specific microbial taxa within the human gut. For treatment purposes, the microbiome has found applications in immunotherapy, chemotherapy, and radiotherapy. Besides these, the microbiome can be modulated to further improve cancer therapy; like microbiome transplantation.

Bacterial Biofilms and Antimicrobial Resistance: A Rising Threat in Microbial Communities

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Abstract

Group B Streptococcus (GBS) poses a significant threat to newborns, pregnant women, and immunocompromised individuals, highlighting the importance of understanding its antibiotic resistance profile for effective prophylaxis strategies. Like other streptococci, GBS forms biofilms, aiding in colonization, immune evasion, and antibiotic protection, complicating treatment. This study aimed to evaluate biofilm formation and antibiotic susceptibility among clinical GBS isolates. Thirty GBS isolates were identified using biochemical, microbiological, and molecular tests and assessed against six commonly used antibiotics. Results showed resistance to all antibiotics tested, with penicillin resistance emerging as a major concern. Ofloxacin demonstrated the highest susceptibility, followed by azithromycin. GBS, like other Gram-positive bacteria, can form biofilms, facilitating colonization. Biofilm assays revealed most strains as strong biofilm producers, with some showing moderate production. Interestingly, a negative correlation was observed between strong biofilm formation and penicillin resistance, suggesting a potential relationship.

Furthermore, most isolates carried virulence genes associated with invasion and colonization, with no significant association between biofilm formation and virulence gene expression observed. These findings underscore the need for comprehensive strategies to address antibiotic resistance and biofilm formation in managing GBS infections.

Microbial Nanostructures and Their Application in Soil Remediation

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Abstract

The field of nanobiotechnology is rapidly gaining prominence since it involves the construction of inorganic nanoparticles using plants, plant extracts, fungi, and bacteria that mitigate the risks related to their physicochemical methods of synthesis. This biogenic approach also improves its applicability in various biomedical and bioremediation fields. Nanoparticles exhibit higher reactivity and sorption capacity in comparison to larger particles therefore, they are far more superior in tackling the issues of environmental pollution and ecological restoration. Studies also indicate that they are better substitutes to the more traditional and aggressive methods of decontamination. The concept of nanobioremediation further explores the synthesis of sustainable nanostructures and their potential in the removal of impurities from the soil, water, and air. This study explores the efficiency of biogenically produced nanoscale metallic iron (nZVI), metal oxide nanostructures (CuO, ZnO, TiO2, CeO2, MnO2), Au, Ag, Pd, PbS, and CdS nanostructures in soil remediation and highlights their versatility in the removal of both inorganic and organic soil pollutants along with the risks and drawbacks associated with their use. Modifications of nZVI such as assistance by Electrokinetics, coating with macromolecules or surfactants, and its integration with microbes is further highlighted as it greatly reduces the ecotoxicity associated with bare nZVI.

Keywords: Microbial nanostructures, soil remediation, nanobioremediation, soil pollutants

Assemblage of Benthic Macroinvertebrates in the Headwater Tributaries of River Alaknanda in Garhwal Region of Uttarakhand (India)

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Abstract

Benthic insects have been used comprehensively for biomonitoring of various environmental stresses and have received significant attention for the study of lotic ecosystems. The assemblage structures of benthic insects are sensitive to watershed conditions and are useful for monitoring the stream health. In present study the assemblage of benthic macroinvertebrates along with their habitat characteristics in the three major headwater tributaries of river Alaknanda between 1040m to 3150m above sea level were recorded. Benthic macroinvertebrates were represented by 13 genera belonging to 10 families and 06 orders. The total density of benthic fauna was recorded maximum at tributary Dhauli Ganga, whereas the diversity was recorded maximum at Birahi Ganga. The River Saraswati at Mana, has the least diversity of benthic macroinvertebrates as it was represented by single order Ephemeroptera attributed to its extreme conditions.

Keywords: Benthic Insects, Identification, Habitats, Indicators

Understanding in-situ pesticide biodegradation using stable isotope probing (SIP)

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Abstract

Pesticides have become one of the inevitable components of modern agriculture. Its usage can only be anticipated to rise in the future given the current situation of a growing population, changing land use patterns, and climate circumstances. Stable isotope probing (SIP) has been widely used in environmental microbiology to link active microbial communities with their functions. Using heavy isotope labeled DNA, RNA, proteins, lipids, and/or metabolites as biomarkers, it enables us to explore the potential of vastly unculturable microbial populations leading to discoveries of wealth of novel microbes, genes, enzymes, and metabolic pathways. Its potential and applicability have increased beyond comprehension with the integration of several cutting-edge technologies. Nevertheless, a number of issues, including the high cost and the commercial unavailability of appropriate labeled substrates, have restricted its uses in the study of multi-carbon substrates, such as pesticides. Consequently, the biodegradation of pesticides employing stable-isotope probing has been the subject of very little research. The present study reviewed these researches, highlighted various challenges and discussed future perspectives of using stable isotope probing in the pesticide's biodegradation study. Besides the potential of discovering novel biodegrading agents, understanding in-situ biodegradation of pesticides has huge implications in developing appropriate bioremediation techniques.

Keywords: Stable isotope probing, Pesticide, In-situ biodegradation, Heavy isotope, Biomarkers,

Expression and characterization of novel chimeric endolysin CHAPk-SH3bk against biofilm-forming methicillin-resistant *Staphylococcus aureus*

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Abstract

The continuous evolution of antibiotic resistance in methicillin-resistant *Staphylococcus aureus* (MRSA) due to the misuse of antibiotics lays out the need for the development of new antimicrobials with higher activity and lower resistance. This study includes the expression of novel chimeric endolysin CHAPk-SH3bk to investigate its antibacterial activity against planktonic and biofilm-forming MRSA. The molecular docking and MD simulation results identified critical amino acids (ASP47, ASP56, ARG71, and Gly74) of CHAPk domain responsible for its catalytic activity. Chimeric endolysin CHAPk-SH3bk showed an effective binding to peptidoglycan fragment using 14 hydrogen bonds. The chimeric endolysin CHAPk-SH3bk derived from endolysin LysK was cloned, expressed, and characterized. The in-vitro antibacterial assays displayed higher activity of CHAPk against planktonic MRSA with 2-$\log_{10}$ reduction in 2 h. Both CHAPk and CHAPk-SH3bk displayed bactericidal activity against MRSA with ~4$\log_{10}$ and ~3.5$\log_{10}$ reduction in 24 h. Biofilm reduction activity displayed CHAPk-SH3bk reduced 33 % and 60 % of hospital-associated ATCC®BAA-44™ and bovine origin SA1 respectively. The CHAPk treatment reduced 47 % of the preformed biofilm formed by bovine-origin MRSA SA1. This study indicates an effective reduction of preformed MRSA biofilms of human and animal origin using novel chimeric construct CHAPk-SH3bk. Stating that the combination and shuffling of different domains of phage endolysin potentially increase its bacteriolytic effectiveness against MRSA.

Keywords: Biofilm, MRSA, Bacteriophage endolysin, Chimeric endolysin, Antibacterial activity, Bacteriophage

Mitigation of solid waste generated in campus by compost

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Abstract

Domestic, industrial and academic practices yield large quantities of solid waste daily. Unregulated disposal and cause dumping are responsible for soil contamination and groundwater, deterioration of soil and hazardous to the ecosystem. Composting is an established sustainable method to eradicate degradable organic wastes and an ecological alternative for waste management. However, significant advancements in the composting process are required to overcome pathogen detection, low nutrient status, long duration of composting, long mineralization duration, and odor production to enable its extensive and effective usage. In this context, a Composting Unit has been established in the college to mitigate campus waste based on a modified Aerated Static Pile Composting technique which combines organic waste in a big pile with layers of bulking agents-like wood chips or shredded newspaper for aeration as physical turning over is prevented. Physical-chemical characterisation of the generated compost as per FCO-1985 will provide useful information to develop the composting unit that can serve as a prototype for a decentralized organic waste-to-compost system.

Keywords: waste management, compost

Faunistic study on the freshwater ciliate diversity with description of a novel urostylid species from Delhi, India

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Abstract

Ciliates, highly diverse eukaryotic microorganisms, exhibit the utmost morphological complexity and differentiation among single-celled organisms. They are found in diverse ecosystems. The present study aimed to elucidate the ciliate diversity in three freshwater sites within the Delhi region of India: Okhla Bird Sanctuary (OBS), Sanjay Lake (SL), and Raj Ghat pond (RJ). Ciliates were identified using live cell microscopy, staining techniques, and molecular methods. The highest number of species was observed at the OBS site (43 species), followed by SL (27 species), and RJ site (21 species). Ciliates from eight classes – Spirotrichea, Oligohymenophorea, Prostomatea, Litostomatea, Phyllopharyngea, Karyorelictea, Heterotrichea, and Colpodea – were observed. A novel species from the order Urostylida (class Spirotrichea), isolated from the OBS site, was described. *Diaxonella multimarginata* n. sp., *in vivo,* measured about 120–150 x 40–70 µm with a length to width ratio of about 2:1. The body appeared flexible, slender, and elongated ellipsoidal, with both ends rounded and brightly coloured with rose-coloured granules. The adoral zone covered 35% of the body size, with an average of 33 membranelles, and undulating membranes optically intersected. Multiple macronuclei and micronuclei were observed. The ciliate exhibited three frontal cirri, four to six buccal cirri, four frontal row cirri, two fronto-terminal cirri, a midventral complex with 15–26 pairs of cirri, two to four pre transverse, and six or seven transverse cirri arranged in J-shaped row. Additionally, a single row of right marginal cirri with 40 cirri and more than four rows of left marginal cirri with an average of 22 cirri on each row (LMR_{1-6}) were observed. Three rows of dorsal kineties were present, with caudal cirri absent. Frequent encystment was observed frequent while conjugation was not observed. Molecular analyses suggested that the new species was distinct from its closest congeners, *D. trimarginata* and *D. pseudorubra.*

Keywords: Delhi, Diversity, Freshwater ciliates, Taxonomy, Urostylid species.

Expanding the Spectrum of Outer Membrane Proteins in Lyme Disease Pathogen *Borrelia burgdorferi*

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Abstract

Lyme disease (LD) constitutes a zoonotic disease transmitted by tick vectors and is prevalent in temperate regions worldwide. The etiological agent of LD is the tick-borne bacterium *Borrelia burgdorferi*- a gram-negative, motile, spiral-shaped spirochete. Cases of LD have emerged across diverse regions in India. However, the prevalence of LD in India remains obscure due to the varied manifestations of the disease and limited awareness among the population. This lack of awareness is resulting in underreporting and thereby presenting a challenge in accurately determining the true prevalence of LD in Indian population. Termed the "great imitator," LD manifests diverse symptoms in patients, with majority resembling symptoms of various other diseases. *B. burgdorferi* has a double-membrane envelope and contains outer membrane proteins (OMPs) with β- barrel structures. OMPs play pivotal roles in nutrient import, efflux, adhesion, proteolysis, and membrane biogenesis. *B. burgdorferi* relies on external sources for essential substances due to its lack of cellular biosynthetic genes, emphasizing OMP significance. Hence, determining the OMP repertoire is crucial for unravelling the mechanisms of LD pathogenesis. Majority of the Borrelial OMPs remain undiscovered and unexplored. We have employed an integrated in silico approach, combining multiple OMP prediction tools and beta-barrel structure prediction methods. From these analyses, 17 putative B-barrel OMPs were manually selected. Homology-based models were constructed, revealing structural insights into these proteins. Amino acid sequence variations, obtained from clinical strains, were mapped onto the structural models, highlighting the significance of surface exposed loops in the adaptation and evolution of these proteins. The findings suggest that these surface-exposed regions are under constant selection pressure, which implies their importance in bacterial pathogenesis. Through this work we have identified novel OMPs of *B. burgdorferi*, highlighting their structural features which may have potential role in bacterial pathogenesis.

Key words: Lyme Disease, *Borrelia burgdorferi*, outer membrane, beta-barrels, protein structure-function.

Nanopolymeric micelles formulations of *Emblica officinalisis* (Amla) and its antibacterial evaluation

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Abstract

In today's scenario SDG3 is focusing on antimicrobial resistance (AMR) and Ayurveda is very promising approach to deal with AMR. Nanoparticles are very promising in drug delivery development. In this study, N-Isopropyl acryl amide-N-Vinyl 2-pyrollidone (NIPAAm-VP) co-polymeric micelles are fabricated by radical copolymerization and the alcoholic extract of *Emblica officinalisis* (Amla) entrapped in this polymeric micelles to evaluate its antibacterial activity. The size of nanoparticles was measured 80-120 nm and 1 % drug is loaded. In this work, the dried fruit extract has been loaded into the polymeric micelle and its effectiveness has been evaluated against various bacteria strains. *Emblica officinalisis* (Amla) loaded polymeric micelles found many times efficient in comparison of the crud drug and marketed formulation (Ampicillin). The research findings revealed that this nanopolymeric micelles would more effectively release the drug into the body when infectious states are functional and may have high possibility to apply as a novel drug delivery system for more herbal drugs for patient compliance.

Key Words: *Emblica officinalisis* (Amla), Polymeric micelles, AMR, SDG3, Ayurveda, NIPAAM

Cross-genera colonization of salt tolerant endophytes in tomato and their contribution in mitigating salt stress in tomato cultivation

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Abstract

The problem of growing area under salinity is alarming and different tools and techniques are being explored to mitigate the stress from crop plants. In this study, we have assessed the cross-genera establishment of bacterial endophytes from two niches in the tomato with an aim to find salt stress mitigators. In the first experiment, we have isolated and characterized the salt tolerant bacterial endophytes from holi basil (*Ocimum tenuiflorum*) and in another set, we have used endophytes from 4 halophytic plants of Runn of Kutch. These endophytes were first tested for their establishment in the tomato system and the same was tracked by confocal scanning laser microscopy. Upon inoculation to the tomato plants under salinity stress, we could find that these endophytes were having supporting potential to the plant under stress. These endophytes treated plants could experience lesser oxidative stress and accumulation of free radicals. This was confirmed by DAB and NBT staining, gene expression studies, and quantification of respective antioxidant enzyme levels. Upregulation of salinity stress related genes e.g. LKT1, SlWRKY39, SlERF16, aquaporins, antiporter genes, etc. were reported in the endophyte treated plants. Using light-excitable Na^+ indicator, the sodium absorption in different treatments also indicated protective effects of these endophytes on salinity tolerance of tomato. Accumulation of different compatible solutes, electrolyte leakage, chlorophyll content, etc. have also indicated the complementary benefits of using these endophytes for salinity stress tolerance. Cell tracker system have indicated that some of the endophytes of halophytic plants could establish themselves in a plant of different genera (tomato) and can reduce the stress in the plant system and helping then in recovery from oxidative stress. This could open a wide application possibility of endophytes for stress mitigation.

KEYWORDS: Endophytes, salinity, inter-genera colonization, root architecture, *Bacillus*, oxidative stress, reactive oxygen species, Na^+/K^+ balance, Cell tracking

Bacterial composition and their plant-beneficial function contributing (PBFC) genes in rhizospheric soil microbiomes of tropical and temperate forests

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Abstract

Rhizosphere soil microbiome compositions are profoundly affected by the host tree species, aboveground plants, and habitat. Soil microbes including plant growth-promoting bacteria can assist plants to withstand the abiotic challenges caused by the current climate change events. In this study, we have unravelled the soil microbiome composition of tropical and temperate forest soils. Further, the plant-beneficial function contributing (PBFC) genes present in major bacteria reported were investigated. The soil samples were collected from the Sal tree rhizospheres of the tropical forests (West Bengal) and the Oak tree rhizospheres of the temperate forests (Arunachal Pradesh). Nanopore sequencing of the isolated soil DNA was performed on GridION ×5 (Oxford Nanopore Technologies, Oxford, UK), to determine the soil microbiome composition. The predominant bacterial taxa found in tropical and temperate forests were significantly varying from one another. The major bacterial species found in tropical forests were *Bradyrhizobium diazoefficiens, Bradyrhizobium erythrophlei, Bradyrhizobium elkanii, Afipia broomeae, Bradyrhizobium sp. STM 3843, and Rhodopseudomonas palustris*. Whereas the temperate forest mushroom rhizosphere was predominantly composed of bacterial species like *Candidatus Solibacter usitatus, Candidatus Koribacter versatilis, Bacillus cereus, Granulicella tundricola, Granulicella mallensis, Bradyrhizobium icense, Bacillus weihaiensis,* and *Planococcus sp.* MB-3u-03. The major plant-beneficial functions of the predominant bacteria were identified using the presence of PBFC genes reported earlier in the respective species. Phosphate solubilization, Nitrogen fixation, and auxin synthesis were the major plant-beneficial functions investigated using the presence *pqq*, *nif, nir*, and *ppd* genes. PATRIC BV-BRC, NCBI genes, Blast Koala, and antiSMASH were the major bioinformatic tools and databases employed for finding these genes. We found out that various phosphate-solubilizing and nitrogen-fixing bacteria co-exist in the same ecological niche of these forests and may have a significant contribution to plant nutrition and growth thereby facilitating the existence of a sustainable ecosystem.

Keywords: Bacterial composition, Plant-beneficial function contributing (PBFC), tropical forest, temperate forests, Soil microbiome, Bioinformatics, Metagenomics

The influence of *Leucaena leucocephala's* decomposing leaf litter on the soil's fungal community and its contribution to enhancing soil fertility

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Abstract

To assess if Multipurpose Tree (MPT) species can serve as nutrient sources for crop cultivation, it's essential to examine the decomposition rate and patterns of their residual leaf matter. An extensive investigation was carried out to observe the nutrients discharged into the soil from the decaying leaf litter of Leucaena leucocephala and its effect on the surrounding soil mycoflora, soil fertility, and the plant's growth and yield metrics. The impact of incorporating leaf litter into the soil was evaluated by measuring the soil's pH, nutrient levels, and organic content at various crop growth stages. The enhancement of soil fertility for agricultural purposes was gauged through diverse growth and yield indicators of Trigonella foenum-graecum. The populations of fungi in the rhizosphere and non-rhizosphere from both the enriched and unaltered soils were estimated, with results presented as a percentage frequency of occurrence. Enriching the soil with leaf litter led to a fungal population increase (18,000/g soil) compared to the unaltered soil (7,200/g soil). The addition of this organic layer promoted mycorrhizal root colonization. After 90 days of plant growth, the colonization percentage was over double that of plants in unaltered soil, with 90% of roots exhibiting mycorrhizal colonization. The soil amendment with leaf litter also raised the levels of organic carbon and matter. The peak phosphorus level in the soil of the control plot (32.27 mg/g) was lower than that in the experimental plot (38.79 mg/g). Soils enriched with leaf litter yielded higher crop outputs compared to control soils. Therefore, Leucaena leucocephala, commonly planted for reforestation in semi-arid and arid zones, markedly enhances soil fertility through its decaying leaves.

Surfactant Protein-D, an Innate Immune Molecule with anti-leukemic activity

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Abstract

Surfactant Protein D (SP-D), a member of the collectin family, has indispensable role in host defense and control of inflammation in the lungs. Although initially discovered from the lung where it is secreted by type II and Clara cells, extra-pulmonary existence of SP-D is also reported. Our study showed apoptotic effect on eosinophilic leukemia cells. SP-D is shown to decrease viability of AML14.3D10 cell line (eosinophilic leukemic cell line), acute myeloid leukemia cell line (THP-1), acute lymphoid leukemia cell lines (Jurkat, Raji), human breast epithelial cell line (MCF-7), etc.

Our preliminary studies using proteomics also indicated SP-D mediated induction of specific pro-apoptotic molecules, changes in mRNA processing, rate of translation and chaperones involved in protein processing and degradation. Similarly, in a membrane interactome of recombinant fragment of SP-D with PC3, a metastatic prostate cancer cell line, showed GRP78 (an ER resident chaperone, known as HSPA5) as a novel membrane binding partner to SP-D, having cytoplasmic, mitochondrial and nuclear localization, facilitating protein maturation & degradation, regulating ER stress signalling- important in anti-cancer therapeutic targeting. Many publications since then have appeared and the efficacy has been further proved in lung cancer, breast cancer, pancreatic cancer cell lines. Therapeutic immunogenic potential of SP-D to treat immunologically unresponsive prostate tumour in a Transgenic Adenocarcinoma of Mouse Prostate (TRAMP) model has also been recently shown. These lead discoveries marked beginning of new research areas that needs to be further explored.

Keywords: Innate Immune molecule, Surfactant Protein-D, anti-leukemic activity, molecular mechanism, proteomics

Biodegradation of Nitro-explosives in soil using microbial based water dispersible granular (WDG) formulation

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Abstract

Nitro explosives are commonly used in military, mining and demolition processes. Due to their recalcitrant nature, there has been continuous increase in soil contamination by various nitroexplosive compounds. They can undergo various transformations in soil and causes harmful effects on soil biota as well as human health. Octahydro-1,3,5,7-tetranitro-1,3,5,7-tetrazocine (HMX) is one of the widely used nitroexplosive. In the present study, aerobic degradation HMX has been investigated using self-developed water-dispersible granular (WDG) formulation of HMX-degrading microbes. Initially, six bacterial strains were screened for their potential of HMX degradation in soil. On the basis of degradation efficiency, *Pelomonas aquatica,* which degrade 65% HMX within 30 days, was selected for formulation development. *P. aquatica* formulated as WDGs has a shelf-life of up to 6 months at 30˚C with only a 16% loss in viability. An enhancement of 19.64% in HMX degradation in soil was observed with the use of WDGs as compared to use of fresh bacterial culture. LCMS analysis revealed the presence of nitroso derivate of HMX (1-NO-HMX) at 325 m/z as an intermediate metabolite indicating the single nitrite elimination pathway for HMX degradation leading to the formation of nitrite, nitrate, and CO_2 as end products during degradation. The current study provides the base for the development of efficient microbial formulations for enhanced remediation of HMX contaminated soils.

Keywords: Biodegradation, HMX, LC-MS, Microbial formulation, Water Dispersible Granules (WDGs)

Comparative study of Physico-Chemical Parameters of Lonar Crater, India.

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Abstract

Currently declared Ramsar site of India, is Lonar Crater India. Lonar Crater is situated in Buldhana District, Maharshtra, India $19^{0}58'$N $76^{0}32'$E. It is third largest impact crater and famous about its salinity and alkalinity. During the study periods various both physic-chemical parameters was studied, physical parameters like Water Colour, Temperature, pH, Electrical conductivity, Total dissolved solids (TDS), Transparency and Chemical Parameters like Dissolved Oxygen, free Carbon dioxide were absent due to that it converted in to Carbonate and Bicarbonate. Total Hardness, Calcium Hardness and Magnesium Hardness are also studied. The most important parameters that is Chloride and Salinity this crater alake is famous about its Salinity, Phosphate, Sulphate, Silicate, Iron, Nitrogen and Nitrogen compounds like Ammonia, Nitrite, Nitrate, Biological Oxygen Demand and Chemical Oxygen Demand was studied. In this research article we studied the comparative analysis of different parameters during the both years. The water body of Lake was terms towards the Eutrophication.

Key words: Lonar, Crater, Physico-chemical, Eutrophication.

Strigolactones and Rhizospheric Microflora- An Overview on its Role in Plant Growth Enhancement

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Abstract

Strigolactones (SLs) are signaling molecule derived through carotenoid biosynthetic pathway. Recently in 2008 it is now well established as plant hormone. They play diverse roles in plants, both as plant growth regulator and as a signaling molecule in the rhizospheric soil. Their crosstalk with several other plant hormones brings about different physiological responses in the plants. In addition, they are also secreted into the rhizosphere in the root exudates. There are several studies which have reported that SLs play an important role in the microbiome diversity in the rhizosphere and the phylloplane. Initially SLs have been observed as germination stimulant for seeds of parasitic weeds like *Striga* and *Orobanche* and as an important factor for presence of arbuscular mycorrhizae fungi (AMF) association in plants. It is well established that it promotes hyphal branching in AMF. Recently various researchers are studying the direct relation of amount and type of SLs in root exudates and diversity - density of microbiome population in the rhizosphere. The type of SLs is specific for showing particular response in the rhizosphere. SLs also influence the establishment of symbiosis of plants with other fungi and the growth of plant pathogenic fungi in the rhizospheric soil. Relationship of SLs and vegetative plant growth is also reported by researchers. SLs also play an important role in establishment of various plant growth promoting rhizobacteria like *Rhizobia* with the plants. They also enhance the nodulation in leguminous plants. The present paper presents an overview on the interaction of SLs with other soil microflora and effect of this interaction in plant growth and development.

Keywords: Strigolactone, Rhizosphere, AMF

Tackling global health challenges like pandemic preparedness, sustainability and health inequity by the use of virus like particles and viral nanotechnology platforms

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Abstract

The COVID 19 pandemic and the continuous emergence or re-emergence of infectious diseases have exposed the lack of global preparedness and wide health system disparities. Health inequity has exposed the fractures in the global public health, leaving the poor countries more vulnerable and unprotected. The lifesaving drugs and vaccines have been inaccessible and unaffordable to the poor in developing countries. Therefore, cost effective and rapid biomanufacturing of vaccine antigens, biosimilars like monoclonal antibodies, etc. at a large scale for remedy against such future pandemics/epidemics, will be urgently needed. Their quick safe production in a timely manner, their scalability, accessibility, etc. are of utmost importance for global public health. However, traditional production methods for biomolecules of prophylactic and therapeutic properties often face challenges to cost effectiveness, affordability and cold storage requirements. Virus like particles and viral nanotechnology along with allied fields like protein, and lipid nano technology (for m-RNA vaccines) have emerged as potential and now well proven modern tools in achieving the unmet goals in public health.

However, the plant-based nanotechnology platforms using Virus like Particles (VLPs) and Virus Nanoparticles (VNPs) have shown the best results for the production of biopharmaceuticals like vaccine, monoclonal antibodies and several therapeutic proteins like interferons, cytokines, immunomodulators etc. Not only is this technology inexpensive, easy to produce and scale up, it is also highly efficacious and safe. Such biopharmaceuticals produced by viral nanotechnology using plant bioreactors are free from human pathogenic contaminants, very easy to produce and scale up on a short notice and the products can be easily transported in stored at ambient temperatures.

This nanomedical plant-based platform has proven to be highly economical and very promising and can be easily adopted by the poorest of the poor countries. Thereby, the issues of health disparities can not only be tackled but the public health systems of low- and middle-income countries can be strengthened and be better prepared to fight against disease outbreaks of both acute and chronic diseases, before they assume epidemic proportions. This nanomedicine approach, using plant based platforms can not only help the low resource countries lacking sophisticated infrastructure but also make them self sufficient and provide them sustainability.

In this presentation, I shall be explaining the tools and methods used in this technology, in detail, their unique advantages *vis a vis* other platform. I shall also discuss a few success case studies where using this approach has brought about very good results.

Keywords: Virus Like Particles, Viral Nanotechnology, Plant Platform, Vaccines, Global Public Health, Health Inequity

Efficacy of microbes as a potent shield against pathogens and in conferring immunity against microbial diseases

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Abstract

Generally, the micro-organisms/ microbes (bacteria, viruses, protozoans, etc.) have been studied as the causative organisms of various diseases, ranging from the common cold, chicken pox,shingles, to the serious ones like HIV/AIDS and there is exhaustive literature available on this subject. Until recently, scientific research focussed on eliminating these microbes from in and around our body systems/ environment/ (micro)habitats in which they survive and thrive. Accordingly, various types of measures, especially the chemical formulations) were developed which became readily available for use by the end-users or consumers like us. However, in spite of the ready availability of anti-microbials (with advocated efficacy of '99.99%') customized (in the laboratory conditions) for dealing with specific microbes in relation to their microhabitats, the infants and children exhibit weakened immunity and frequently suffer from one or the other microbial disease during their growing years. In light of these observations, researchers are directing their efforts to unravel the complex intricacies of the human microbiome, and some investigations have revealed the role of 'friendly' microbes in fighting out the 'pathogenic' microbes, thereby conferring long-lasting immunity to human beings and playing a very significant role in the maintenance of overall health and well-being. Future studies in this field should involve all aspects of microbiology including asking 'How could the microbes be used for maintaining the health and well-being of human beings?'. To address questions of how microbes can be beneficial, numerous general mechanisms have been proposed such as strengthening of the friendly microbiome which would provide a strong shield against colonization of pathogens, modulation of the immune system, the digestion, detoxification, and production of nutrients, stimulation of cellular differentiation, improvement of barrier function, and alteration of the gut-brain axis. Hence, there is a lot of scope for the budding scientists to fill-in the lacunaein this important field of study to help comprehend the underlying molecular mechanisms and successful application in medical science.

Keywords: Microbiome, modulation of the immune system, microbes and immunity, microbial diseases, health and well-being

Characterization of Faecal Sludge and Water Quality Assessment of Groundwater and River Water of Lucknow City

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Abstract

The present study aims at Faecal Sludge (FS) characterization and assessing groundwater and river water quality due to impact of waste dumping in one of the India most polluted city, Lucknow. Currently, FS is dumped into the urban and peri-urban environment, posing great risks to the soil, surface water and groundwater quality. FS sample was collected from septic tank in the study area to measure pH, EC, BOD, COD, TN, TP and heavy metals. To assess the water quality, 55 groundwater and 23 surface water were sampled and analyzed by water quality index (WQI) and multivariate statistical analysis. Groundwater samples were collected from different locations covering solid waste dumping area, residential area and slum area while river water samples collected from nearby drains of upstream to downstream region of the Gomti River. The groundwater were gather into class I , II and III, while river water grouped as class II, III, IV and V by water quality index. Irrigation water quality determined by Wilcox's diagram and US salinity laboratory classification, most of the groundwater and river water samples are suitable for irrigation. River water was found to be more polluted at the downstream of the stretch as compared to the other sampling sites due to direct discharge of untreated domestic waste, human excreta, sewage waste, polythenes, municipal garbage and toxic elements from the factories. The principal component analysis identified four major components that explained 76.10% of the variance in the dataset for ground water. In River water, three major components accounts for 85.40% of the total variance. Hierarchical cluster analysis depicts seven types of clusters for ground water and 4 types of cluster for surface water in the study area. Due to the impact of waste disposal on groundwater and river water resources, it is suggested to treat waste before disposal into the land and water resources. Appropriate measures such as construction of fecal sludge treatment plant, landfill site has to develop to minimize the pollutant levels in water.

Keywords: Faecal sludge, ground water, river water, water quality index, multivariate statistical analysis

Field-scale bioremediation of hexachlorocyclohexane (HCH) -a persistent organochlorine Pesticide

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Abstract

Hexachlorocyclohexane (HCH) is a persistent organochlorine compound formerly known as Benzene hexachloride (BHC). Due to its insecticidal properties, it was used globally to control agricultural pests and vector-borne diseases like malaria. But soon, this pesticide became a menace due to the nature of its production and use. HCH was sold as technical HCH (t-HCH) containing a mixture of α- (60-70%), β- (5-12%), γ- (10-12%), δ- (6-10%) and ε-HCH (2-3%) until the 1950ties and as lindane consisting chiefly of γ-HCH (99%) from 1950 to 1980ies because only γ-HCH possesses insecticidal properties. Purifying one ton of γ-HCH led to the formation of 8 to 12 tons of 'HCH muck' containing remaining isomers, which were discarded creating HCH dumpsites. Due to the nontarget toxicity and persistence of HCH isomers α-HCH, β-HCH, and lindane were officially listed as persistent organic pollutants (POPs) in Annex A to the Stockholm Convention in 2009. Over the past years, several HCH-degrading microbes have been isolated from dumpsites worldwide. The present study focuses on using them to treat HCH-contaminated soils. In the present study HCH contaminated soils were treated for 64 days *in situ* (HCH dumpsite, Lucknow) and *ex situ* (University of Delhi) in line with three bioremediation approaches. The first approach, biostimulation, involved the addition of ammonium phosphate and molasses, while the second approach, bioaugmentation, involved the addition of a microbial consortium consisting of a group of HCH-degrading sphingomonads that were isolated from HCH-contaminated sites. The third approach involved a combination of biostimulation and bioaugmentation. The efficiency of the consortium was investigated in laboratory-scale experiments, in a pot-scale study, and a full-scale field trial. Combining biostimulation and bioaugmentation was most effective in reducing the levels of α- and β-HCH. The application of a bacterial consortium compared to the action of a single HCH-degrading bacterial strain was more successful.

Keywords: Hexachlorocyclohexane, Biostimulation, Bioaugmentation, Consortium, Toxicity

Role of Gut Microbiome in Neurodevelopmental Disorders

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Abstract

Gut microbiome homeostasis plays an important role in human health. Gut-brain axis refers to complex interrelationship between central nervous system and gastrointestinal system. Recent studies have highlighted the importance of commensal gut microbes to normal gut function and neurobehavioral health especially the Neurodevelopmental disorders (NDD). As per the epidemiological and clinical evidences co-morbid gut dysfunction exists in many individuals with neurodevelopmental disorders. There has been increase in number of cases of NDD especially Autism Spectrum Disorder (ASD) and Attention Deficit Hyperactivity Disorder (ADHD). Autism spectrum disorder is of particular interest as a highly prevalent neurodevelopmental disorder in which a significant subset of patients' present gastrointestinal problems and in which microbial dysbiosis has been highlighted as a potential contributing factor to gastrointestinal and neurodevelopmental abnormalities. Recent case studies suggest that the gut microbiota plays a role in shaping cognitive networks encompassing emotional and social domains in neurodevelopmental disorders. There are several factors that may affect and may alter the gut microbiome like breastfeeding, mode of delivery, use of antibiotics or exposure to other chemicals. Based on pre-clinical and clinical evidences, this work tries to correlate the potential role of the gut microbiota in the origins and development of social and emotional domains related to Autism spectrum disorders and also tries to identify if there is a possible role of microbiome in treating NDDs.

Keywords: Microbiota, Autism Spectrum Disorder, Neurobehavioural, Dysbiosis, Neurodevelopmental disorder

Omics approach and strategies to study Saffron and its associated microbes

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Abstract

Saffron, the dried stigma of *Crocus sativus* flowers, is referred as the "golden condiment" being the world's most expensive spice costing about 11000 USD per pound. Even though saffron is cultivated in various country worldwide, India ranks second after Iran in its global production. *Crocus sativus* is sterile triploid plant (3n=24), bearing no seeds and reproducing via vegetative propagation. Lack of genetic variations has been reported in various accession of saffron grown worldwide due to its vegetative propagation. However, the microbes associated with different parts of saffron are reported to vary. The microbes associated with the different underground parts of saffron (rhizosphere and cormosphere) were studied using culturomics and metagenomics approaches. It was observed that saffron rhizomicrobiome was distinct from cormomicrobiome with few overlapping bacterial species, thereby indicating that microbes are niche specific. Variations in saffron microbiome were also observed temporally i.e. across the different growth stages i.e. the cormomicrobiome during flowering stage were distinct from dormant stage. Additionally, spatial variations were also observed in saffron microbiome wherein rhizomicrobiome and cormomicrobiome across were significantly varying different geographical regions respectively even though there is no genetic variation in saffron plant across different geographical locations. In-spite of the variation in the microbiome, a core microbiome i.e. the microbes that remain same irrespective of geography was identified in saffron.

Due to the absence of whole genome sequence of saffron, the genetic diversity in this plant was established by conventional genetic markers such as RAPD, SSR, AFLP etc. Our group has reported the first draft genome of *C. sativus* with 3.5 Gb genome size and with N50 value of 1860 using Illumina sequencing technologies. The genome was functionally annotated and 53,546 genes were identified including the 5726 transcription factors. *C. sativus* genes were compared with the closely related plants namely *Asparagus officinalis, Phalaenopsis equestris, Apostatia shenzhenica* along with a model monocot plant *Oryza sativa* (Rice) and was found phylogenetically closer to *A. officinalis.* This was due to the presence of more orthologous protein clusters in *A. officinalis* as compared to other selected plants. 85.2% of total identified genes (45632 genes) were found orthologous with one or more plants, however only 7914 were specific to *C. sativus* that need further investigation. In addition, all the genes encoding the enzymes involved in apocarotene biosynthesis pathway were identified in the *C. sativus* genome. A total of 862,275 repeats were identified in assembled genome wherein simple repeat (48.41%) and LTR (30.34%) were the most abundant. 964,231 SSR markers were identified in the assembled genome that can be further evaluated for their application in *C. sativus*.

Exposure of plant growth hormone herbicides on growth of isolated bacterial strains

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Abstract

Plant growth hormone herbicides 2,4-dichlorophenoxy acetic acid (2,4-D) and 4-chloro-2-methylphenoxy- acetic acid (MCPA) which are regularly applied on agricultural fields to kill weeds. Microorganisms are utilized in bioremediation for the detoxification and degradation of pollutants. There has been increased attention given to this technology since it has shown to be both effective and reliable in removing pesticides from polluted environments. In present study, 5 pure bacterial strains were isolated from exposed agricultural field in the presence of herbicides individually at constant concentration which is recommended on land. Identification and characterization of isolated strains were done by sanger sequencing, observed *Micrococcus luteus*, *Klebsiella oxytoca*, *Pseudomonas aeruginosas*, *Porphyromonas gulae* and *Escherichia coli* and submitted on NCBI GenBank. Impact of herbicides on the growth pattern and growth curve of these different microbial strains in enriched medium and in minimal medium observed differently. Microbial strains with different genera having same environmental and atmospheric conditions shows slightly different pattern in their growth curve, with and without presence of both herbicides individually at a constant concentration of 500mg/L. In enriched media with and without presence of herbicides growth curve is similar showing 2-4hrs of lag phase in 4 strains and 6hrs in one strain with maximum optical density of around 1.5 to 2 at 600nm. While in minimal medium with 0.2% glucose concentration shows maximum of 0.25 to 0.35 OD at 600nm wavelength.

Keywords: Detoxification, Plant growth hormone, Bioremediation, Sanger sequencing, NCBI



Isolation and characterization of Algae isolated from marine costal samples of Arabian Sea near Mumbai for the detection of antioxidant and anticancer properties

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Abstract

Algae are an important and distinct phytoplankton group of marine ecosystems. Marine algae have multiple applications, including nutritional supplements, fish farming, medicines, personal care products, agriculture fertilizers, biofuel manufacturing, and cattle feed. With all of these benefits, algae create a significant number of bioactive chemicals. In the current context, antibiotic resistance is rising among bacteria, food has lower nutritional contents, and due to other causes isolation of novel marine algae and separation of new bioactive compounds is current need. The vast algae diversity in India is shaped by biogeographical and environmental variations. Despite this richness, there's been limited exploration of Indian algae for ecological and industrial purposes. In this study we have successfully isolated seven different algal species from the sample taken from the sea shore of Bandra beach Mumbai. On the basis of morphological characters and microscopic observations all the isolates found to be distinct from each other. Isolated algae are of three distinct categories macro algae, microalgae and a distinct group of cyanobacteria i.e. blue green algae. Three Macro algae are subdivided in to two green algae, and a red algae. One micro algae and three Cyanobacteria. On the basis of distinct microscopic characters microalgae found to be of the genus *Selenastrum*. For the clear demarcation up to the species level isolates are yet to be identified on the basis of molecular identification.

Keywords: Marine microalgae, Cyanobacteria, Diatoms, Green algae, Red algae

Integrating cyanobacteria as a climate resilient option in rice under elevated CO_2 environment

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Abstract

Soil is an essential global sink for organic carbon, however, the role of cyanobacterial C and N fixation potential and its linkage with its availability in soil and uptake by plants is less investigated under elevated CO_2. Evaluation of two selected rice varieties *Pusa Basmati 1718* and *Pusa Basmati 1509* (*PB1718* and *PB1509*) under ambient and elevated CO_2 environments, illustrated that the former variety exhibited significantly higher values for nutrient accretion and growth-related plant attributes. Inoculation with *Anabaena torulosa* (BF1; along with 66% N + Full dose PK) led to significant increment in C-N related parameters in soil under both environments. Photosynthetic pigments were significantly higher in ambient condition, with cyanobacterial inoculation increasing leaf pigmentation and leaf enzyme activities. BF1 inoculation led to highest value for PEP carboxylase activity under elevated CO_2 conditions, while it led to enhanced dehydrogenase activity, microbial biomass and micronutrient content (Fe and Zn) in soil, under ambient conditions. Biomass yield was positively impacted by elevated CO_2 in *Pusa Basmati 1718*, however, BF1 formulation led to better yield. Among the two varieties, *Pusa Basmati 1718* outperformed the other variety in terms of leaf pigments, while *Pusa Basmati 1509* exhibited higher PEP carboxylase activity. Metagenomic analyses of abundance of the N-and CO_2-assimilating gene copies illustrated significant differences, as influenced by variety, environments and cyanobacterial inoculation. This study provides interesting insights into the significance of alternative fertilization strategies, such as partial N fertilizer substitution by cyanobacteria to acclimatize plants, without compromising grain yield in rice.

Keywords: ambient, elevated, metagenomic, environment, cyanobacteria

Assessing Industrial Impact on Bhilwara Soil: A Comparative Analysis

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Abstract

Today industries play a vital role in our economy. Bhilwara, a prominent industrial district in Rajasthan, India, faces potential soil degradation due to its thriving textile industries. This study investigates the impact of industrial activity on soil health by comparing soil samples from three distinct Bhilwara locations: the industrial area, agricultural land, and urban areas. We collected soil samples from each location and analyzed them for key parameters including pH, electrical conductivity, organic matter content, and presence of heavy metals. By comparing the results across these sites, we aim to identify potential industrial contamination and its impact on soil fertility. This research will contribute to a better understanding of industrial influence on Bhilwara's soil health and inform strategies for sustainable land management practices.

Keywords: Bhilwara, Industrial Soil Contamination, Soil Quality, Agriculture, Urban Soil

Virome Analysis of the Yamuna River: Taxonomy and Genomic Characteristics

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Abstract

Bacteriophages, widely present in the environment, have not undergone thorough exploration as promising alternatives for antimicrobial interventions. despite their ability to target bacteria that may act as carriers for antibiotic resistance genes. With the evolving environment, aquatic systems, such as river water, reflect modifications in genomic and protein sequences among aquatic inhabitants, including microbes and bacteriophages. In this context, the present study aims to systematically examine the virome in the Yamuna River water stream through metagenomic analysis. Upon metagenomic assembly, our results reveal 11,132 sequences classified into 26 distinct virus classes. Significantly, 66% of these viruses belong to the Caudiviricetes class, followed by Herivicetes, Naldavircetes, Megaviricetes, Reutraviricetes, Pisoniviricte, and Pokkesviricetes. Despite the lack of complete representative genomes for the majority of sequences in prominent public virome databases. These taxonomic diversity demonstrates a variety of genomic features, are predicted to infect a wide range of microbial hosts, and collectively constitute less than 1% of metagenomic reads. Consequently, this study aims to explore the potential applications of the Caudiviricetes class in healthcare, with a specific focus on addressing antimicrobial challenges.

Keywords: Antibacterial, Bacteriophages, Caudiviricetes, Metagenomics, Yamuna

Unveiling the characteristics and microbial community structure of biogas slurry for its implications in improved biomethanation in household biogas plants of Sub-Himalayan region

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Abstract

The microbial communities play a significant role in anaerobic digesters for biogas production. A deeper understanding of the composition and activity of microbial flora is crucial for further optimizing the performance of biogas reactors. Reports on lower biogas production from sub-Himalayan regions like Palampur during winters are available; however, there has been no attempt to understand the microbial community of household biogas plants. In the current study, physico-chemical properties and microbial community structure of household biogas plants in the sub-Himalayan region were explored, and compared with publicly available metagenomes of advanced biogas reactors to understand the relative microbial structure. The nutrient contents of the slurry are in line with Fertilizer Control Order standards for values of liquid fermented organic manure, indicating its suitability for agricultural use. 16S rRNA gene amplicon sequencing reveals microbial diversity, showing a higher abundance of Firmicutes (70.9%) and Euryarchaeota (9.52%) in advanced biogas reactors compared to household biogas plants. Alpha diversity indices (Chao1, Shannon, and Simpson) indicate bacterial richness and diversity of household biogas plants were quite similar to advanced biogas reactors. Beta diversity analysis reveals differences in community structures between household biogas plants and advanced reactors. Additionally, differential abundance and core microbiome analysis revealed higher abundance of Firmicutes and Euryarchaeota in advanced reactors compared to household biogas plants. The lack of beneficial microbiome might be the reason for inefficient biogas production in household biogas plants in the sub-Himalayan region. This study emphasizes the establishment of efficient microbial consortia for enhanced degradation rates that may increase methane yield in biogas plants.

Keywords: Household biogas plant; Metagenomes; Methane; Microbial community structure; Sub-Himalayan region.

Deciphering the impact of Polycyclic aromatic hydrocarbons in altering the rhizosphere's properties and microbial profile

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Abstract

Polycyclic aromatic hydrocarbons (PAH) are among the most hazardous, ubiquitous and persistent organic compounds emitted from various anthropogenic activities which have become major concern globally. Among the priority pollutants for the environment, Phenanthrene (Phe) (low molecular weight) and Fluoranthene (Flu) (high molecular weight) are considered as the most abundant and toxic PAH reported in the soil. The current study has determined their effect on soil physico-chemical profile (pH, electrical conductivity, nitrogen, phosphorous and potassium), microbial density and diversity under different Phe and Flu concentrations. The results have shown that their presence in rhizosphere affects not only soil physico-chemical properties, but also their microbial profile, resulting in altered soil ecosystem.

Some microbes were found to be highly sensitive to the presence of even lower concentration of both Phe and Flu, whereas abundance of few bacteria fluctuated only at higher concentration of these PAH. The study has also showed that even changes in the ratio of abundance of two microbes resulted in physical disturbances that lead to decreased nutrient availability and electrical conductivity. An increase in CFU count was also visible with an increase in the concentration of these PAH. The results have shown significantly lowered soil enzymatic activity with increase in Phe and Flu concentrations, affirming a positive correlation with concentration of PAH. The study concluded that high concentration of PAH led to compromised quality of soil both in terms of nutrient and enzymatic properties as well as healthy microbiota profile.

Keywords: Fluoranthene, urease, dehydrogenase, Phenanthrene, colony-forming unit, physico-chemical properties

Ciliates as Symbionts: Exploring Symbiotic Relationships

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Abstract

Ciliates, a diverse group of unicellular eukaryotic organisms, have recently emerged as fascinating symbiotic partners. Endosymbiotic relationships between ciliates and other organisms are critical for their ecological roles, physiological adaptations, and evolutionary implications. These can be obligate and facultative. These symbionts play various roles in nutrient cycling, host defense, and ecosystem stability. Using transcriptomic and genomic investigations, we ascertain the genetic foundation of ciliate symbiosis, clarifying the adaptive strategies utilized by these organisms to flourish inside their hosts. A systematic survey of these endosymbionts has been conducted using both traditional and metagenomic approaches. Ciliates can establish symbiotic relationships with a variety of hosts, ranging from protists to metazoans. Ciliate symbiosis has implications for host health and resilience in the face of environmental stressors, and potential applications in bioremediation and agriculture. Understanding ciliate symbiosis can provide useful insights into the complex relationships that drive microbial communities and ecosystems in general. Endosymbiotic partnerships have attracted particular attention in phycology, zoology, microbiology, and virology.

Keywords: Ciliates, Ecosystems, Endosymbionts, Metagenomic, Microbiology, Partnerships

Assessing Soil health through Macronutrient and physiochemical Analysis in Mahendergarh District, Haryana

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Abstract

The physicochemical properties, macronutrients, and micronutrients of the soil in the South Haryana district of Mahendergarh are thoroughly examined in this study to assess the condition of the soil. The four primary macronutrients (nitrogen, phosphorus, potassium, and sulfur) as well as pH, electrical conductivity (EC), organic carbon, and total organic matter were analyzed in soil samples collected from three blocks. pH and EC were analyzed and found in the range of 7.39 to 9.07. EC was analyzed and was observed in the normal range (0.11- 0.41 S/m). pH was in the normal to saline range which interprets into the presence of calcium carbonate ions. Extreme pH levels can hinder nutrient uptake, affecting plant growth. Organic carbon and total organic matter were found in the low range (0.07 to 0.38 mg/l). Nitrogen was found in the range of (55-163 kg/ha). Potassium, phosphorus and sulphur was estimated and phosphorus was found in the range of 7.06-13.62 kg/ha. Potassium was observed in the range of 83.27-262 kg/ha. Sulphur was found in the range of 6.80-59.53 kg/ha. These findings provide insights into the soil's fertility and potential challenges for agricultural productivity in the studied region.

Keywords: Soil health; Physiochemical parameters; Macronutrients, Micronutrients, Agricultural productivity

Understanding soil immunity against phytopathogens for enhancing soil health

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Abstract

Organic soils are able to suppress a wide range of phytopathogens, with this ability known as general disease suppression. However, the mechanisms and factors contributing to this phenomenon remain largely unknown due to soil heterogeneity and the limited studies on general disease suppressiveness. It is also unclear how the soil's biological activity of general disease suppression relates to its physicochemical factors. Therefore, this study aimed to establish a correlation between physicochemical parameters, soil biological activity, and disease suppression, adopting a polyphasic approach to attain this objective. Rhizospheric soil samples were collected from farmers' fields in the North-Western Himalayan region of India, from comparable organic and conventional farming fields. The collected soil samples were screened for their *in vitro* suppression of phytopathogens, physicochemical properties, molecular markers, and enzymatic activities. It was found that organically managed soils were more pathogen-suppressive, and had higher enzymatic activities, available macronutrients, and total organic carbon than conventionally-managed soils. Furthermore, concentrations of available micronutrients, such as Mn, Cu, and Fe, showed a negative correlation with the pathogen suppression efficacy of soils. The current study highlights the potential of organic soils as a sustainable agriculture strategy by outlining the significance of soil biotic and abiotic components in disease suppression mechanisms in Himalayan soils.

Keywords: Phytopathogens, micronutrients, disease suppression, organic farming

Rise of infectious diseases

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Abstract

Infectious diseases are defined as those who occur due to a microorganism or its toxic products that appear after the transmission of the infectious agent (or its toxic products) from an infected person, an animal, or a reservoir to a susceptible host, directly or through an intermediary agent (animal, vector, or inanimate environment). Despite vaccinations, improvements in hygiene and food safety, and the availability of antimicrobials, infectious diseases continue to be an important cause of mortality and have given us a sense of vulnerability to the microbial world. The impact of these diseases is greater in less developed countries, but in our environment, travel, ageing, advances in medical (oncological and immune-modulated) and surgical treatments (transplants and prostheses) consequently, re-emerged (west nile virus), accidently emerged (vaccine derived polio virus), truly emerged (HIV) pathogens. In a recent pandemic risk assessment study of 50 new viruses, the family with highest risk was coronaviruses, followed by bunya viruses, filoviruses and paramyxoviruses and the most dangerous animal reservoir is that of bats. Compared to other diseases, infectious diseases are unique because of their transmissible nature. But also due to its unpredictable pandemic potential, the evolutionary adaptability of the causative microorganisms and their ability to induce a more or less effective immune response. The possibility of preventing them and even eradicating them in some cases depends on the close relationship with human behavior, its frequent origin in animal species (zoonosis), and the additional effects that its treatments may have. Anthropozoic era represents aggressive, harmful, and unbalanced interactions with nature that favor the emergence of new infectious diseases. Having good diagnostic capacity, well-funded public health services, and the ability to treat and isolate those who are infected are essential in controlling infectious diseases. Every action carries risk but we should never underestimate the risk of inaction.

Keywords: Infectious diseases, microorganism, pathogens, viruses.

Comparing diversity of unicellular eukaryotes (ciliates) through morphological and metabarcoding approach in various ecotypes

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Abstract

Soil biodiversity include different life forms like bacteria, algae, fungi, nematodes and ciliates that are essential to maintain healthy ecosystem. Soil ciliates comprise important microbial group as they play important role in microbial loop, nutrient recycling, enhancing the soil microbial biomass, regulating the size and composition of bacterial communities in the soil by grazing which ultimately helps in plant growth. The present study was aimed to compare the spatial and temporal variations in eukaryotic microbial diversity by using morphological and metabarcoding approach. Soil samples were analyzed with the non-flooded Petri Dish method for morphological analysis. The environmental DNA (eDNA) was extracted from undisturbed soil, soil contaminated with leachate and digested sludge and were used for sequencing 18S V4 barcode region, followed by phylogenetic analysis. Various diversity indices were analyzed in both the approaches. Maximum number of Amplicon sequence variants (ASVs) were observed in Jahanpanah Forest Land (1899), followed by Okhla landfill (694) and Okhla sewage treatment plant (628). Variations were also observed in species abundance of all the three sites in different seasons. The metabarcoding approach has unraveled the hidden diversity of ciliates including *Paramecium, Stylonychia sp. Arcuospathidium sp., Hamiurosomoida longa, Cyrtohymena citrina, Cyclidium glaucoma, Leptopharynx bromelicola, Acineria incurvata, Cyrtolophosidida sp., Pseudoholophrya terricola, Frontonia terricola, Pseudouroleptus caudatus, Blepharisma elongatum, Bryometopus pseudochilodon, Pseudoplatyophyra nana, Eschaneustyla lugeri* that were not observed in morphological approach. This study shows how metabarcoding strategy can be used to decipher new and rare species of ciliates.

Keywords: Ciliates, Metabarcoding, Environmental DNA, Forest land, Digested sludge, Leachate

Exploring Microbial Diversity for Sustainable Tannery Effluent Remediation: A Bioremediation Approach

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Abstract

Tannery effluent, laden with various pollutants including heavy metals and organic compounds, poses significant environmental hazards if not treated effectively. Bioremediation, employing microbial communities isolated from effluent, emerges as a sustainable and eco-friendly approach for mitigating the adverse effects of tannery effluent. This study investigates the efficacy of microbial isolates obtained from tannery effluent in degrading pollutants present in tannery effluent. Microbial isolates were characterized for their ability to tolerate and degrade complex pollutants commonly found in tannery effluent. Subsequently, the selected microbial consortia were employed in batch experiments to assess their effectiveness in degrading organic pollutants and reducing heavy metal concentrations in tannery effluent. Results obtained using a micro plate reader and HPLC demonstrate the potential of indigenous microbial communities to efficiently remediate tannery effluent, offering a promising strategy for sustainable waste management in the leather industry. The findings underscore the importance of harnessing microbial diversity for environmental remediation and advocate for the integration of bioremediation practices in industrial waste treatment protocols.

Characterization of the bacterial microbiome structure and identification of the beneficial genera in the leaf litter compost for its potential application as bio-organic fertilizer

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Abstract

The abundance of beneficial microbes found in organic waste composts plays a vital role in enhancing soil health and supporting plant growth. Globally generated waste can be transformed into organic compost that can be used as bio-organic fertilizers. This research delved into exploring the viability of leaf and various organic waste composts as bio-organic fertilizers using 16S rRNA metagenomics. Through an analysis of the bacterial microbial richness and diversity, employing both alpha and beta diversity indices, notable variations influenced by organic substrates during composting were revealed. The leaf compost exhibited a high total OTU count (70,554) but lower microbial diversity (Chao 1 index = 272.27), while the kitchen waste compost displayed the highest microbial diversity (Chao 1 index = 429.18). There was a positive correlation between microbial biomass, diversity, and compost quality, underscoring the significant role of microbial activity. The presence of beneficial genera was identified across all the compost samples. The beneficial genera identified across all the bio-composts were *Lactobacillus, Leuconostoc, Sphingobacterium, Paenibacillus, Pseudomonas,* and *Clostridium*. Some pathogenic genera were also detected in all the composts analysed viz. *Prevotella, Agrobacterium, Fusobacterium,* and *Streptococcus*. However, the ratio of beneficial to pathogenic genera remained generally high in all composts, indicating enrichment with beneficial microorganisms. Notably, the leaf compost displayed the highest proportion of beneficial genera, approximately 92%, and a low presence of pathogenic genera at about 3%, suggesting substantial potential as bio-organic fertilizers. This underscored the importance of understanding the microbial composition of organic composts for their effective utilization as bio-fertilizers.

Key words: Bio-organic fertilizer, 16S rRNA Metagenomics, Microbial diversity, Organic waste compost

16S rRNA metagenomic profiling of red amaranth grown organically with different composts and soils

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Abstract

In recent years, organic food has surged in popularity due to its perceived benefits for human health and soil sustainability. However, concerns persist regarding potential pathogens in organic produce. The aim of this study was to investigate how various composts and soils impact the microbiome of organically cultivated leafy vegetables. 16S rRNA metagenomic profiling of the leaves was done, and data was analyzed. The study found that organic produce, when supplemented with compost, had a higher microbiome diversity compared to conventional produce. Beneficial genera like plant growth promoters (*Achromobacter, Paenibacillus, Pseudomonas, Sphingobacterium*) and probiotics (*Lactobacillus*) were more abundant in organic samples. While some pathogenic genera viz. plant pathogenic bacteria (*Cellvibrio, Georgenia*) and human pathogenic bacteria (*Corynebacterium, Acinetobacter, Streptococcus, Streptomyces*) were present, their levels were relatively low in organic produce, indicating lower pathogen contamination compared to chemical fertilizer produce.

Key words: Microbiome, 16S rRNA Metagenomics, Organic, Composts, Pathogens

Metagenomics and Medicinal Sulfur Waters

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Abstract

This study delves into the metagenomic analysis of sulfur-enriched water from the Gandhak-ki-baoli, a notable stepwell in Delhi, amidst the broader context of abandoned wells in northwestern India. Despite the prevalent dysfunctionality of the wells in the urbanization era, Gandhak-ki-baoli stands out for its well-preserved water, characterized by a distinctive sulfur content believed to possess medicinal attributes. The investigation revealed a substantial dataset of 17,488 Operational Taxonomic Unit (OTU) sequences, showcasing the dominance of S*ulfuricurvum kujiense* at 5.5% abundance, capable of releasing elemental sulfur into the environment.Other bacterial strains from genera such as *Novosphingobium, Desulfofustis, Ruegeria, Hyphomicrobium, Phaeobacter, Desulfobulbus, Desulfuromonas, Desulfococcus,* and *Desulfosporosinus* were identified as integral contributors to sulfur metabolism in this ancient stepwell. Moreover, certain strains were explored for their production of secondary bioactive metabolites, contributing to the medicinal aspect of the water. These taxonomic investigations collectively offer compelling evidence for the therapeutic potential associated with sulfur-enriched water.

Keywords: Metagenomics, Delhi, Stepwell, Sulphur water, Gandhak-ki-baoli

Synergistic Strategies with Bioinoculants: Enhancing Crop Productivity and Health

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Abstract:

Bioinoculants have emerged as essential components of modern agriculture, offering multifaceted benefits for enhancing crop productivity, mitigating biotic and abiotic stresses, and promoting sustainable agricultural practices. These microbial formulations, including biofertilizers and biopesticides, play pivotal roles in fostering plant-microbe interactions, improving nutrient uptake, bolstering defense mechanisms against pathogens, and contributing to soil health and fertility. Recent research highlights the significant potential of bioinoculants in degrading pesticides, reducing chemical residues, and promoting sustainable agricultural practices. Moreover, bioinoculants exhibit antagonistic activity against plant pathogens, induce systemic resistance in plants, and contribute to disease suppression, reducing the dependence on synthetic pesticides. Studies underscore the importance of synergistic interactions among different strains of bioinoculants, optimizing application methods, and evaluating long-term effects on soil health and ecosystem resilience. By harnessing the capabilities of bioinoculants, modern agriculture can transition towards a more balanced and efficient system that minimizes negative environmental impacts while enhancing crop yields and promoting long-term sustainability. This abstract provides insights into the recent advancements in leveraging bioinoculants to achieve synergistic effects on crop productivity and health, emphasizing their strategic importance in sustainable agricultural practices.

Key words: Bioinoculants, Sustainable agriculture, Crop productivity, Plant-microbe interactions, Pesticide degradation, Soil health, Disease suppression, Synergistic interactions, Biofertilizers, Biopesticides.

To study the rise in Shingles cases as an aftermath of COVID-19

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Abstract

The Varicella-zoster virus (VZV) (or human herpes virus 3) is a neurotropic human alpha herpes virus responsible for chickenpox/varicella and shingles/Herpes zoster (HZ). HZ is secondary to varicella which is caused only after the reactivation of VZV. Recently, reports suggest a rise in shingles cases COVID-19 and its vaccination. This is a statistical study to assess whether COVID-19 or its vaccination has any role in the reactivation of the VZV in such a form as to cause Herpes Zoster (Shingles). A cross-sectional survey was conducted through a Google form-based analytical and semi-structured questionnaire among 220 subjects (18-70 years) from India. Statistical analysis was performed using MS Excel and R software. p-value was calculated through the chi-square method (as the data available is in non-numeric form). Results indicated **that** out of 67 COVID-19 patients 24 (36.3%) got shingles while among the 153 non-COVID-19 subjects only 13 (9.15%) developed shingles. Interestingly, all the non-COVID-19 subjects who developed Shingles were vaccinated for COVID-19. 21 out of 24 COVID patients who developed shingles and 10 out of 13 non-COVID vaccinated subjects who developed Shingles, all had a history of chickenpox. Furthermore, occurrence of Shingles could be correlated with the age of the subjects. The results clearly indicate that COVID-19 virus (SARS-CoV2) can cause reactivation of VZV particularly in patients above 50 years of age.

Management of *Listeria monocytogenes* in Indian arable land by harnessing the potential of soil microbiota

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Abstract

Listeria monocytogenes is a pathogen of growing concern, with many fatal outbreaks linked to the consumption of infected fresh food, documented all over the world. The CDC estimates that it is the third leading cause of death from foodborne illness in the United States. The gut microbiota of farm animals contains a variety of human pathogens, including *Listeria monocytogenes*. These contaminants persist in their feces, which are used to produce animal manure on organic farms. The use of such manure on soil may cause the transfer of *L. monocytogenes* to plants, vegetables, and farm animals, resulting in infections in humans after consuming contaminated fresh produce. Despite recent cases of listeriosis in various parts of India, little effort has gone into systematic surveillance of the pathogen in soil and compost. There have been few studies on the use of plant growth-promoting rhizobacteria (PGPR) against human pathogens, which are also members of the indigenous microbial population in soil. In light of this, soil and compost samples were collected from 15 different sites across India. Both culture-dependent and culture-independent approaches were employed to detect *Listeria* species. *Listeria* species were detected in some samples. Furthermore, a SynCom of 11 plant growth-promoting strains with diverse PGP features and biocontrol activities against *Listeria monocytogenes* was generated. The findings of this study showed the presence of *Listeria* spp. in Indian soil and reflects on the potential of native soil microbes in providing an environment-friendly approach of the mitigation of human pathogens from arable ecosystems.

Alzheimer's disease, a brief discussion on emerging treatment methods and strategies for the future

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Abstract

Alzheimer's disease, the most prevalent and serious form of dementia, requires more of our attention. Currently, there is no complete cure, and existing treatments only manage symptoms rather than providing a complete cure. However, global efforts are underway to address the disease. Recent research literature shows promising results for future therapeutics, categorized by different proposed pathological mechanisms of Alzheimer's. While the exact mechanism remains unknown, several hypotheses, including the Amyloid-β, Tau, Mitochondrial cascade, and oxidative stress hypotheses, are among the most plausible. This review compiles promising research literature regarding therapeutics from each major mechanism of the disease, as well as unconventional approaches such as altering gut microbial composition, utilizing phytocompounds, and appropriate supplementation to manage disease severity. The review also discusses major FDA-approved and repurposed drugs for treating Alzheimer's. Looking ahead, suggestions for the future include improving drug delivery methods, early detection of biomarkers, and leveraging computer applications for more efficient and paced-up solutions. Although the path to a cure remains unclear, the literature offers hopeful prospects for treating Alzheimer's disease. This review aims to provide a brief insight on Alzheimer's disease, its causes, emerging conventional and unconventional treatment strategies, and finally, some future suggestions aiming to reduce the disease burden worldwide.

Key words: Amyloid-β, Mitochondrial cascade, Tau tangles, Acetylcholinesterase, Cholinergic neuron.

Translational Studies in the Applications of Quorum-Sensing in Gut-Brain Axis-Associated Disorders and Drug Targeting

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Abstract

Quorum sensing (QS) is a sophisticated 'social' behaviour demonstrated by various bacteria to coordinate group behaviours based on population density. It enables bacterial adaptability, and increases their ability to survive in changing environments - such as the intestines they inhabit. The coordinated behaviours mediated by QS confer numerous advantages to bacterial populations. For instance, biofilm formation provides protection against environmental stresses, enhances nutrient acquisition, and promotes survival in hostile conditions. QS also regulates the expression of virulence factors, enabling bacteria to launch coordinated attacks on host organisms and evade immune responses. Targeting QS pathways presents a promising alternative to antibiotics, and serves as a strategy for combating bacterial infections, disrupting virulence and biofilm formation. At the core of QS are signalling molecules known as autoinducers, which are released by bacteria into their surroundings. Autoinducers vary chemically, including acyl-homoserine lactones (AHLs) and peptides among others. AHL-mediated QS systems are currently being researched as potentially moderating psychological disorders associated with the Gut-Brain-Axis; including Autism Spectrum Disorders (ASDs).

The gastrointestinal disorders associated with ASDs first introduced the idea that gut health might significantly impact disease symptoms, and this hypothesis has been backed by modern studies of biomarkers in autistic individuals and dysbiosis within their microbiota. Behavioural studies and the use of healthy faecal transplants in mice models of ASDs have been shown to induce normobiosis. QS Peptide-Modified micelles are being explored as options for targeted drug delivery systems to treat gliomas in nude mice models. This review explores the importance of understanding QS within our microbiomes, and applying this knowledge towards the potential treatment of disorders of the mind and body will ultimately help to identify prevalent markers for risk assessment and pre-disposition, while also highlighting the ethical obligations that must be upheld while pursuing a course of action.

Key words: Quorum Sensing, Normobiosis, Autism Spectrum Disorders, Gliomas

Breaking the Bacterial Banter: Disrupting Quorum Sensing for Infection Control

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Abstract

Bacterial biofilm poses challenges in chronic infections and is a major challenge in infection control and therapeutic strategies. Biofilm helps bacteria to evade the host defence mechanisms and persist longer in the host. Quorum sensing (QS) primarily regulates biofilm formation in chronic infections and plays a major role in eliciting virulence. The challenge of controlling infections is compounded by the antibiotic resistance and the ability to promote chronic infections by the biofilms. Inhibiting signalling molecules through interference with QS might be one way to prevent occurrence of biofilms and reduce adverse effects due to contamination.

Recent investigations have showcased successes associated with these approaches that counteract such biofilm-associated infections. Synthetic chemicals, like *meta-bromo-thiolactone (mBTL)*, which hinder QS receptors, prevent virulence and formation of biofilms by pathogens like Pseudomonas aeruginosa. For example Baicalin has been identified as an effective natural compound that disrupts QS mediated biofilm formation and virulence; hence promises new therapeutic windows. For next-generation antibiotics, it is essential to manage drug resistance based on Gram-negative and Gram-positive bacterial QS disruption.

These findings broaden our comprehension regarding the usefulness of QS disruption against Biofilm related infections as well as combating increasing antibiotic resistance. It analyses present strategies employed in curbing bacterial QS and production of Biofilms putting more emphasis on their relevance towards disease management and medication. In this review, we will discuss some of the strategies employed currently to inhibit bacteria quorum sensing and the biofilm formation. It will also examine the opportunities and challenges facing in this field and try to suggest potential future research areas and clinical applications.

Key words: Biofilm, Quorum sensing (QS), Quorum Quenching (QQ), Antibiotic Resistance, Non-antimicrobial Strategies for QQ

An industrially feasible approach for denim biobleaching: Reuse of a novel laccase and recycling of its mediator for repeated bleaching cycles

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Abstract

The preference for the worn-out look of denim is popular among various generations, mainly achieved through conventional "stone washing". In this process, denim is washed with pumice stone in the presence of various oxidising chemicals. However, due to toxic chemicals, this process has several limitations. To make the process environmentally friendly, the use of enzymes such as laccase mediator system (LMS) has been explored. In the present study, an economical and commercially viable process has been standardized using a novel strategy for recycling the mediator and reusing the enzyme for multiple cycles of denim bleaching. *Bacillus cabrialesii* SJ2 produced an extracellular laccase active/ stable in wide range of temperature (40-70°C) and pH (6-9). The enzyme yield was significantly enhanced, showing a 154-fold increase in yield (2216.5 $IUml^{-1}$) under the optimized conditions. The enzyme efficiently degraded indigo carmine within 30 and 45 minutes at 50°C/8.5 pH with and without a laccase-mediator, respectively. Enzyme was able to bleach denim without any mediator however effective bleaching was achieved in the presence of ABTS. To make the process economical the cost of bleaching reactions was reduced by recycling the mediator and adding a reduced dose of enzyme. In recycling studies, the same bleaching effect on fabric was maintained for up to eight cycles with the same mediator in the reaction mixture (500µM ABTS) and the addition of reduced doses of enzyme (10U in the first cycle and 5U in subsequent cycles). The mechanical properties of the enzymatically bleached fabric, elongation (7.6mm) and tensile strength (1105N) were comparable to those of the control and superior to the chemically bleached samples. This study represents the first report of standardizing a process by recycling the mediator and reusing the enzyme, making it economically viable and thus a practical alternative for application on an industrial scale.

Key words: Laccase, Laccase-Mediator, Denim, Biobleaching, Recycling



Genomic Characterization and Comparative Analysis of Seven Strains of Methanocaldococcus Spp. and Their Potential for the Treatment of Wastewater and Aqueous Organic Pollutants

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Abstract

Methanocaldococcus is a genus within the phylum Euryarchaeota, containing single-celled, methane-producing archaea belonging to the class Methanococci, which utilise methanogenesis to generate methane as their primary energy source. Their metabolism involves the reduction of carbon dioxide with hydrogen or formate as electron donors. This allows them to play a major role in the global carbon cycle by contributing significantly to methane production in various ecosystems and the geochemical cycling of carbon and sulfur. Given the ecological importance and potential biotechnological applications of *Methanocaldococcus* species, there's a pressing need for comparative genomic studies within this genus.

The complete genomes of seven *Methanocaldococcus* strains (*M. bathoardescens* JH146*, M. fervens* AG86*, M. infernus* ME*, M. jannaschii* DSM 2661*, M. vulcanius* M7*, Methanocaldococcus sp.* FS406-22 *and M. lauensis* SG7) were collected from NCBI database for this study. Initially, the genomes were annotated using Rapid Annotation using Subsystem Technology (RAST). Then, we derived the pairwise Average Amino-acid Identity (AAI) matrix for genomes and their phylogenetic relationships were constructed using iTOL. This was followed by Functional Annotation using the KAAS and MinPath Server.

The analysed strains exhibited genome sizes from 1.749 to 1.773 Mb, while their GC content ranged from 31.6 to 32.8% with a variation of only 1.2%. ANI analysis uncovered a close relationship between strains *M. jannaschii* DSM 2661 and *Methanocaldococcus* sp. FS406-22, however, ANI = 91% suggests their phylogenetic divergence as distant species. Analysis of the core genome revealed a large size of 1083 genes, likely due to the limited number of genomes included. In this case, even after incorporating the seventh genome, the pan-genome continues to grow suggesting a considerable degree of genetic diversity. Functional analysis provided insights into the metabolic potential of these strains, suggesting their utility in various applications for treating wastewater and aqueous organic pollutants.

Key words: *Methanocaldococcus,* Comparative genomics, Methane-producing archaea, Phylogenomic analysis, Wastewater Treatment

An investigation of the Genome of Antibiotic resistance bacteria *Micrococcus endophyticus*

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Abstract

Antibiotic resistance is among the most challenging issues due to limited information on bacterial species and their associated antibiotic-resistant genes and proteins. The current study was designed to assess the presence of antibiotic-resistant bacteria in Yamuna River water and to assess the attributes of the bacteria using genomic sequencing.

The water samples were collected from three distinct sites of the Yamuna River, specifically the Wazirabad stretch. This stretch is significant as it is a major source of water supply for Delhi, making it a crucial area to study for potential antibiotic resistance. Aliquots were systematically diluted, spread on Luria Bertani agar plates, and incubated for 24–48 h at 30 °C. Bacterial colonies were quantified as CFU/ml. The pure bacterial colony was subjected to whole genome sequencing. 16 s Ribosomal DNA sequence was used to construct the phylogenetic tree. The genomic sequence was explored for the presence of heavy metal genes and the identification of AMR genes. The results indicated that the isolated bacterial strain's 16S ribosomal RNA showed similarity to *Micrococcus endophyticus*. Analysis of the DNA sequence revealed the presence of several heavy metal resistance genes and antibiotic resistance genes. The results add to our understanding of antibiotic resistance in bacteria and its potential impact on public health.

Key words: Whole genome sequencing (WGS), antibiotic-resistance genes (ARGs), antimicrobial resistance (AMR), phylogenetic tree, *Micrococcus endophyticus*

Nanotechnology based approaches for enhancing microbial remediation of contaminated soil current trends & future perspectives

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Abstract

Contaminated soil possesses enormous environmental issues and health risk worldwide, it is very significant to understand the challenges possess by contaminated soil for environment and living organisms. It entails the development of new technologies which gives promising solution and development of innovative remediation strategies.

Nanotechnology offers an exciting approach and boulevard to enhance microbial remediation; it is a process which involves the use of micro organisms to degrade the pollutants. Micro organisms plays crucial role in degradation, transformation & detoxification of various pollutants in contaminated and polluted soil eco-system. This paper reviews the recent trends and futures perspectives for augmenting microbial remediation of the contaminated soil in nanotechnology.

Nanotechnology is emerging as powerful tool, it works by boosting microbial activity, targeted delivery and improved degradation of unwanted particles. This is under development in this we discuss the application of nano-materials for enhancing microbial activity, pollutant degradation, bio availability and transport in soil environment. Thinking holistically it become more powerful when combines with other approaches e.g. nano-phyto remediation which involves combining NPs with hyper accumulator and microbial mediated nano remediation in which indigenous or already present microbes can interact with NPs and work more effectively.

Furthermore, we explore the challenges, opportunities and future direction of integrating nanotechnology with microbial remediation strategies to address soil pollution by understanding the intricate relationship between micro-organisms and plants. We can implement holistic and environmental friendly approaches using NPs that support long term soil health and food security. This paper review provides a comprehensive overview of the diverse function and application of NPs in soil ecosystem

Keywords: Nanotechnology, Biological remediation, Contaminated Soil, Pollutant degradation, Bio availability and Soil health.

Comparative Genomics of Six Strains of *Sulfolobus* Spp. for Interpreting their Abilities to Survive in Extreme Sulfur-Rich Environments

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Abstract

The *Sulfolobus* genus, belonging to the order Sulfolobales within the phylum Thermoproteota, comprises thermoacidophilic archaea that thrive in extreme environments characterized by high temperatures (70-80°C) and low pH (pH 2-4). Sulfur metabolism is a hallmark of *Sulfolobus* species, and they are recognized for their ability to oxidize elemental sulfur, thiosulfate, and other sulfur-containing compounds. Despite the ecological significance of *Sulfolobus* species and their potential biotechnological applications, the number of comparative genomic studies conducted within this genus remains limited. In this study, the genomes of six *Sulfolobus* strains (*S. acidocaldarius DG1, S. islandicus L.D.8.5 and Sulfolobus sp.* strain *E5-1-F,* strain *E11-6,* strain *A20 and* strain *S-194*) were downloaded from NCBI server. The genomes were annotated using Rapid Annotation using Subsystem Technology (RAST) initially. Then, the pairwise Average Amino-acid Identity (AAI) matrix for each genome was prepared, followed by Functional Annotation using the KAAS Server and MinPath server.

The genomes of the analysed strains displayed a range in size, with values between 2.22585 and 2.74865 Mb. Furthermore, the GC content showed some diversity, ranging from 34.7 to 36.7 %. ANI analysis identified a close association between strains E5-1-F and E11-6 with >98% ANI which suggests these strains belongs to a same and likely diverged from a common ancestor more recently compared to the other strains studied. The core genome analysis of genomes further revealed a predicted core genome size of 1193 genes. This is large due to fewer genome representatives. Similarly, the pan-genome, representing the complete gene set across all strains, showed no signs of reaching a stable size even after incorporating the sixth genome. Functional analysis further revealed the metabolic potentials of these strains to survive in a sulfur-rich environment.

Key words: *Sulfolobus,* Sulfur metabolism, Genome Analysis, Extremophiles

Impact of heavy metal pollution on the Community Structure and diversity of ciliates

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Abstract

Heavy metal contamination poses a significant threat to aquatic microorganisms vital for nutrient cycling and ecological stability. However, the effects of heavy metal contamination on microorganisms and the interactions between them are still unclear. This research aims to assess the impact of heavy metal pollution on ciliate communities in different seasons, identifying tolerant species and offering insights for bioremediation. The most probable number method (MPN) was used to investigate the abundance and structural diversity of the ciliate community in five different sites of the Yamuna River. Results revealed Wazirabad After Drain (WBAD) as the most perturbed site, exceeding BIS permissible limits for Pb, Fe, Mn, Cr, and Ni, and exhibiting the lowest species diversity in the pre-monsoon season. However, maximum species richness was observed at Prayagraj in pre-monsoon and Wazirabad before drain (WBBD) in post-monsoon. Notably, *Coleps* sp. emerged as the predominant in the study area, while highly polluted water harboured *Euplotes woodruffi*, *Sterkiella* sp., and *Dileptus* sp. Furthermore, significant negative correlations were found between heavy metal concentrations (Fe, Mn, Cr, Pb) and diversity indices, indicating potential tolerance and bioremediation efficacy of certain ciliate species. Overall, these findings offer valuable insights into the intricate relationship between heavy metal contamination and ciliate communities, highlighting the potential of ciliates in biomonitoring and bioremediation.

Key words: Biomonitoring, Bioremediation, Ciliate community, Ecological stability

Hybrid Assembly approach: A case study on thermoactive serratiopeptidase producer *Serratia marcescens AD-W2*

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Abstract

A highly contiguous whole genome sequence of *Serratia marcescens* presents the genes responsible for the production of prodigiosin as well as serratiopeptidase. To unveil its complete genetic blueprint, we employed a hybrid assembly approach using Illumina short-read and Nanopore long-read technologies. This strategy successfully generated a highly-contiguous assembly. Functional annotation revealed a diverse repertoire of genes responsible for metabolite production. Furthermore, comparative analysis with other strains highlighted its identification as *Serratia marcescens* and characterization at strain level. The WGS approach lays the foundation for in-depth exploration of *S. marcescens* AD-W2 for its industrial applications. The Anti-Smash based prediction of secondary metabolite clusters revealed 9 clusters, out of which only one cluster was found to have 100% similarity with known metabolite prodgiosin. The annotation was successfully performed using Prokka, by which around 4582 CDS, 22 rRNA gene and 93 tRNA gene were annotated. The N50 and N90 of the assembly obtained were 4989359. The presented case study on the hybrid assembly approach, lays a foundation for in-depth exploration of *S. marcescens* AD-W2, a thermoactive serratiopeptidase producer for further industrial applications.

Key words: *Serratia marcescens*, hybrid sequencing, Illumina, Nanopore, single-contig assembly, serratiopeptidase, prodgiosin

Harnessing DHA Producing *Schizochytrium Spp* for Phytase Expression By Electroporation

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Abstract

The marine oleaginous protist *Aurantiochytrium sp. (Schizochytrium spp.)* is a well-known docosahexaenoic acid (DHA) producer and its different DHA products are the ideal substitute for the traditional fish oil resource. Studies revealed the inclusion of microalgae in animal diets could improve goat and cow fat milk quality, and meat quality in ruminants, pigs, poultry, and rabbits essentially due to its high content of docosahexaenoic acid (DHA). The use of marine microalgae in laying hen diets improved egg production and quality, increasing yolk DHA levels. In this study, we explored an innovative approach using electroporation to introduce the phytase gene into the Schizochytrium spp. Phytase is an enzyme that plays a crucial role in the digestion of phytic acid (salt form: phytate) to release usable inorganic phosphorus. In ruminant animals such as cattle and sheep, utilize bacterial phytase in the gut to access the phosphorus content in grains, which would otherwise be indigestible. But Non-ruminant animals such as pigs, poultry, and fish lack phytase to effectively break down phytic acid. Therefore, exogenous phytase supplementation becomes essential to enhance bioavailability. Electroporation effectively facilitated the transfer of the exogenous phytase gene in pRI201-AN vector into Schizochytrium spp. The transformants were cultured and screened on G418 Plates and confirmed the presence of phytase gene by analysis in colony PCR. Eight colonies were tested positive with colony PCR having 1.5 kb and with a phytase activity of 1.77 U/ml of crude lysate. Through our findings, we have addressed two critical challenges by mitigating phosphorus pollution and enhancing ruminant nutrition. Thus Schizochytrium spp. which belongs to GRAS (generally recognized as safe) can be incorporated at levels of up to 2.8% for broilers and 4.7% for layers as feed. The essential fatty acids maintain overall health and support various physiological functions in these animals. Besides DHA it also provides antioxidants that contribute to immune function in poultry.

Key words: Assay, Cloning, Docosahexaenoic acid, omega-3-fatty acid, Phytase, Phytic acid, *Schizochytrium sp.*

Indian Laboulbeniomycetes

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Abstract

Fungi of the order Laboulbeniales are a large group of obligate parasites on living arthropods. They spend their entire life cycle on their host. The group includes around 2200 described species in 142 genera found on their hosts around the world. They exhibit some level of host specificity as well. Since they live as a parasite they can be used for the myco-biocontrol of insect pests. In the present study we collected insects like the common cockroaches (*Periplaneta americana, Blatta* sp.), ladybug (Members of Family Coccinellidae) and the Alates ant species. Screening of the collected host specimens was followed by isolation of fungi using fine needles and the mountant Hoyer's medium. This study has expanded the taxonomic base of the fungi in India.

Key words: Laboulbeniales, Cockroach, Ladybug, Parasite

Studies on the role of enzymes in degrading explosives present in environmental samples

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Abstract

Environmental contamination by explosives leads to deterioration in the quality of human health and ecosystem. It is necessary to treat explosives to ensure environmental safety. Technologies based on bioremediation (BR) have gained importance in recent times due to their eco-friendly nature. Among the BR approaches, enzyme-mediated explosive degradation is being evaluated for explosive remediation. Various classes of enzymes have been reported for the degradation of explosives, and can be classified as a) nitro-reductases, which are responsible for the initial reduction and conversion of nitro groups to amino groups, b) oxidases such as peroxidases or dehydrogenases that lead to the oxidation of reduced compounds into less toxic molecules; c) hydrolases like esterase and nitro-reductases that catalyze the breakdown of ester and nitro groups, and d) lyases, that break the specific carbon-nitrogen bonds. Enzymatic degradation of explosives involves several biochemical processes viz; recognition, binding, electron transfer; and sequential degradation reactions. Different analytical techniques are being used for qualitative & quantitative estimation of enzymatic degradation of explosives viz., Liquid Chromatography-Tandem Mass Spectrometry, Gas Chromatography-Mass Spectrometry, Enzyme-linked Immunosorbent Assay, and Polymerase Chain Reaction. These can provide valuable insights into potential enzymatic pathways aiding in the understanding of degradation mechanisms. Studies have been planned to evaluate the role of enzymes involved in BR of explosives-contaminated wastewater (WW) and soil. In biological WW studies, investigation of enzymes involved in a treatment chain consisting of a continuous stirred tank reactor (CSTR1 & CSTR2) operated in sequential mode followed by a hybrid anoxic reactor (HAR) will be done with the help of acclimatized chemoheterotrophs and chemoautotrophs. In soil BR studies, both the aerobic & anaerobic conditions will be evaluated by maintaining saturated (water-flooded) and unsaturated conditions at field level. Understanding the enzymatic role will help in safe disposal and efficient degradation of explosives.

Keywords: Bioremediation, Explosives, Enzymes, Nitro-reductases, Wastewater

Treatment technologies for field-scale remediation of explosive contaminated soil

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Abstract

Explosive contamination in soil occurs as result of production of munitions, explosives transportation, testing of ammunitions and training or waste disposal activities of unexploded ordnance (UXO) etc. Soil contamination due to persistent explosives has been reported across the world and needs to be remediated. War zones often have remnants of unexploded ordnance and explosive chemicals deposited in the form of chunks, particulates, both on surface/ subsurface soil. Natural processes such as leaching, runoff, rainfall, etc can cause migration of these explosive chemicals from soil to surface and groundwater resources posing a long-term threat to the ecosystem. As explosives are hazardous chemicals and are known to possess toxic and reactive properties, environmental contamination by explosives pose serious threats to the ecosystem affecting both flora and fauna. Human health related ailments such as convulsions, anaemia, liver damage, neurological disorders etc. have been reported due to repeated exposure to explosive contamination. Remediation technologies based on biological, chemical and biological methods have been extensively studied at lab-scale levels for treating explosives contaminated soil. Further testing and validation at pilot/ Field scale level is necessary before actual implementation at site. The field scale studies also provide a road map for further amendments or research to enhance the efficiency of method/technology at field scale. This review assesses the various biological, chemical, and physical treatment technologies, both ex-situ and in-situ available for pilot and field scale remediation of explosive contaminated soil, along with their technical feasibility, cost-effectiveness, advantages, and disadvantages. Few integrated field scale remediation methods are also discussed. In the study, the biological integrated methods of treatment are found to remediate the contaminated ecosystem more effectively. These integrated methods also incorporate the sustainable development approach by being cost effective and having less environmental footprint. This paper also throws light on the emerging trends in field-scale remediation of explosive soil. We have explored the existing knowledge gaps and key challenges in field scale soil remediation for explosives and finally future research prospects are discussed. This review aims to provide useful information to scientific and industrial community on the development and application of more suitable site-specific remediation technology for explosive contaminated soil.

Keywords: Field-scale Studies, Explosives, Soil, Sediments, Treatment methods



Unveiling the power of microorganisms in nanotechnology

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Abstract

Microorganisms coexist with almost every living creature on Earth and are an integral element of life as we know it. Compared to the human microbiome, the environmental microbiome is far more varied. It has been stated that cultivating most environmental microorganisms in a lab is a challenging task. The human body can include three types of bacteria: pathogenic, opportunistic pathogenic, and beneficial, despite the fact that both pathogenic and beneficial microbes may be prevalent in the environment. Microbes as a normal flora are essential to human survival since they have at least ten times the number of cells as human cells. Human health is largely dependent on the bacteria that inhabit our bodies, and the composition of our microbiomes is influenced by the microbiome in our surroundings. Microbes have emerged as an invaluable resource for human advancement in the fields of agriculture, medicine, the environment, and industry within the revolutionary field of microbiological technology. The process of creating nanomaterials is driven by the various proteins found in biological systems, and it is straightforward, economical, easily scalable, and environmentally benign. Microbes are the most significant of these living entities due to their diversity in terms of population and ecological niches, high rate of productivity, effective and dynamic metabolic machinery, simplicity of manipulation, and susceptibility to artificial growth and culture. As a result, they are now the subject of research in the developing field of microbial nanobiotechnology, where nanomaterials are being created for a variety of uses. In this regard, it has been discovered that several substances, including proteins, enzymes, lipids, pigments, polysaccharides, and biosurfactants, are helpful to microorganisms in the intra- or extracellular production of nanomaterials.

Keywords ***-Microbiology, Microbial technology, Nanotechnology ,nanobiotechnology, microorganisms, environment.***

Controlling microbes by using natural herbs instead of fully reliance on medicine

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Abstract

This study explores the potential of natural herbs in treating life threating Diseases and their action on human body. Using natural herbs such as turmeric, sage, dandelion, ginger, Echinacea. They contain a wide range of bioactive compounds that can work together synergistically to promote health. Addressing not just the symptoms but also the root cause of an ailment with almost no side effects.

This study also explores the using both allopathy medicine as well as herbs in treating various diseases. we know that allopathy medicines has many side effects.

Furthermore, the herbs as a sustainable alternative to conventional chemical using in medicines, contributing the advancements of eco- conscious practices in medicinal field.

This experiment setup involves study of the components, which are present in natural herbs that helping in treating disease and try to find that these bioactive compounds make artificially or not.

Key words: Controlling microbes, using natural herbs

Mitigating the Global Gut Microbiota Crisis through Sustainable Development: An Interdisciplinary Approach

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Abstract

The global gut microbiota crisis poses a critical threat, caused by factors such as dietary shifts, antibiotic misuse, and environmental pollutants native to modern life. Statistical projections indicate an alarming acceleration in dysbiosis rates, demanding urgent intervention to avert severe consequences. This paper proposes a multifaceted approach to addressing the crisis through sustainable development practices by analyzing various mitigative proposals from around the world and hopes to implement them before we face any more extinctions of the microbial species in the gut. By analyzing the statistical data via mathematical models of disappearing gut microbiota species, this paper seeks to draw attention to the severity of this crisis in hopes of mitigating this critical situation in time. By integrating sustainable strategies into microbiome restoration efforts, we aim to identify and tackle its root causes. Statistical analysis is used to identify critical intervention points, emphasizing the potential impact of sustainable practices on crisis mitigation. Practical implementation of these strategies is explored, showcasing their feasibility and efficacy in promoting gut microbiome health and environmental sustainability focussing on India. By recognizing the interconnectedness of microbiome health and sustainable development goals, an effort is made to align it with principles of responsible consumption, environmental conservation, and equitable healthcare access. Case studies demonstrating successful integration models from around the world are used to highlight the symbiotic relationship between human health and global ecosystem well-being. This approach calls for interdisciplinary collaboration prioritizing microbiome restoration within global health and environmental governance frameworks. By heeding this call to action, we can collectively steer away from crisis and pave a path towards a healthier, more sustainable future for India.

Key words: Mathematical models, Gut microbiota, Intervention point, Microbiome restoration, Case studies, Interdisciplinary collaboration

Assessment of synergistic effect of *Azardiarachta indica* extract in limiting the growth of *Micrococcus luteus* by kanamycin

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Abstract

Bacterial resistance to antibiotics poses a significant global health concern, prompting exploration into alternative treatments. Medicinal plants offer a potential solution due to their historical use in combating infectious diseases. *Azadirachta indica*, commonly known as neem, is one such plant with promising bioactive compounds. This study was carried out to investigate the synergistic effects between *Azadirachta indica*-derived compounds and antibiotic (Kanamycin) for combating bacterial resistance using a gram-positive bacterium, *Micrococcus luteus*.

The experiment proceeded in two stages. Initially, n-hexane, Chloroform, Methanol, and aqueous extracts of phytochemical compounds from plant were prepared from the leaves of *Azadirachta indica* using Solvent extraction methods. Subsequently, the synergistic effects of combining these compounds with antibiotics were studied across various concentrations. Minimum inhibitory concentrations (MIC) were determined through Disc Diffusion analysis to assess the efficacy of the combination of Antibiotic and plant extracts. Out of all the extracts the maximum results were observed in the Chloroform extract of the plant with zone of Inhibition of 17 mm togethear with antibiotic as 10 mm was observed in case of antibiotic and 5 mm in case of Chloroform extract of the plant alone. While other extracts showed no shift in their activity. We are further carrying forward the study in more diversified ways.

Key words- bacterial resistance, synergistic effects, antibiotics, Micrococcus luteus, Minimum inhibitory concentrations

Quality and yield enhancement of spinach using a novel cyanobacterial nutri-fertigation strategy

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Abstract

Spinach is a highly popular flavorful and nutritious leafy vegetable crop, accessible and enjoyed by all sections of the society. Hence, making it more enriched in phytonutrients assumes significance in agri-horticulture, towards the SDG's goals aimed towards ensuring *good health and well-being*. The use of microbials, as seed coating, and follow-up with drench application at different stages of maturity, through the use of cyanobacteria-based mixes was envisaged towards stimulating the growth, soil nutrient availability and quality aspects of Spinach (*Spinacia oleracea; Pusa All Green variety*), grown under shade net conditions. Cyanobacterial treatments led to substantial enhancement, along with significantly higher values in terms of pigment content, enzyme activities of N and C-assimilation enzymes such as nitrate reductase, glutamine synthetase and in leaves. Among them, the use of *Anabaena laxa* (RPAN8) led to a notable increase in spinach yield, while *Nostoc carneum* (BF2) stimulated quality traits, including ascorbic acid, antioxidants and β carotene. The treatment with *Anabaena laxa* (C11) was significantly superior in terms of growth, soil microbiological, yield and quality attributes. Principal Component and Path coefficient analyses illustrated interesting and strong positive correlation of leaf ascorbic acid with soil chlorophyll and available iron, as well as direct effects of availability of nitrogen in soil with leaf attributes at all growth stages. The novelty of this research lies in the development of a nutrient-enriching strategy, which is also an eco-friendly organic option, for boosting spinach cultivation.

One Health Approach: Integrating Human, Animal, and Environmental Microbiology

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Abstract

The microbiological realm, with an extensive variety of microscopic creatures, is of great importance to human health and environmental sustainability. The various roles that bacteria play are examined in this abstract, from their vital contributions to human health to their crucial involvement in preserving ecological equilibrium. Microbes have two roles in the context of human health: they can be both allies and enemies. Beneficial microorganisms fill a variety of specialized roles in the human body, supporting vital processes including mood management, immunity, and digestion. Additionally, new studies have shown that some microbial strains may be used therapeutically to treat a variety of illnesses, from mental health issues to gastrointestinal disorders. On the other hand, pathogenic microorganisms present serious risks to human health, leading to infectious diseases that have traditionally presented enormous obstacles to the advancement of medical knowledge. In order to develop strategies to promote health and combat disease, it is essential to comprehend the complex interactions between beneficial and dangerous bacteria. Outside the boundaries of human physiology, bacteria have a significant impact on the sustainability of the environment. Microbial communities in natural environments are responsible for waste breakdown, soil fertility, and nutrient cycling, which supports the stability and productivity of both terrestrial and aquatic ecosystems. Additionally, bacteria are essential to bioremediation because they help pollutants and toxins in soil, water, and air to break down. Using microorganisms' metabolic potential presents a viable strategy for reducing pollution in the environment and repairing damaged ecosystems. Furthermore, cutting-edge developments in biotechnology have opened up new uses for microbial systems in a variety of industries, such as waste management, energy production, and agriculture. Microbial strains that have been engineered are being used to increase crop yields, generate biofuels from renewable resources, and make it easier to turn organic waste into useful goods.

Key words: Microbiology, Human health, Environment, sustainability, Technology, Nanotechnology

Utilizing *Aloe vera* gel as a mordant for dyeing silk fabric using *Jatropha curcas* extract

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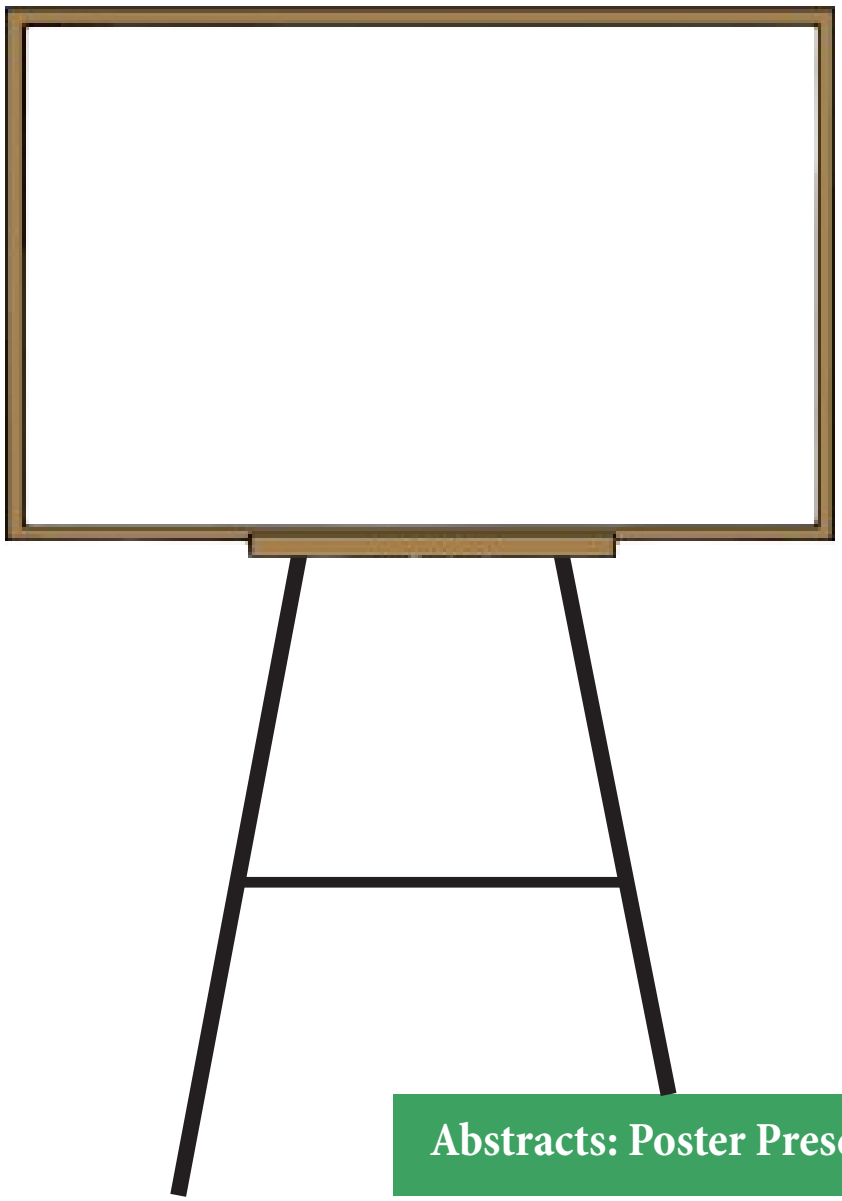
Abstract

This study explores the potential of *Aloe vera* gel as a mordant in the dyeing process of silk fabric using *Jatropha curcas* extract. Silk, renowned for its luxurious feel and sheen, has been historically dyed using various natural dyes for centuries. However, the challenge lies in achieving durable and vibrant colors on silk fabric, which necessitates effective mordanting techniques. ***Jatropha curcas* L.,** a plant recognized for its rich pigment content in its leaves and stems, presents a promising alternative for silk dyeing and therefore we will be using this. ***Aloe vera* L.**, known for its mordant properties and natural affinity to textiles, can be used as a sustainable and eco-friendly option. The experimental setup involves the extraction of pigments from *Jatropha curcas* stems and leaves and subsequent dyeing of silk fabric under varying conditions, including different concentrations of *Aloe vera* gel mordant and dye bath. The effectiveness of *Aloe vera* gel as a mordant is evaluated through various colorfastness tests, such as lightfastness and wash fastness, as well as spectroscopic analysis to ascertain the color intensity and depth achieved. This study will help us to optimize the use of *Aloe vera* gel as a mordant in enhancing the color retention and durability of *Jatropha curcas* dye on silk fabric. Furthermore, the eco-friendly nature of *Aloe vera* gel and *Jatropha curcas* dye complements their potential as a sustainable alternative to conventional chemical mordants and dyes, contributing to the advancement of eco-conscious practices in textile dyeing.

Key words: Natural dye, *Jatropha curcas* extract, *Aloe vera* mordant, Colourfastness, Silk fabric dyeing

Poster Presentation

ABSTRACTS



Abstracts: Poster Presentation

Study of development in the Laboulbeniales

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Abstract

The fungal group Laboulbeniales are a unique group belonging to the Ascomycota. They include an estimated 115 genera, that are obligate exo-parasites of arthropods as biotrophs and for dispersal. They parasitize members of many insect orders, coleopteran insects being the most common targets. This study looks at the developmental details of the fungi. They are unique in that there is a complete lack of a mycelial stage. Since anamorphs have not been observed, it can be assumed that asexual reproduction is absent. The thalli may be monoecious or dioecious. The carpogonium is the female sex organ and the antheridium is the male sex organ. In the monoecious species the antheridia and carpogonia occur on adjacent branches. However, in dioecious species there are separate male and female thalli. They may be very different in structure or show small differences in the final stages of development. The perithecia also show variations. They may be one or more and formed laterally or terminally. The ascospores are produced by free cell formation. When liberated, they attach to the host and germinate to form the new thallus, skipping the mycelial stage throughout the lifecycle.

Keywords: Laboulbeniales, arthropods, development

Phylogenetic relatedness of diverse soil bacteria: an indicator of ecosystem functioning

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Abstract

Soil is an intricate and varied biological niche that is home to a wide variety of microorganisms, predominantly bacteria. Microorganisms in soils are involved in several ecological activities, such as the decomposition of organic matter, the fixation of nitrogen, and the immobilization of nutrients, that are vital to the sustenance of ecosystems. Species richness has traditionally been used to analyze the relationship between biodiversity and ecosystem functioning. Phylogenetic studies would therefore be useful to identify if the species are evolutionarily related and thus depict functional similarities. Comparing and analyzing the genomes of several soil bacteria would be instrumental in order to understand the complexity and evolution of these genomes. In this study molecular phylogenetics of the whole genome, 16S rRNA genes and key housekeeping genes of soil bacterial species belonging to varied soil types was performed. The phylogenetic relationships of bacterial communities in the different soils types consisting of their inherent set of abiotic factors would predict ecosystem functioning and management stratergies.

Keywords: Microorganisms, Soil, Phylogenetics, ecosystem, biodiversity

Developing eco-friendly based modules strategies for management of sheath blight in rice

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Abstract

Rice (*Oryza sativa* L.) is an important and extensively cultivated second largest cereal crop in the world. Production of rice is 111.76 million tones in kharif season of 2021-2022. Efforts for enhancing the productivity are limited by a number of biotic and abiotic stresses. One of the major constraints in rice production in this region is the increasing incidence of diseases and pests. The estimated loss due to sheath blight alone in India has been reported up to 51.3%. Management of diseases has been generally achieved by the use of synthetic pesticides but these are known to pollute the environment, soil and water, besides causing deleterious effects on human health and biosphere. A number of plants are known to possess antifungal activities which could be exploited for environmentally safe and eco-friendly method of disease management (Ray and Kumar, 2006). The use of botanicals an alternative method to chemical control. In an effort to develop eco-friendly measures for the control of this disease, were screened eight plant extracts viz., *Azadirachita indica, Lawsonia inermis, Zingiber officinale, Trachyspermum capcicum, Allium sativum*, *Lantana camara, Ocimum sanctum and Citrus lemon* against *Sclerotium oryzae*. Leaf extracts of *Allium sativum* and *Azadirachita indica* inhibited maximum mycelial growth of *S. oryzae* at all three tested concentrations viz; 5%, 7.5% and 10%, were found significantly more effective as an alternative to conventional chemical fungicide.

A new record of *Oxytricha granulifera* Foissner and Adam (1983) from Delhi, India

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Abstract

Ciliated protists have been found in almost every habitat on Earth, demonstrating their wide global distribution. So far, reports of 700 free-living ciliates from India have been reported. When examined with modern methods, such as live observation and silver staining ('Silver Proteinate' or 'Silver Albumose'), supported by molecular taxonomic analyses, the true diversity of free-living ciliates from India is expected to exceed 2,000 species. The present investigation aims to report a species *Oxytricha granulifera* Foissner and Adam (1983) which is a new record to the Indian diversity. *O. granulifera* is isolated from a pond of Nand Nagri as well as a lake of Kamla Nehru Ridge, Delhi, India. The morphology and morphogenesis of Indian population of *O. granulifera* is described on the basis of protargol impregnation. The morphological features of *O. granulifera* are as follows:Size of protargol impregnated cell about 70x18 µm;two macro-nuclear nodules and 2 micronuclei; 18 Frontal-Ventral-Transverse(F_{1-8},V_{1-5},T_{1-5}) cirri; five dorsal rows of bristles (DK_{1-4} and DM_1); 3 caudal cirri; on an average 27 adoral membranelles; 24each right and left marginal cirri; flexible body; flat and narrow buccal cavity, and the undulating membranes (UM_S) in the typical *Oxytricha* pattern; characteristic colourless cortical granules are present.

Incredible Indian woman scientist: Their contribution to put India in global map

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Abstract

All over the history of science, woman have played a significant role in discovering and developing uprising devices. Science is sometime considered a male influenced area especially in Indian community. But the field is rich with many famous female Indian scientists who contributed their rich knowledge to the society. They have contributed into many important discoveries in several fields of the science. Even their lives are the role models for all girls who aspire to make a mark in the field of science and technology. They left an indescribable effect both before and after the independence. Tessy Thomas, Soumya Swaminathen, Gagandeep Kang, Sunita Sarawagi and Ritu Karidhal are the some of the Indian woman who made the country proud in post-independence era. The dilemma is not that there aren't enough woman in the field of science, but they are not well recognized and not credited for their achievements. Therefore present study is dedicated to bring out success stories of post-independence Indian woman scientist who defied all hurdles and left a magnificent mark on history of Indian science.

Key words: Woman scientist, Woman in science

A new fresh water ciliate *Aponotohymena australis* (Foissner & O'Donoghue, 1990; Foissner, 2016) from Delhi, India

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Abstract

The present study aimsto report and describe the morphology as well as morphogenesis of *Aponotohymena australis* (Foissner & O'Donoghue, 1990; Foissner, 2016)which is a new record to Indian fauna. The cells of *A. australis* are reported from the ponds of Ramghat, Wazirabad & Nehru Vihar, Delhi India. This genus is recently created by Foissner in 2016. The type species of this genus, *A. australis* was first named as *Oxytricha austalis* and later redesignated as *Notohymena australis*. However, recently it is further redesignated as *Aponotohymena australis*. According to Foissner (2016), the genus *Aponotohymena* differs from the genus *Notohymena* only in the number of caudal cirri. Only three species of this genus are reported till date namely *A. australis*, *N. apoaustralis*&*A. isoaustralis*. The morphometric and morphogenetic features are based on protargol staining. The morphometric feature of *A. australis* include: flexible body; size of protargol stained cell 90x26 µm; body shape ellipsoidal; 18 Frontal-ventral-transverse(F_{1-8}, V_{1-5}, T_{1-5}) cirri; Six dorsal rows of bristles (DK_{1-4} and DM_{1-2});7-8 caudal cirri; on an average 35 adoral membranelles; 35 right marginal cirri; 35 left marginal cirri; flexible body; buccal cavity large and deep; undulating membranes (UM_S) in the typical *Notohymena* pattern; yellowish orange sub-pellicular cortical granules present.

Exposure of BPA induces renal toxicity in *Drosophila melanogaster*

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Abstract

Bisphenol A (BPA) is an emerging organic pollutant, widely distributed and frequently detected in soil in recent years. BPA is used as a monomer to manufacture various plastic products**.** Enormous usage of BPA has increased production worldwide, hence the estimated global volume of BPA utilization in 2015 is 7.69 million metric tons, while the production is increased 10.7 million metric tons in 2020 and is expected to reach 12,169 metric tons by 2031. Due to abundance presence in the environment, BPA toxicity is a problem that needs to be solved in terms of both human health and agriculture production. In the present study, we have investigated impact of BPA exposure on renal organs of *Drosophila melanogaster*, a genetically tractable model organism. Our results suggest that BPA causes renal impairment by oxidative stress in *Drosophila melanogaster.*

Prevention methods of microbial infection in fishes

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Abstract

Aquaculture is one of the fast growing sector of agricultural. 44% of the fish production by aquaculture. There are many challenges of fish production due to different infectious diseases. Infectious diseases of fish impact the production of fish. Fish infections caused by Viruses, fungi, parasites. Naturally majority of microbes are occurring in water. Due to poor environmental conditions, and inefficient fish husbandry and limit of nutrition practices, fish only cause diseases. In fresh water fishes infected by Pseudomonas Acinetobacter bacterial gill diseases. Betterment of the fisheries the prevention of fish diseases is essential. This article therefore gives an overview of bacterial fish microbes with a focus on some common features of pathogenicity. This article aims to highlight complete details about parasites and bacterial infections of fish and how they can be prevented in aquaculture.

Keywords: Fish, Pathogenicity, Aquaculture, Diseases

Nanobiofertilizers: Enhancing soil health and sustainable agriculture with Nanotechnology and Plant Growth-Promoting Microorganisms

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Abstract

The indiscriminate use of chemical fertilizers in modern agriculture poses a grave threat to soil integrity, water quality, and overall ecosystem health. This widespread practice leads to soil structural degradation, water pollution, eutrophication, soil toxicity, and nutrient depletion, with far-reaching consequences for both the environment and human well-being. To ensure the long-term sustainability of agriculture, there is an urgent need to prioritize the management of soil health and nutrients. In response to these challenges, the development and adoption of nanobiofertilizers offer a promising avenue for improving soil fertility and agricultural sustainability. Nanobiofertilizers employ various strategies to enhance soil health and nutrient availability. Firstly, they contribute to the restoration of essential nutrients through mechanisms such as nitrogen fixation and phosphorus solubilization, ensuring that crops receive adequate nutrition for optimal growth and yield. Moreover, nanobiofertilizers bolster the soil's nutrient absorption capacity, facilitating efficient uptake by plants and minimizing nutrient leaching. Additionally, nanobiofertilizers play a crucial role in mitigating the harmful effects of heavy metals in soil by producing siderophores that chelate iron and sequester heavy metals, rendering them inaccessible to plants and reducing their toxic impact. Furthermore, these innovative fertilizers stimulate the production of phytohormones and compatible solutes, promoting plant growth and stress tolerance in adverse environmental conditions. By conserving soil moisture and enhancing resistance to both biotic and abiotic stresses, nanobiofertilizers contribute to the overall resilience of agricultural systems. One of the key benefits of nanobiofertilizers is their ability to enhance nutrient use efficiency in plants, optimizing resource utilization and minimizing waste. Through a combination of these diverse strategies, nanobiofertilizers represent a promising solution for sustainable agriculture, offering a path towards improved soil health, increased crop productivity, and reduced environmental impact.

Keywords: Nanobiofertilizers, agricultural sustainability, soil fertility

Physico-chemical properties of Jojari river Western Rajasthan, Jodhpur

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Abstract

In the present study the effects of Textile industrial effluent on Jojari river water was investigated at Jodhpur district of Rajasthan. The physicochemical analysis was done for one year and the present reveals that, the pH of River water is more than the standard levels and the other parameters of the river water was found to be higher in concentration. On the basis of these observation it can concluded that the river water is adversely affecting, which affects on aquatic environment and human beings of surroundings.

Key words: Water, River, Environment, Rajasthan.

Exploration of microbes from Baratang mud volcano of Andaman and Nicobar Islands and study of their iron tolerance behavior

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Abstract

Mud volcanoes are not true volcanoes as they do not produce lava; instead they are mainly topographic elevations builds from active mud discharge triggered by high pressure gas that squeezed out in the fault zones of sedimentary basin. The mud oozes out from the deep subsurface layer of the Earth's crust; it may provide the visualization to the deep, extreme as well as unique microbial environment. In this study the ICP-OES analysis shows the iron concentration is about 57.23 mg/L. Total 16 bacterial isolates were studied from the mud samples, they were capable to tolerate high concentrations of $FeSO_4$ as BRTN (500 mg/L), KS7 (400 mg/L), KS14 (300 mg/L), and KSB3 (300 mg/L). Optimum growth of isolates was found at pH 6.0 and they can tolerate up to 9.0 g/L NaCl. All these 4 isolates can form iron nanoparticle in the presence of 1:1 ratio of $FeSO_4$: bacterial samples, confirmed by color changes. Further characterization of nanoparticle has been done by scanning electron microscopy, transmission electron microscopy, fluorescence and UV-Vis spectrophotometer. Whole genome study and RAST analyses on BRTN identified as Bacillus sp. associated with 3.35 Mb genome, GC 35.9% and 3,514 genes. A significant number of genes related to iron-sulfur cluster assembly (9), siderophore (8), iron acquisition and metabolism (16) have been observed. Genome comparison was also performed using different bioinformatics tools. The genome size of BRTN is small in compared to closely related Bacillus sp. It is known that the iron concentration during the early life of Earth was high, interestingly our mud sample contains high iron concentration and the isolate BRTN can tolerate high concentration of iron about 500 mg/L. So, this present study will help to understand the life of microbes in mud volcano as well as in primitive Earth.

Keywords: iron, microbes, mud volcano, nanoparticle, RAST

Wastewater: Contaminants, implications and solutions

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Abstract

Rapid urbanisation and industrial developments along with agricultural and domestic use has substantially increased the amount of pollutants and untreated wastewater. Wastewater production as extrapolated from aggregation analysis on a regional basis for seven regions: Asia, Sub-Saharan Africa, Middle East and North Africa, Europe, Latin America and Caribbean, North America and Oceania, is estimated to be 360-380 billion m3 annually across the world. The dominating contaminants of wastewater can be categorized into pesticides and hydrocarbons, heavy metals, dye derivatives, petrochemical derivatives, antibiotics and pathogenic microorganisms having proven health effects. Several nations on the recommendation of WHO, have formulated standards and guidelines for wastewater disposal and re-use. Bioremediation and phytoremediation based technologies such as activated sludge, oxidative ponds, trickling filters, biofilters and biofilms, bioreactors have been attempted for the wastewater treatment and re-use purposes. Improvements with the addition of biochar and nanoparticles have also been reported. Recent innovations include use of artificial intelligence for computing predictive models such as artificial neural networks (ANNs), support vector machines (SVMs), and recurrent neural networks (RNNs), adaptive neuro-fuzzy inference system (ANFIS), genetic algorithms (GA), and particle swarm optimization (PSO)
Hence, studies on disposal and treatment of wastewater at global scale are required in compliance with the sustainable development goal 6 (Clean water and sanitation) and SDG 6.3 (SDG 6.3, Improve Water Quality, Wastewater Treatment and Safe Reuse), to achieve improvements in treatment methods for it's safe disposal and reuse.

Key words: Wastewater, SDG goals, bioremediation

Tracking the emergence and spread of antimicrobial resistance (AMR) in bacterial populations: A Metaproteomics Approach

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Abstract

Significant shifts in the composition and diversity of the microbiome are linked to modification of lifestyle, nutrition, and medication over a period of decades. Meanwhile, many diseases associated with these modifications and their consequences thereof, are emerging. Noncommunicable diseases (NCDs) kill 41 million people each year, equivalent to 74% of all deaths globally. Metaproteomic focuses on studying the entire complement of proteins present within a microbial community for disease detection. Unlike traditional proteomics, which typically analyses proteins from a single organism or cell type, metaproteomics aims to characterize the collective proteome of all microorganisms present in a given sample. It offers valuable insights into the structure, function, and dynamics of microbial communities in different environments. Recently, it was shown that in case HIV (Human immunodeficiency syndrome) infection, higher levels of proteins belonging to complement system was detected in CSF (cerebrospinal fluid) of patients. Furthermore, Metaproteomic studies can track the emergence and spread of antimicrobial resistance (AMR) in bacterial populations. Studying the proteome of pathogenic bacteria, one can identify AMR-linked proteins. Such studies can elucidate the specific mechanism and pathways involved in resistance, such as efflux pumps, target enzymes and enzymatic inactivation of antibiotics in resistant bacterial populations. It has far reached applications in environmental monitoring; studying the proteome of microbial communities in soil, water, and other ecosystems. We can assess environmental health, control pollution levels, and diagnose microbes with potential bioremediation capabilities.

Overall, metaproteomic studies offer valuable insights into the structure and function of microbial communities by characterizing the proteome in depth, which was not possible earlier.

Key words: Metaproteomics, Disease, Health, Microbial, Microbiome, Re-emergence

Isolation and Characterization of Lactic Acid Bacteria (LAB) Isolated from Arrowroot (*Maranta arundinacea* L.) for Probiotic Development

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Abstract

Arrowroot (*Maranta arundinacea* L.) is recognized for its abundant reserves of starch, fiber, and carbohydrates including maltodextrin and fructo-oligosaccharides, crucial prebiotics that facilitate the proliferation and viability of lactic acid bacteria. This aim of this study is to isolate and characterize potential lactic acid bacteria from the arrowroot, with the objective of formulating an arrowroot-based probiotic beverage. Arrowroot samples, encompassing fresh rhizo mes were collected from the Palakkad district, Kerala, India. Lactic acid bacteria (LAB) were directly isolated from fresh arrowroot and enriched arrowroot samples at the dilutions of 10^{-6} and 10^{-8}, employing MRS (de Mann, Rogosa, and Sharpe) selective agar medium. Five isolates, designated as PAR-1 to PAR-5, were selected and characterized for their probiotic properties and morphology. Each of the isolates stained gram-positive with coccus and rod-shaped cell. In terms of sugar utilization, PAR-3 and PAR-5 demonstrated metabolic activity with all five sugars (dextrose, sucrose, maltose, lactose, and fructose) without gas formation. Notably, PAR-3 and 4 exhibited substantial growth even at elevated concentrations of bile salts (3% and 5%), whereas PAR-1 and 2 displayed reduced growth under these conditions. Similarly, PAR-3 displayed maximum growth at lower pH levels (2, 3, and 4) after 4 hours of incubation. Consistent results were observed across various temperatures (4°C and 37°C) and NaCl concentrations (8% and 10%). Antibiotic susceptibility test showed PAR-3 and PAR-5 were resistant to penicillin, gentamicin, and vancomycin. Hence, PAR-3 and PAR-5 were selected as the most promising isolates suitable for the development of arrowroot probiotic beverages.



Linking Sleep Deprivation to its impact on Gut Microbiome

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Abstract

Sleep is a periodic occurrence in a living organism's schedule. From the simplest bacteria to the highest-level vertebrates, the complexity of sleep has evolved with life itself. In the past decade, there has been an exponential growth in research linking the microbiome-rich 'gut-brain' in higher animals, to the phenomenon of sleep. It is largely described as a bidirectional relationship along the microbiome-gut-brain axis, where microbial taxa and their short-chain fatty acid metabolites significantly impact the circadian rhythm while anomalies in this rhythm have been shown to disrupt the gut microbiome. With sleep deprivation rapidly becoming a global public health epidemic, this literature review chooses to focus on the second aspect, connecting circadian disruptions to their impact on the gut microbiome. Research papers from the past ten years have been considered for this review in order to provide an overview of the most recent developments. As antibiotics also significantly alter the gut microbiota and are known to decrease diversity, this review hopes to offer further insights to medical practitioners while prescribing antibiotic medications to patients with existing sleep disorders. Studies have shown that a deficit in sleep can change the composition of the gut microbiota within a few hours. Sleep deprivation has been correlated with abnormality in hormone secretions, damage to intestinal barriers, and with disorders like Inflammatory Bowel Disease (IBD). Interventions in the form of improved sleep quality for extended periods or external melatonin supplements appear to impact the gut by increasing short-chain fatty acid production. This reinforces how sleep deprivation alters the gut ecosystem and places it as another important factor to be considered when studying the far-reaching effects of sleep deprivation on human health.

Keywords: Gut microbiome, microbiota, microbiome-gut-brain axis, sleep deprivation, antibiotics

Standardisation and testing the efficacy of thermostable DNA polymerase from Indian isolate *Thermus parvatiensis* strain RL

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Abstract

The hot water springs have always attracted considerable attention as they provide an ideal niche to exploit microbes for biotechnological application and understand microbial life under such environment of high temperature. The genus *Thermus* is the most dominant group concerning thermophilic bacteria studied so far. The first thermostable DNA polymerase characterized and applied in PCR was Taq DNA polymerase isolated from *Thermus aquaticus*. Today this enzyme (Taq DNA polymerase) has formed the basis of million-dollar industry. According to the report of Market Future Insights, DNA polymerase market is of US$ 353.9 million and expected market value in 2033 is US$ 647.5 million. Our group has successfully cloned and expressed DNA polymerase gene (*Tpa)* from *Thermus parvatiensis* in *E. coli*. We are now planning to scale-up the production of this thermostable DNA polymerase in *E. coli* by developing a cost effective and scalable fermentation medium that supports high density cell growth and optimal polymerase production. Optimization of downstream processing and pilot scale testing will be done to validate the feasibility and efficiency of the process. This poster represents experimental plan for the upscaling of this thermostable polymerase using pilot scale fermentation and transition it to industrial scale. Overall, this "Made in India" initiative for enzyme production holds significant promise for India's economic growth, scientific advancement, and strategic security. By addressing the challenges and leveraging its vast biological resources and scientific talent, India can become a major player in the global enzyme market.

Keywords: Thermozymes, thermostable polymerase, fermentation, protein-processing, industrial application.

Effect of evolutionary influence on high antimicrobial resistance of *Clostridioides difficile* and its possible implications

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Abstract

Clostridioides difficile (*Clostridium difficile*) formerly a member of the anaerobic Gram-positive bacterial genus *Clostridium* was reclassified to the family *Peptostreptococcaceae*, genus *Clostridioides*. Infections caused by *Clostridioides difficile* pose serious threat to public health due to them being highly resistant to antibiotic treatment. The pathogen shows resistance to antibiotics like fluoroquinolones, penicillin, clindamycin etc. and disinfectants used in hospitals like ethanol. This study dives into the process of evolution of antibiotic resistance in *Clostridioides difficile* through bacteriophages, transposable elements and homologous recombination while also comparing its characteristics to similar bacteria within the genus, *Clostridium*. *Clostridioides difficile*'s commendable capacity to adapt quickly, particularly in response to the pressures generated by antibiotics treatment is what is explored here. Furthermore, we draw comparisons between the evolutionary trends observed in antimicrobial resistance among *Clostridioides difficile* strains and those seen in other species of *Clostridium* bacteria, illuminating potential differences in their genetic makeup and clinical implications. Methods like restriction endonuclease analysis and pulse field gel electrophoresis are used for microanalysis of genome architecture. Procedures like PCR ribotyping and toxinotyping are commonly used for identification of single regions within the chromosome of the species genome. MLVA, and MLST can be used for strain discrimination, followed by high-throughput sequencing methods like Illumina can be used for genome analysis. Whole-genome sequencing has advanced the knowledge of *Clostridioides difficile* infection outbreaks, transmission, and recurrence significantly, shedding light on zoonotic transmission potential of the disease caused by the species. Moreover, the scope of this can be expanded to the study other antibiotic resistant bacteria showing similar modes of contagion. Ultimately, this study aims to widen our 'understanding of the complex evolutionary processes driving antimicrobial resistance in *Clostridioides difficile* infections, thereby providing essential insights for devising more effective strategies to manage and control these challenging infections.'

Keywords: *Clostridioides difficile,* antibiotic resistance, *Clostridioides difficile* Infections (CDI), Evolution

Lack of life history trade-off in *Drosophila melanogaster* populations with reduced lipid reserves

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Abstract

Immune system is constitutively active in all living organisms and maintenance of active immune function is energetically costly. In the context of life-history trade-offs hypothesis, any energy allocated to physiological systems responsible for maintenance of health and thus enhancing survival probability will not be available for reproduction- thus leading to reduced overall fitness. In order to test this, we used two populations of *Drosophila melanogaster*, one of which is selected for faster pre-adult development and elongated reproductive longevity and hence has reduced over all lipid reserves at emergence as adult compared to their control population, and tested the hypothesis that populations with reduced lipid reserves should invest less energy in immune function and thus should not be able to survive infection by *Pseudomonas entomophila*. Contrary to the hypothesis, the selected flies had longer survival under infection by pathogenic bacteria due to non-significantly heightened immune function suggesting the same.

CRISPR: From bacterial immune system to a promising cure for sickle cell disease

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Abstract

The world of microbiology has been a rich source of scientific breakthroughs. Among them, the discovery of CRISPR and its applications have gained an unprecedented level of attention and critique. Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)/CRISPR-associated (Cas) systems are a bacterial defence mechanism against bacteriophage invasion. These systems are of various types, with type II systems featuring Cas9 proteins, which rely on a base-paired structure formed between trans-activating RNA (tracrRNA) and targeting CRISPR RNA (crRNA) transcribed from the CRISPR locus. This complex mediates the cleavage of a specific region of the target double-stranded DNA (dsDNA) of the virus, thereby safeguarding the bacterium. The Cas9 endonuclease family can be programmed with single guide RNA molecules, enabling cleavage at specific DNA sites, underscoring their potential in gene editing.

Despite the longstanding debate surrounding the use of CRISPR-based therapies for human diseases since the advent of this system, the successful treatment of Sickle Cell disease using this technology represents a monumental breakthrough. A prevalent strategy in CRISPR sickle cell gene therapy involves gene knockout, silencing the gene responsible for suppressing foetal haemoglobin, thereby promoting the expression of foetal haemoglobin (haemoglobin F) to replace the mutated adult haemoglobin. An investigational new drug application, co-sponsored by CRISPR Therapeutics and Vertex Pharmaceuticals, represents a promising avenue for treating sickle cell disease. This illuminates the vast potential CRISPR-based therapies hold for disorders that have long evaded effective treatments and leaves us contemplating that our current understanding of this technology merely scratches the surface of its capabilities.

Key words: CRISPR, Sickle cell disease, Gene therapy.

Unraveling the impact of pathogenic infection on the insect microbiome

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Abstract

The microbiome is the community of all symbiotic microbes living on or in an organism, whether mutualistic, commensal, or pathogenic. The symbiotic association between insects and their microbiome plays a crucial role in enabling insects to survive in extreme conditions, shaping each other's evolutionary trajectory. Insect endosymbionts provide insights into the microbiome's impact on various biological processes. Effective antimicrobial signaling in insects to eradicate pathogens while tolerating commensal species allows the microbiome to actively participate in the gut homeostasis and immunity of the host. Moreover, increased pathogenic infection poses environmental pressures on insects, thereby driving microbiome adaptations that are crucial for their survival. We conducted microbiome analyses using our proprietary computational pipeline. Our results reveal that viral infections in insects such as *Drosophila melanogaster, Acyrthosiphon pisum, and Antheraea pernyi* result in dysbiosis of the microbiome, which is in contrast to *Culex pipiens*, potentially due to the presence of *Wolbachia* that is associated with reduced rates of viral infection. Nevertheless, bacterial and fungal infections in *Drosophila* showed effects, with no consistent trends in microbiome changes. These findings emphasize the role of viral infections in driving microbiome dysbiosis, providing insights into host-microbe interactions that are relevant to higher organisms, including humans.

Keywords: Microbiome, Endosymbionts, Pathogenic infection.

Myo-inositol and Beta-alanine as potential regulatory molecules for Human Prdx6

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Abstract

The protein Prdx6 is known for its multifunctional nature, displaying peroxidase, phospholipase, and lysophosphatidylcholine acyl transferase (LPCAT) activities. Despite extensive research, the specific domain responsible for regulating its enzymatic activities has remained elusive. Prdx6 comprises a thioredoxin fold and a C-terminal domain. While the thioredoxin fold is implicated in all observed activities of Prdx6, the precise role of the C-terminal domain remains unclear. It is suggested that alterations in the C-terminal region may influence the structure of the thioredoxin fold, thereby affecting its functionality. Studies involving systematic mutations within the C-terminal region have shown increased enzymatic activity, indicating a potential crosstalk between this domain and the thioredoxin fold. The C-terminal domain may act as a cis-acting regulatory site, with additional trans-acting elements likely involved in regulating the enzyme's structure and function. One intriguing possibility is the involvement of small molecule metabolites, which organisms accumulate alongside antioxidant enzymes like Prdx6 to safeguard against stressful conditions. In our investigation, we identified Myo-Inositol and Beta-Alanine as potential trans-acting regulatory molecules for human PRDX6. These molecules likely bind to the cis-acting regulatory site of Prdx6, modulating its function in response to cellular demands and environmental stressors. This discovery sheds light on the intricate regulatory mechanisms governing the activity of Prdx6 and provides insights into potential therapeutic interventions targeting this enzyme.

Estimation of bioaerosol concentration in the educational institutional environment: A case study from urban city of Delhi, India

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Abstract

Aerial suspension of dead or living biological particles found in aggregation with particulate matter are called bioaerosol, and is synonymous with the term "biological particulate matter" (bioPM).

Bioaerosol constitutes organisms such as bacteria, fungi, virus, pollen, plant debris, dander, etc. and their products like beta-glucans, endotoxins, mycotoxins, etc. that can be pathogenic or non-pathogenic in nature. Majority of the Indian population is below the age of 44 years, of which country specific reproductive fit age group ranged between 22-25 years. College students belonging to this age group spend most of their time (≈ 8-10 hours/day) inside the institutional campus and are continuously exposed to the biological contaminants present within indoor and outdoor built-up environments. The higher concentration of bioaerosol is responsible for the adverse indoor and outdoor air quality which relates to poor respiratory and general health effects, so monitoring of bioaerosol concentration at educational institutions is the need of the hour. This study aimed to determine the bioaerosol load in the different microenvironments of an educational institution using the traditional passive open plate method. It was also observed that bioaerosol concentration was crossing permissible limit (500 CFU m-3) set by various non-governmental and governmental agencies in indoor sites with poor ventilation and high occupancy (1392-1736 CFU m-2 min-1) compared to the indoor sites with good ventilation and low occupancy (142-189 CFU m-2 min-1). Also, there was a positive correlation of the bioaerosol concentration with temperature and negative correlation with relative humidity. Thus, to avoid exposure and potential health risk of attendees, documentation of source apportionment of each microenvironment within campus is urgently needed.

Keywords: bioaerosol, educational institution, indoor, outdoor, Delhi

In-Silico Study of the Phenolic Compounds on DNA Methlase 3A

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Abstract

Polyphenol are secondary plant metabolites which are used in several important activities in plant body for example protecting plant from the harmful UV radiation and several diseases. In nature these can be found in variety of sources like fresh fruits, vegetables, berries. Their structure is characterized by the presence of aromatic ring with at least one hydroxyl group, which help them to reduce the reactivity of nitrogen and oxygen generated as a result of the various metabolic activities. Thus, these can be considered as a good Antioxidants which can work in combination with Vitamins to reduce the inflammation. DNA methylation is an important epigenetic process which plays an important role during the cell growth and transfer of genetic material from one generation to other. In mammalian cell the methylation mainly occurs at the 5th position of carbon in cytosine within the CpG dinucleotides which forms around 80% of all the methylation occurring in the genome. Dysregulation in the vital process of DNA Methylation is subjected to diseases like 'Prostate Cancer'. It is one of the second major cause of death among males worldwide. Treatment of the Tumor Micro Environment (TME) may be helpful in the treatment of the Prostate Cancer. Polyphenol can be used as a major compound in the treatment with its 'Anti-Oxidant' activity. In this study a comprehensive library of Phenolic compounds was virtually screened and studied for the interaction and ADME properties using the software like the Pyrx, AutoDock 4.0, Discovery Studio Visualizer and SwissADME.

Effectiveness and Advancements of mRNA Vaccines in Combating Infectious Diseases

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Abstract

Messenger RNA (mRNA) vaccines have seen rapid advancements in the post-COVID era giving a new dimension to the vaccination strategies against infectious diseases. Recently, the use of mRNA vaccines for COVID-19 across the globe has proven the therapeutic efficacy in combating SARS-CoV-2 infections in human populations of different demographics.

The mRNA vaccination strategy largely depends on the effective delivery of modified mRNA encoding the antigen of interest in the Open Reading Frame (ORF) via suitable lipid nanoparticles (LNPs) into the host cells. These modified mRNAs must structurally mimic the eukaryotic mRNA in the host system to effectively trigger innate and adaptive immune response against the pathogen. This should also ensure stability and protection against recognition by cytoplasmic sensors of viral RNA and lead to the successful translation of the mRNA in the host cell.

mRNA vaccines are advantageous due to a variety of reasons especially in the case of pathogenic diseases with multiple variants like SARS-CoV-2, HIV, etc. as these vaccines are flexible and more resilient in response to rapidly mutating pathogens. These vaccines are relatively safer as they do not enter the nucleus thus, lowering the chances of integration in the genome or insertional mutagenesis. Owing to their cost-effective and large-scale production in cell-free systems they are free of contaminants compared to conventional vaccines. However, the logistic challenges concerning thermal conditions affecting the stability of the mRNA, the suitable selection of effective delivery systems, and long-term immune impacts are the constraints leveraging areas of further study.

Keywords - mRNA vaccines, Lipid nanoparticles (LNPs), infectious diseases

Gut dysbiosis-associated molecular pathways leading to carcinogenesis

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Abstract

With the initiation of the Human Microbiome Project in 2007, understanding the gastrointestinal (GI) tract microbiota has contributed to the knowledge of a mutualistic interplay between host and microbes. About 99% of microbial mass in the human body is contained in the GI tract. The crosstalk - established between the resident microbes and the Gut-Brain Axis (GBA) - has been the pillar of host-microbial homeostasis. Evidence suggests that alterations in the gut bacterial composition or 'gut dysbiosis' are associated with the onset of diseases and health implications involving human nutrition, metabolism, and immune function. One such partly discussed correlation is between dysregulation of the gut microbiome and carcinogenesis. Neoplastic initiation by the resident microbes is mediated by several methods, such as by affecting signaling pathways, manipulating the DNA of proximate cells, or directly inhibiting the function of certain immune cells, to name a few. In this study, we aim to highlight specific microbes that exhibit pro-tumorigenic effects and the molecular mechanisms that contribute to the development and progression of cancer. Here we also attempt to draw a parallel between the incidence of cancer and infectious diseases caused by microbes.

Keywords: Gut dysbiosis, cancer, p53, bacterial toxins, JAK-STAT pathway, colorectal cancer.

Nanomaterials-based chemisensors for detecting toxic nerve agents via DMMP simulant

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Abstract

The necessity to investigate and create reliable, long-lasting chemical sensors with fast reaction times and high sensitivity has been accelerated by recent terrorist activities . Nerve agents are known to be the most dangerous type of chemical warfare weapons. Severe hazardous consequences might occur even with brief contact. Even years after these gases were employed, humans unintentionally suffer from their after effects. Chemical warfare agents (CWAs)with severe toxicity, even at low doses, include Sarin, Soman, and VX. Therefore, handling these substances for research purposes carries a significant risk and needs to be done with extra caution and authorization in designated facilities. The majority of CWA research is conducted using simulant molecules rather than actual CWAs in order to reduce this danger. Dimethyl methylphosphonate (DMMP) is the most widely used simulant of nerve agents, often employed in labs as a replacement of real time warfare nerve agents. DMMP can imitate the effects of nerve agents since its chemical structure is almost the same as that of nerve agents. A number of chemical sensors, such as mass-sensitive sensors, chemicapacitors, chemiresistors, and field-effect transistors, have been developed and utilized to detect DMMP in recent years. A diverse range of chemi-sensors such as graphene based, metal oxide based, macrocyclic based, and polymer-based nanomaterials have been designed and tested successfully as chemical sensors with efficient sensing performance in terms of sensitivity, limit of detection, linearity, recovery and response times, etc., for the detection of DMMP.

Keywords: Nerve agents, sensor, DMMP, response time, sensing efficiency

From the Gut to the Mind: Unravelling the Microbiome-Anorexia Connection

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Abstract

Anorexia nervosa (AN) is a severe mental illness and eating disorder characterized by distorted body image, obsessive thoughts about food, ritualistic behaviours including reduced eating, weight loss, increased physical activity, and emotional rigidity. It is dominated in women with a population prevalence of 1%. The study done on 77 females with AN and 70 healthy females implies that disrupted gut microbiota and associated bacterial metabolites contribute to AN pathogenesis.

This research suggests a connection between gut bacteria and Anorexia Nervosa (AN). People with AN have altered gut bacteria composition, potentially linked to eating behaviours, mental health, and metabolism. The study explored bacterial functionalities, growth rates, and interactions with metabolites, suggesting these factors might influence AN development. This research strengthens the link between gut bacteria and Anorexia Nervosa (AN). Mice receiving gut bacteria from AN patients showed weight gain issues and metabolic changes, mimicking AN symptom. Additionally, the study identified specific bacterial variations in AN patient and linked them to certain eating behaviours, suggesting a potential role in the development of the disorder.

As a result, the study sheds light on putative processes behind the biology of this severe mental health disease and eating disorder. It also offers complete insights into the intricate relationships between the gut microbiota, serum metabolites, and host phenotypes in AN. The results provide new insights into the function of the gut microbiota in AN and pave the way for future investigations and possible treatment approaches.

Key words: Anorexia nervosa, gut microbiota, metabolites, phenotypes

Resolving the enigma: Multiplex testing's role in combating antimicrobial resistance

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Abstract

To enhance antibiotic stewardship, there's been advocacy for multiplex testing, enabling the simultaneous assessment of a broad panel of pathogens. While nucleic acid amplification-based tests now serve as the gold standard for respiratory virus confirmation, their broad application can be cost-prohibitive. Multiplex testing offers a potential solution by actively diagnosing multiple pathogens at once, thereby optimizing resources and expediting diagnoses.

The failure of interventions to curb antimicrobial use in acutely ill adults may stem from clinicians' apprehension regarding adverse outcomes. However, recent studies indicate promising outcomes with the adoption of rapid sample-to-answer multiplex PCR for respiratory virus detection in adults with acute illness. This approach significantly reduces time to results and shortens hospital stays compared to routine laboratory-based PCR testing.

Implementing multiplex testing in clinical settings holds promise for more effectively managing drug-resistant infections and enhancing patient outcomes. By streamlining diagnostic processes and facilitating targeted treatment approaches, multiplex testing stands as a pivotal tool in combating the escalating threat of antimicrobial resistanceAddressing drug resistance is a paramount concern within healthcare, demanding innovative approaches for its effective management. Whether intrinsic or acquired, drug resistance poses a formidable challenge across all chemotherapeutic agents. Clinical differentiation between bacterial and viral infections often proves intricate, frequently resulting in empirical antibacterial therapy, exacerbating the burden of antimicrobial resistance.

Drug resistance typically arises through various mechanisms, including target alterations, diminished internal drug concentration, and drug inactivation or failure of activation. Given that drugs typically target vital cellular mechanisms, mutational resistance commonly correlates with reduced replicative fitness.

Unfolding the impact of urban-environment induced factors on gut microbiome-driven cardio-metabolic disease

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Abstract

The world is experiencing a sudden surge in the urban population, especially in developing Asian-African countries. Consequently, the global burden of cardio-metabolic diseases (CMD) is also rising owing to the dysbiotic shift in the gut microbial composition due to environmental and lifestyle-associated changes during urbanization. A dysbiotic gut microbiome indicated by an altered *Firmicutes* to *Bacteroides* ratio and loss of short-chain fatty acids (SCFAs) producing bacteria, may disrupt host-intestinal homeostasis by altering the host immune response, gut barrier integrity, or microbial metabolism. This could lead to the establishment of a pro-inflammatory gut characterized by the overproduction of pro-inflammatory cytokines such as Tumor necrosis factor (TNF)-α, Interleukin (IL)-6, IL-2, IL-12, and interferon (IFN)-γ, or metabolic endotoxemia due to leaky gut formation characterized by the increased blood serum levels of toxic bacterial products such as lipopolysaccharide (LPS). All of these physiological characteristics are associated with an increased CMD risk. In this review, we aim to elucidate the effect of urbanization on CMD via gut dysbiosis caused by the interplay of different vertical (mother to infant) and horizontal (environment to individual) urban-environment induced factors such as mode of birth, breastfeeding, diet, environmental pollutants, and soil exposure. We further elucidate the targeting of the gut microbiome and its associated pathways for potential preventative and therapeutic applications for CMD.

Keywords: Urbanization, Gut microbiome, Cardio-metabolic disease, Inflammation, Dysbiosis.

Comparative genomics of two strains of *Fusarium oxysporum* with different life styles associated saffron, *Crocus sativus* L.

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Abstract

Two *Fusarium oxysporum* strains already isolated and characterized from the saffron corm have been taken for this study *Fusarium oxysporum* R1 has been isolated from the rotten corm and its pathogenecity has been confirmed. *Fusarium oxysporum* CSE15 is an endophyte isolated from the healthy corm by Wani et al., 2016 and it also causes moderate rotting on inoculation. The aim of the present study is to compare the genomes of two fungal strains associated with the same host and to understand the difference in their genome that directs their their lifestyle. The *in-vitro* dual plate study between two fungi indicated that both the fungi are not inhibiting each other rather they are showing competition for food and niche. Earlier differential transcriptomics of *Fusarium oxysporum* R1 has resulted in the identification of pathogenicity related genes. Similar study needs to be done in case of *Fusarium oxysporum* CSE15. Additionally in order to study their interaction at genome level both the fungi were sequenced for short and long reads by illumina and pac Bio respectively. About 6Gb (Fox R1) and 13Gb (Fox CSE15) data has been generated by illumina sequencing and 9.4Gb (Fox R1) and 14Gb (Fox CSE15) data by PacBio sequencing. The sequence data for both fungal genomes has been assembled using different assemblers with different parameters. The assembled genome of both fungi has shown difference in their genome size, this will be counter confirmed by fluorescent activator cell sorter. The assembled genome was subjected for genome completeness which resulted in approximately 98% of genome coverage. Also, hybrid assembly and Polishing was done to remove mis assemblies. Further, genome annotation of both fungal genomes will be done to understand the difference between the two genomes at gene level. The goal of the current research is to understand how endophytes and pathogens interact with one another and the host plant.

Determination of Physicochemical Parameters in Microbial Communities Isolated from Drill Oil Contaminated Soil

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Abstract

Assam's petroleum production causes environmental and community concerns. Oil exposure may lead to health problems and soil fertility depletion. The environmental contamination caused by oil is teeming with microbiota that can utilize hydrocarbon for metabolic activity and growth. Considering the important role of microbes, the present study was carried out in which the soil was collected from four different sites of an oil field in Makum, Tinsukia (Assam), and the physio-chemical and nutrient analysis of the soil was performed. The results of contaminated soil were – pH: 9.34, Organic Carbon: 0.52%, and Electrical Conductivity: 0.07dS/m. The macronutrient content is: Zn - 225.14 ppm, Cu - 274.03 ppm, Mn - 1046.94 ppm, and Fe - 994.2 ppm; while the micronutrient content is: N - 225.42 kg/ha, Ca - 0.5mEq/L, Mg - 0.7mEq/L, K - 187.55 kg/ha, 23.15 kg/ha. The microbial population of the soil was isolated, and 3 strains DLI, DLII, and DLIII were obtained in pure culture. The biochemical analysis were conducted for these 3 isolates which showed isolate DLI was positive for Catalase, Mortality, and Citrate test, DLII was positive for Catalase, Motility, and MacConkey test and DLIII showed positive for Catalase and Citrate test. The antibiotic sensitivity test showed DLI was sensitive to Kanamycin DLII was sensitive to Ampicillin and Kanamycin while DLIII was sensitive to Tetracycline and Kanamycin. Here, we are presenting the physicochemical properties that have been currently inferred by our research team.

Keywords: Drill oil soil, contaminated soil, Antibiotic Sensitivity, Micronutrient, Macronutrient

In Silico Analysis of Uncharacterized gene ML0472 of *Mycobacterium leprae*

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Abstract

Mycobacterium leprae is an obligate intracellular parasite, which is the causative agent of chronic neurological and dermatological disease called leprosy or Hansen disease. *M. leprae* forms a complex with *M. lepromatosis* called *M. leprae* complex to cause infection. The Genome of *M. leprae* contains fewer protein-coding genes as compared to non-coding genes and pseudogenes, it relies on the host cells for survival as well as replication. It has the highest number of pseudogenes as compared to any other microbe. It mainly infects the Schwann cells of PNS leading to demyelination and loss of axonal conductance. ML0472 is a type of hypothetical protein in it whose function is uncharacterized. It has *Mycobacterium tuberculosis* as its orthologue, which is the causative agent of one of the deadliest disease tuberculosis. ML0472 has 243 bp of gene length with 81 amino acids in sequence. The computational analysis of ML0472 predicts its role in metabolism and to a few extents in cellular processes. It acts as a missing gene that has an enzymatic function in its metabolism. Also, proteomic analysis shows that it has a moderately positive instability index shows that it is a stable protein with a huge number of aliphatic chains. *M.leprae* is mainly spread through the respiratory tract with a huge amount of bacilli in untreated patients. Moreover, the cure of Leprosy requires a Multi Drug Treatment (MTD) approach, which is also insufficient for many patients hence further research on its drug and vaccine development is required.

Key words: Leprosy, Pseudogenes, Hypothetical protein, Metabolism

Tracking the molecular responses of gut-associated microbes in the physiology of the *Anopheles stephensi*

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Abstract

Mosquitoes are carriers of several infectious diseases dangerous to humans, including malaria-causing mortality worldwide. As a dominant vector species, *Anopheles stephensi* poses a major threat to human health in urban areas and several small, medium, and metropolitan cities in India. Presently, strategies to control malaria are limited due to emerging insecticide resistance in mosquito vectors and the unavailability of an effective vaccine. Thereby, there is an urgent call for the development of new vector control tool in order to reduce/mitigate the burden of malaria transmission. Mosquito midgut-associated microbes have gained considerable attention for the development of novel transmission-blocking tools against vector-borne diseases. Mosquito midgut has an unique ecosystem with a diversity of microbiota. Commensal bacteria in the midgut of mosquito can suppress parasite development and impact vector physiology. The malaria parasite development involves critical steps within the mosquito midgut, an environment shared with gut-residing bacteria making it important to decipher interaction of these host gut microbes with the parasite to help/restrict the growth of plasmodium. In the present study, microbial diversity of *Anopheles*-associated midgut microbiota is being studied by a culturable approach so that the molecular interaction at individual microbe levels can be found out. Isolation of gut microbes on selectable media depending on the physiological conditions of the vector mosquito is carried out. The isolated colonies on various media can be purified and characterized by biochemical and molecular approach. Further whole genome sequencing of the isolates will be used to find out the networks of various host - vector – parasite. Physiological and metabolic pathways will be identified and characterized by microbiological and molecular techniques. This study will conceptualize an understanding by interfering gut-microbe-mosquito interaction that may guide the development of new eco- friendly molecular tools.

Keywords: microbiota, midgut, Malaria, *Anopheles stephensi,* mosquito

Tree of Life: Unveiling the Viral Lineage

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Abstract

The origin and evolution of life has always been a topic of interest for evolutionary biologist which led to the formation of a universal Tree of Life (ToL). The current understanding depicts a branching system with three main branches: bacteria, archaea, and eukarya. Archaea and Eukarya are seen as closely related groups within this system.

The location of viruses in the ToL as the fourth domain has always been a mystery. The living and non-living characteristics of virus creates a state of uncertainty while placement of viruses in ToL. Phylogenetic tree including viruses have been constructed by scientist but addition of a fourth domain in ToL is still unclear. The discovery of giant viruses having larger genomes such as *Mimivirus* sharing common genes with the other three branches of the ToL points towards the need for placement of viruses in the universal Tree of Life.

Viruses should be considered as an integral part of the tree of life as they have interacted with their hosts since the dawn of life thus parallelly evolving and forming genetic similarities. Viruses are important agents for Horizontal Gene Transfer (HGT) as they cause genetic reshaping in themselves their host thus coevolving. Though a perfect phylogenetic lineage of viruses cannot be expected due to their constant evolution with their hosts that are domain specific, but the placement of viruses in the universal ToL is as crucial as any other cellular entity.

Keywords: Tree of Life, Giant viruses and Coevolution.

Saptio-temporal variation in microbial and physico-chemical characteristics of institutional water environment

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Abstract

Water is an essential component for overall health and wellbeing, and is one of the basic need of humankind. As pollution levels continue to increase, our available freshwater resources are facing growing threats from a variety of contaminants, such as ….. The toxic metal contamination also requires urgent attention due to their potential to cause acute or chronic illnesses. It is therefore necessary that the quality of water should be assessed at regular intervals for its biological and physico-chemical properties. The study aims to examine the biological and physico-chemical properties of fresh water (Ground, Tap and Pond water) within institutional areas in North Delhi. The study focuses on spatio-temporal variations in factors such as toxic metal analysis, temperature, Chemical Oxygen demand, Electrical Conductivity, Salinity, ORP (Oxidation-reduction potential), pH, TDS (Total dissolved solids), Dissolved Oxygen, and Alkalinity. Microbial contaminations are screened using conventional culture technique. The analysis was performed using APHA (American Public Health Association) standard methods and the instruments used were Atomic Absorption Spectrophotometer (Shimadzu) and Multiparameter Water Quality Analyser (Hanna). These results are then compared with existing safety standards of World Health Organization (WHO), the Bureau of Indian Standards (BIS) and Central Pollution Control Board (CPCB) specifications.

The Preliminary results obtained from the month of December 2023; January-February 2024 will be presented in the study. Assessment of physicochemical and microbial parameters reveals that the chosen sites are significantly impacted, highlighting the necessity for treating water prior to utilization to prevent waterborne diseases that pose risks to both human health and aquatic life.

Keywords: Water Quality, Pollution, Assessment, Water-borne, Physico-chemical, Spatio-temporal, Pathogens, Contamination, Institutional areas

Integrated Deep Eutectic Solvents and Nanoparticles: A Pathway towards Green Chemistry Principles and Sustainability Goals

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Abstract

Deep Eutectic Solvents (DES) combined with nanotechnology have emerged as a promising idea in modern chemistry, aligning with the principles of Green Chemistry and contributing to achieving sustainability goals. DES is a versatile, low-toxicity, and easily prepared solvent from renewable resources.

Nanotechnology's pivotal role stems from its ability to manipulate matter at the nanoscale, enhancing reactivity, selectivity, and efficiency. The synergy between DES and nanomaterials minimises environmental impact, reduces waste generation, and optimises resource utilisation. This synergy facilitates the design of greener synthetic routes, thereby mitigating the environmental footprint associated with conventional chemical processes. Using nanoparticles,mostly of Silver(Ag), Gold(Au), Copper(Cu) and Platinum(Pt^{+4}) for novel applications in various fields is substantially enhanced which covers catalysis, separation processes, and material sciences.

The integration of DES with nanoparticles (NPs) catalyses advancements toward sustainability goals outlined by international frameworks. By enabling more efficient processes, reduced energy consumption, and waste generation, this approach contributes directly to targets such as resource efficiency, pollution prevention, and sustainable production patterns. In addition, the inherent biocompatibility and eco-friendliness in DES-NP systems open avenues for sustainable solutions in diverse sectors, including pharmaceuticals, energy, and environmental remediation.

This poster presentation explores the multifaceted applications and benefits of the DES-NP system in advancing green chemistry principles and supporting sustainability objectives. It covers recent advancements, challenges, and future directions in harnessing this innovative approach to address pressing societal and environmental concerns. Consequently, integrating DES and NPs represents a step towards establishing more sustainable and environmentally conscious practices in the chemical sciences and beyond.

Key words: Deep Eutectic Solvent, Green chemistry, Nanoparticles, Sustainable

MDM2 polymorphism analysis uncovers novel mechanism for cancer resistance

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Abstract

MDM2, a major oncogene known to be overexpressed in several cancers, is a E3 ubiquitinin protein ligase, which interacts with TP53 and promote its degradation, thus this interaction is also an important therapeutic target, We have identified a mutation in TP53 interacting domain of MDM2 which is conserved in four cancer resistant organisms (*Loxodonta africana*, *Balaena mysticetus*, *Heterocephalus glaber* and *Nannospalax galili*),this mutated residue is known to be involved in MDM2 /TP53 interaction. So, in this study we tried to investigate using insilico approach that whether this difference is giving any advantageous affect to these cancer resistant organisms. Molecular Dynamics Simulation and Docking results of Wild type and Mutated structures indicated that this mutation can alter the MDM2-TP53 interaction, which might be reducing TP53 degradation. Simulation results also suggest that this mutation mediates such functional alterations by effectively altering the flexibility of several highly conserved domains of MDM2. Our results indicate that such repercussions of the butterfly effect of this mutation on MDM2 structure and function might be an important underlier for enhancing cancer resistance.

Non-ionizing electromagnetic radiation and microorganisms

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Abstract

The use of cell phones and related gadgets that produce radiofrequency radiation is growing constantly as a result of the electronic revolution and civilization's modernization. Although there are several studies on the effects of this type of electromagnetic radiation on plant and animal systems, the effects on microbial systems are somewhat confusing. This article discusses the possibility that microwave radiation may affect the ability of microbes to survive, grow, and perform other essential functions. According to published research, electromagnetic radiation have a substantial impact on the growth of microbial cultures. These impacts might range from the death of microorganisms to the stimulation of their growth. The microwave frequency and the total energy absorbed by the microorganisms determine the type and magnitude of the effect. Microorganisms are more likely to develop when exposed to low energy, low frequency microwaves rather than high energy, high frequency microwaves. Nevertheless, no research has been done on the impacts of a broad spectrum of frequencies or a large range of absorbed energy. Given that microwave radiation may have a negative impact on the symbiotic relationship between microorganisms and their human hosts, more investigation is needed to determine how the full frequency and energy spectrum of microwave radiation affects the development of microorganisms

In-Depth Exploration into the Environmental Dynamics of Human Enteric Pathogens in Ready-to-Eat Fresh Produce

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Abstract

A spurred uptick of food borne illness primarily stemming from pathogenic strains of E. coli, with connections established to the consumption of vegetable and leafy greens. In the gastrointestinal tracts of human and animals E. coli and Salmonella are prevalent commensal organisms' servings as versatile pathogens that pose significant public health concerns. Plants are typically not viewed as hosts for human enteric pathogens. Nevertheless, multiple reports of foodborne illness cases have highlighted the occurrence of Shiga toxin-producing E. coli (STEC) and Salmonella in the plants profound interactions between plants and microbes have been noted, encompassing factors like biofilm, antimicrobial resistance (AMR) and others. The synthesis of extracellular matrices, like cellulose and curli-fimbriae amplifies the ability of pathogens to thrive in plants. Consequently, the study sought to investigate the colonization and persistence of E. coli and Salmonella in Ready-to-Eat fresh product. A total of 480 samples of fresh vegetables underwent analysis. The E. coli and Salmonella strains derived from vegetables and fruits were subsequently evaluated for antimicrobial resistance/ biofilm production/ extracellular matrix production and sequence analysis. 82 E. coli and 24 Salmonella strains in total were identified demonstrating the capacity to generate biofilms with elevated cellulose/ curli-fimbriae production. Noteworthy resistance was noted against the tested antimicrobials. The findings reveal the existence of Shiga toxin-producing E. coli and Salmonella in plant posing a potential health risk to consumers. This raises concerns regarding food safety and offers a potential explanation for their capacity to colonize plants or their association with the ongoing increase in foodborne outbreaks. It offers essential foundational information, suggesting that human enteric pathogens have the potential to utilize plants as an alternative host, holding considerable clinical significance.

Keywords: Foodborne illness, pathogenic E. coli, Salmonella, human enteric pathogens, Shiga toxin-producing E. coli (STEC), plant-microbe interactions.

Emphasis on role of microbiota on human mental health: Stress, Anxiety and Depression

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Abstract

Stress, anxiety and depression are most prevalent mood disorders worldwide caused by *allostasis* failure which is experimentally proven. A bidirectional relationship exists between gut microbiota and brain via microbiome gut-brain axis. After the brain, the human intestine contains the second-highest concentration of neurons. Microbiota via diet and lifestyle patterns affect the mental health as diet rich in processed, fried, frozen, high-fat dairy products increase the likeliness of these disorders while food rich in dietary fibres (fermentation of which leads to production of short chain fatty acids; SCFAs which regulate metabolism) promotes good mental health. Microbiome-diversity concerned studies shows that there is an alteration in the abundance of common bacterial taxa- reduction in Bacteroidetes, Firmicutes (*Lactobacillus sp*.) and Actinobacteria (*Bifidobacterium sp.*) and; outgrowth of Proteobacteria, *Oscillibacter* and *Alistipes* in major depressive disorders. Additionally, microbiota regulates various immunological functions. Gut microbiome also produces some epigenetic enzymes that regulate 'human holobiont'. Potential treatments for disrupted microbiota include administration of prebiotics (non-digestible polysaccharides), probiotics (cocktail of beneficial microbes), postbiotics (pasteurized probiotics), synbiotics (combination of pre- and post-biotics), microbiota transplantation. These enhance the 'normal microflora' thereby improving mental health. Differential individual diversity poses a major limitation in order to specifically design drugs and therapeutics, but demographically can be administered.

Key words: Allostasis, Microbiota, Gut-Brain Axis, SCFAs, Probiotics

Characterization of vegetal associated microflora: Exploring aspects to obtain efficient bioinoculants

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Abstract

Bioinoculants offer a promising avenue for sustainable agriculture by harnessing the natural capabilities of microorganisms to enhance soil fertility, plant health, and overall crop productivity. These play vital roles in nutrient supplementation and cycling, disease suppression, and stress management in plants. Various environmental factors, including soil type, pH, moisture levels, and climatic conditions, alongside interactions with specific crop varieties, influence the variety of bioinoculants. This research paper aims on isolation and characterization of useful microbial strains from different vegetal associated soil samples in an attempt to comparatively characterize microflora best suited for formulation of bioinoculants.

Soil samples from various sources decaying wood and leaves, manure, four types of plant varieties viz., ajwain, jackfruit, moringa, and chickpea, were collected. The samples were screened for phosphate solubilizers, free living nitrogen fixers, indole, urease, catalase production by biochemical analysis or by using selective media. Our group generated 18 different microbial isolates from these samples which were characterized further for Gram characters, morphology and colony characteristics. These isolates exhibited beneficial traits like nitrogen-fixing, phosphate-solubilizing, indole production, and ammonium production. Notably, ajwain soil isolates were proficient in nitrogen-fixing and phosphate-solubilizing abilities, while jackfruit soil isolates showed phosphate-solubilizing and indole-positive traits. Moringa soil isolates displayed nitrogen-fixing, phosphate-solubilizing, and indole-positive abilities. Chickpea field isolates exhibited nitrogen-fixing and phosphate-solubilizing traits. Overall, the findings highlight the rich diversity of beneficial microorganisms present in different soil environments, each potentially contributing to plant growth promotion and soil fertility enhancement through various mechanisms. The findings underscore the presence of specific types of microbes with useful properties with different plant varieties. Further work on confirmation of these associations would be required. Future work on application of these isolates could lead to the development of tailored bioinoculants for sustainable agriculture practices.

Comparative genomics of staphylococcus: insights into host-related genetic attributes

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Abstract

Staphylococcus aureus is a pathogenic bacterial species with significant genetic diversity. This pervasive bacterium is responsible for deleterious soft tissue related infections in humans and livestock. Comprehensive genomic analysis of 96 gene sequences retrieved from the National Center for Biotechnology Information unveiled genetic elements underscoring the zoonotic dissemination characteristics of S. aureus. With the help of computational methodologies, we have conducted an intricate examination of the core and pan-genome, which deciphers the conserved segment section of the variable host-associated strains (human, macaca, cattle, camel, and swine), to shed light on different features of host-pathogen interaction, biofilm formation, and the host-specific molecular mechanism. The comparative genome analysis of strains isolated from macaca, humans, and other livestock with the help of average nucleotide identity describes the evolutionary dynamics of bacteria and their potential habitat adaptation. The aim of this study is an in-depth analysis of S. aureus strains to provide valuable aspects for the advancement of targeted strategies and medication and for promoting healthy livelihoods.

In silico analysis of Tecovirimat a repurposed drug against the monkeypox virus, its off-target human proteins, and impact on human health

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Abstract

Objective: In this study, *in silico* analysis of human off-target proteins of tecovirimat was performed. Tecovirimat is an investigational drug reported to stop monkey pox virus infection by binding to a protein that the virus uses to enter host cells, thereby aiding in understanding its off-target long-term and short-term effects on various biological systems in patients over time.
Methods: The drug's target and off-target proteins, along with their characteristics, protein-protein interactions, and associated pathways, were extensively examined through various databases such as Drug Bank, NCBI Gene Database, BLAST, Gene MANIA, UCSC Gene Sorter, STRING, and the Kyoto Encyclopedia of Genes and Genomes (KEGG) Pathway Database.
Results: The study demonstrated that tecovirimat, a repurposed drug, helps treat monkeypox by binding to the viral p37 protein. However, it may also accidentally disrupt crucial human biological processes by interacting with off-target proteins or indirectly affecting proteins that interact with the target proteins in humans.
Conclusion: The results emphasize the necessity of thoroughly examining and evaluating all repurposed medications for any off-target effects prior to their release to the general public.

Key words: Monkeypox, Tecovirimat, p37 protein, Rheumatoid arthritis, Alzheimer's disease

A sneak peak into quinoline-based ionic liquids as artificial chaperones and anti-biofilm agents

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Abstract

The unfolding of proteins under stressful conditions is one of the prevailing challenges in maintaining their activity. Ionic Liquids (ILs) are currently dominating the biomedical industry, by endowing great solubility and stability to bio-molecules. Quinoline and its derivatives are recognized to manifest medicinal properties and hence are utilized in the formulation of a wide range of antimicrobial compounds. We present the molecular chaperone, antimicrobial and anti-biofilm activity of quinoline-based biocompatible ionic liquids (ILs) with their toxicological effects. A series of quinoline-based ionic liquids ([C_{12}quin]Br}, [C_{16}quin]Br}, [C_{21}quin]Br}) were synthesized and validated using Nuclear Magnetic Resonance (NMR) spectroscopy and Infrared Spectroscopy. The structural changes induced in BSA were corroborated with UV-Visible, Steady-State Fluorescence, Circular Dichroism (CD) spectroscopy and Dynamic light scattering (DLS) measurements. The morphology of the BSA amyloid fibrils was characterized using Scanning Electron Microscopy (SEM) and Transmission Electron microscopy (TEM). The protein-IL interaction was validated using in-silico studies. The antimicrobial and anti-biofilm activity was substantiated using various biological assays and toxicity analysis was performed using *Caenorhabditis elegans* as the model organism.

Discern spoilage caused by microorganisms from that of spoiled fruits and vegetables

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Abstract

Recognizing the origins of spoilage in fruits and vegetables holds paramount importance in upholding food safety and quality standards. This research endeavours to differentiate spoilage induced by microorganisms from that arising from the natural degradation processes of fruits and vegetables. Various methodologies, encompassing microbial analysis and visual examination, were applied to discriminate between these two forms of spoilage. The deterioration of fruits and vegetables may stem from the enzymatic activity of microorganisms. Decomposition occurs due to saprophytic organisms. Fruits and vegetables, characterized by high moisture content (85%) and sugar content (13%), along with an abundance of vitamins, minerals, and organic compounds, provide an ideal environment for the proliferation of bacteria, yeast, and molds. The broader pH range further encourages the growth of spoilage microbes. Sugar breakdown transpires through fermentation, resulting in the production of alcohol and CO_2. Common spoilage agents for fruits and vegetables include *Penicillium, Aspergillus,* and *Fusarium,* while *Corynebacterium, Pseudomonas, Xanthomonas*, and *Streptomyces* are typical bacterial spoilers. Fruits with low pH levels (below 4.5), such as oranges, grapes, and guavas, typically evade bacterial spoilage and are more susceptible to degradation by yeasts and molds, as observed in our findings. The results highlight distinct attributes linked with microbial-induced spoilage, including unpleasant odours, irregular discoloration, and visible microbial growth. Grasping these distinctions is imperative for devising effective preservation and storage techniques aimed at mitigating microbial spoilage and preserving the freshness of fruits and vegetables.

Keywords: Degradation, fruits, vegetables, microbial analysis, preservation, storage.

Effect of microbial metabolites on host aging and longevity

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Abstract

Aging refers to the decline in physiological health of an organism. It is detrimental for an organism's survival, making it more susceptible to age related diseases. Recent discoveries have unveiled the connection between host health to the microbiota residing in the host body. Several studies have found connection between the microorganisms living in the host body to the affect they produce on the host's health and ultimately towards their aging process. The metabolites produced by the microorganisms in the host body influence several pathways involved in inflammation, senescence, and eventually aging of the body, therefore it is important to understand the microbes and their metabolites that help in longevity of the host. We shall understand how gut microbiota, skin microbiota and other such microbiota influence the immune system, cell protection mechanism, and other physiological functions and pathways affecting the aging process. We delve into the current research and advancements in the field and peek into the future potential developments.

Keywords: microbiota, microbiome, microbial metabolites, aging, longevity, senescence

Gut metabolite effect on atherosclerosis

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Abstract

Atherosclerosis is a chronic disease characterized by abnormal lipid metabolism and inflammation in the blood vessel walls, resulting in cardiovascular issues, which are a leading cause of mortality. Trimethylamine-N-oxide (TMAO) is a gut metabolite known to exacerbate atherosclerosis by increasing in concentration in the blood during the condition. Various studies suggest that TMAO can trigger the release of pro-inflammatory cytokines (such as IL-6, IL1B), disrupt lipid balance by affecting receptors like CD36 and ABCA1 in macrophages, and enhance the expression of adhesion molecules (e.g., SELE, ICAM1, MCP1) and pro-inflammatory cytokines in endothelial cells. However, the precise mechanism through which TMAO influences the expression of these molecules remains unclear.

One proposed hypothesis is that TMAO might interact with proteins upregulated in atherosclerosis (e.g., Antitrypsin, Thrombin, Fibrinogen) potentially exacerbating plaque vulnerability. These proteins increase during inflammation and significantly in chronic inflammatory conditions like atherosclerosis. These proteins are also known to bind with various metabolites like TMAO and drugs. Certain natural compounds, such as resveratrol and curcumin, have demonstrated promising effects in reducing plaque vulnerability and size in both laboratory and animal models without adverse effects.

To identify potential compounds that could mitigate atherosclerosis induced by TMAO-modulated proteins, we aim to screen thousands of phytochemicals from the HERB database. Our goal is to select 2-3 phytochemicals that show efficacy in inhibiting the progression of atherosclerosis influenced by TMAO-modulated proteins.

Biological Contamination Assessment of Water Resources and Its Water Quality Implications

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Abstract

Water is a fundamental resource, playing a crucial role in various aspects of human existence, from sustenance to sanitation. However, many people do not have access to safe drinking water due to escalating pollution of water bodies. Microbial contamination, being one of the serious pollutants of water, poses a concerning threat to global public health. Pathogens such as bacteria, viruses and protozoa can contaminate water sources causing diseases like cholera, typhoid, gastroenteritis, bacillary dysentery, etc. Addressing these challenges requires a comprehensive understanding of water quality and the impact of microbial contamination on human health, highlighting the urgent need for monitoring and effective management strategies. This aligns with the Sustainable Development Goal-6 (SDG-6), which aims to ensure availability and sustainable management of water and sanitation for all. In this study, we examined the quality of water from the institutional areas in North Delhi for their probable microbial contamination that might have an impact on the health of students and people associated with the institutions. Water samples are being collected from the selected sites of the institutional area. The screening of water samples for the presence of microbial contamination is achieved by using microbiological culturable techniques. To identify potential pathogens in the water samples, metagenomic DNA will be isolated and microbial diversity will be determined further using bioinformatics tools. The preliminary results obtained from the months of December 2023 – January - March 2024 will be presented in the poster. The water ecosystem is disturbed due to the water pollutants and the high levels of microbial contamination is concerning. For this, microbial control of drinking water should be a norm everywhere and regular monitoring and awareness among the people regarding safe drinking water must be performed.

Keywords: water, SDG-6, microbial contamination, pathogen

Influence of 16S rRNA gene hypervariable regions for study of soil microbes from mining sites undergoing ecological restoration

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Abstract

Monitoring below-ground diversity is important to evaluate effectiveness of long-term ecological restoration programs and to understand linkages between re-established plant communities with their rhizospheres. This study explores the best-suited 16S rRNA gene hypervariable regions for detecting rhizospheric soil microbial communities of two native "indicator" plant species sampled from limestone-dolomite and iron ore mining sites in Odisha, at different stages of ecological restoration. Total DNAs were isolated from soil samples for constructing clonal libraries. Identification and characterisation of various taxa was done by comparing different hypervariable regions (V3-V6) of microbial 16S rRNA genes using near to full-length sequences. The generated data was compared with results from NGS of selected rhizospheric microbiomes. Restoration of degraded soils and re-establishment of plant communities influenced microbial profiles of sampled rhizospheres. Remediation of contaminated soils was accompanied by changes in abundance of the bacterial phyla *Acidobacteriota*, *Proteobacteria* and *Actinobacteriota*. Shifts in occurrence of genera like *Halobacillus, Burkholderia, Nitrosophaera, Acinetobacter*, *Sphingobium* and *Bacillus* was evident in the sampled rhizospheric soils. These microbial groups are known to sustain biotic communities in contaminated soils and contribute to processes underlying bioremediation and restoration of such degraded ecosystems. A better understanding of the targeted 16S rRNA gene hypervariable regions selected for molecular characterization of microbial communities in degraded soils undergoing restoration can be pivotal for an accurate interpretation of diversity associated with these complex ecological niches.

Key words: Ecological restoration, rhizosphere soil, microbial community

A study on identifying bacterial prey of filter feeding ciliates in Pringsheim's medium: Methodologies and Future Prospects

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Abstract

Microbes in the laboratory are grown on chemically defined media. Pringsheim's medium (PM) was used for routine culturing at Ciliate Biology Lab (CBL), ANDC. It promoted ciliate growth by performing pH buffering and osmolarity maintenance. Ciliates prey on organisms ranging from bacteria, flagellates and other ciliates. There are 3 types of ciliates based on mode of phagocytic food uptake and filter feeders actively grow on bacteria in PM cultures while difficulty in growing raptorial types was reported. Bacteria in PM grow by decomposing externally placed cabbage/rice. This produces diverse bacterial species as ciliate culturing is performed axenically but without following conventional aseptic techniques. The aim of the present study was to identify these specific bacterial strains and define an appropriate isolation technique. Three PM samples, in triplicate, were kept in open atmosphere of the laboratory for a day after which they were incubated for 3 days at 23°C in a BOD incubator. Samples were serially diluted to a value of 10^{-5} and plated on PM Cabbage Agar which included Amphotericin B. Result showed development of 7 distinct bacterial colonies across dilution plates in 3 triplicates. Two tests were performed for identification. The catalase assay yielded 5 positives and 2 negatives. The 5 of 7 cultured colonies were those of gram -ve bacteria and their shapes and arrangements varied. Results of these tests along with the observed colony morphology characteristics were compared with data from literature indicating that the bacterial colonies resembled species like *Ekhidna lutea*, *Klebsiella pneumoniae* and *Moraxella catarrhalis.* Further 16S sequencing and phylogenetic analysis will prove species level identity. Experiments on prey preference and prey inoculation are also intended to be performed in an attempt to optimize ciliate growth in laboratory.

Keywords: Media, Ciliates, Filter-feeders, Gram staining, Catalase assay, Phylogenetic analysis

Microbial immunomodulation in psoriasis: A comprehensive review

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Abstract

The autoimmune skin disease psoriasis is a long-term condition marked by hyperproliferation and inflammation of the skin due to abnormal immune responses. Changes in microbial diversity, abundance, and species composition have been revealed in the skin microbiome of psoriatic individuals by a number of studies. Both local and systemic immune responses have been linked to psoriasis, with bacterial species like *Staphylococcus aureus* and fungal species like *Candida albicans* being involved. Reduction in bacteria *Faecalibacterium prausnitzii* and *Akkermansia muciniphila* were significantly observed, high bacterial load was also identified in the psoriatic lesions compared with unaffected skin and controls in several studies. Microbial dysbiosis has influenced the immunomodulation in psoriasis. A wide range of interventions are included in immunomodulation, such as modifications to T-cell differentiation, cytokine production, and the stimulation of important signalling pathways. Pro- and anti-inflammatory responses are sensitively balanced by the complex interactions these microbes have with the host immune system. Pro-inflammatory cytokines like interleukin-17 (IL-17) and tumour necrosis factor-alpha (TNF-α) are upregulated as a result of mechanisms involving the activation of pattern recognition receptors (PRRs). This review brings together current knowledge on microbial immunomodulation in psoriasis, providing a thorough investigation of the intricate interaction between specific bacteria and the dysregulated immune responses that underpin the pathogenesis of this chronic skin disease.

Key words: Psoriasis, immune system, cytokines, immunomodulation, microbiome

Role of Epigenetic Marks in Memory Formation and their effects in Aged brain and Neurodegenerative Disorders

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Abstract

Epigenetic marks are the chemical changes on DNA sequence and histone proteins, which regulate gene expression, without changes to DNA sequence. Various processes including DNA methylation, chromatin remodelling, addition of epigenetic marks (acetyl group, methyl group, ubiquitin) on histone proteins and various environmental changes lead to these heritable alterations. Key players in Epigenetics are Writers (add mark, Histone Acetylases), Readers (recognize that mark, Bromodomains) and Erasers (remove mark, Histone Deacetylases). Epigenetic modifications play a crucial role in regulating gene expression, especially in brain, where learning and memory formation are facilitated. Two major functions of epigenetic regulation have been identified in this context: a "gating" mechanism that permits changes in gene expression for learning and a "stabilizing" mechanism that helps maintain gene expression for memory consolidation. Recent findings have shown modifications of epigenetic marks in the aged brain and in neurodegenerative disorders, including Alzheimer's disease. The purpose of this poster is to highlight the various forms of epigenetic alterations and their function in memory formation and synaptic plasticity in healthy brain. It also focuses on how Alzheimer's disease and aging related memory loss are caused by dysregulation of these processes.

Keywords: Epigenetic Modifications, Aging, Synaptic Plasticity

Influence of Indigenously Isolated Nitrogen Fixing Bacteria on the growth of *Triticum aestivum*

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Abstract

Food crops require increased indigenous organic inputs for enhancement of the plant productivity. In this investigation we have attempted to isolate and characterize nitrogen fixing bacteria for increasing the productivity of *Triticum aestivum*. Isolation of Nitrogen Fixing Bacteria was done from soil samples collected from areas such as agricultural land, forest, garden, lake along with banyan and guava tree rhizosphere. Selective isolation on nitrogen free medium was performed to develop a collection of 23 cultures. The cultures were screened for nitrogen fixation ability. All the cultures exhibited positive ammonia production in the preliminary screening process but ten were found to be better. Eight out of ten cultures were positive for oxidase and nine for catalase test. None of the cultures could utilize citrate as a sole source of carbon but all were positive for indole production test. The best performing isolate N7G was able to utilize 7 sugars out of 8 and N6 could utilize 4 whereas other isolates could utilize only 2 or 3 sugars. N9 exhibited amylase production and none of the cultures could show HCN production.

Nitrogenase enzyme activity was found to be good in three isolates named NP-2, NP-9 and N7G which were picked up for *in-vivo* testing by pot assay method. The seeds of *Triticum aestivum* were treated with broth containing these best performing isolates. The *in-vivo* testing in pots revealed 117% increase in plant weight, 42.47% increase in total height of plant, 62.26% increase in the root length and 32.72% enhancement in shoot height. As compared to the 50% seed germination in control plant 91.66% seeds germinated in the plant treated with N7G and we observed a reduction in time required for germination from 72 hrs to 36 hrs. The increased plant productivity has paved way for field trials in future which shall be translated further to commercial level.

Key words: Nitrogen fixation, Pot assay, Nitrogen free medium

Exploiting "Multi-Omic Integration" for prediction of microbial biomarkers in early disease detection and prognosis

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Abstract

Microbial biomarkers have emerged as effective strategies for early disease detection such as metabolic disorders, neurodegenerative diseases, cancer, etc. Beyond infectious diseases, microbial biomarkers have unveiled novel pathways linking the human microbiome to non-communicable diseases as well. Recent developments in artificial intelligence and machine learning have further added to the enhancement of the predictive power of microbial biomarkers by utilising the integration of a multi-omic approach. A multi-omic approach involves the integration of multiple layers of biological functions, including genomics, metabolomics, and microbiomics, to identify diagnostic biomarkers. Specifically, the researchers identified specific bacterial taxa, gene expression patterns, and metabolite profiles that were significantly correlated with particular diseases. For example, techniques like principal component analysis (PCA) or feature selection algorithms like recursive feature elimination (RFE) can help to identify the most crucial features for analysing biomarkers associated with diseases. Recently, a microbial biomarker (*Fusobacterium nucleatum*), a common oral bacterium, was found to be associated with an increased risk of CRC (colorectal cancer). Higher levels are correlated with more advanced stages of CRC, resulting in a poorer prognosis. This finding suggested that *F. nucleatum* could serve as a biomarker for CRC risk prediction. Integration of multi-omic data was utilised to find the predictive capability of microbial biomarkers of gut microbes in individuals with Inflammatory bowel disease (IBD). This approach was also found useful in predicting Crohn's disease and ulcerative colitis. Integrating metagenomic sequencing data to analyze microbial genomic variations, metatranscriptomic data to assess gene expression profiles, and metabolomic data to identify microbial metabolic products has become the new norm for establishing disease risk and prognosis. These models not only improved disease detection but also provided insights into disease mechanisms and potential therapeutic targets. The field is rapidly evolving, and there is a need to keep refining predictive models and developing personalized strategies for the prevention of disease.

Key words: Microbial Biomarkers, Early disease detection, Multi-omic approach, Metabolomic analysis



Resistome Diversity and Priority Pathogens: A Threat Accelerated by Climate Change

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Abstract

Globally, climate change and increasing resistome diversity are two of the top health emergencies and can be considered as two interlinked public health priorities. Therefore, this review aims to investigate this complex correlation from 'One Health' perspective. In 2017, WHO published the first list of "priority pathogens" – a catalogue of 12 families of bacteria that pose the greatest threat to human health. It includes *Acinetobacter baumannii, Pseudomonas aeruginosa, Enterobacteriaceae, Enterococcus faecium, Staphylococcus aureus, Helicobacter pylori, Neisseria gonorrhoeae, Streptococcus pneumoniae, Shigella* spp., etc. based on how deadly the infections they cause are; how easily they spread and how frequently they are resistant to existing antibiotics. Recent researches demonstrated that rise in surgical-site infection (SSI) rates for 1^0 C rise for almost all pathogens including *Streptococcus* spp. and incidence of healthcare-associated bloodstream infections (ha-BSIs), mostly due to gram-negative bacteria are 17% higher in warmer temperatures. Also, higher humidity has been linked to increased colonization and infections with methicillin-resistant *Staphylococcus aureus*. A possible reason for this can be plasmid transfer and resistant gene transfer which can be facilitated by rise in temperature and humidity and decreased ventilation. We conclude that increased transmission of priority pathogens can be seen with climate change, through temperature rise, variations in humidity, precipitation, and wind patterns. Further climate change has been linked to higher rates of antibiotic resistance, increased risk of colonization and pathogen dissemination.

Keywords: Climate Change, Priority pathogens, Resistant gene diversity, Antibiotic-resistant bacteria.

Understanding microbial genomic diversity in Basmati rice root systems of R.S. Pura, Jammu

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Abstract

Understanding the intricate dynamics of plant-microbe interactions within agricultural ecosystems is essential for optimizing productivity and quality. In this study, we delve deeper into the genomic microbial diversity within the rhizospheric compartments of two Basmati rice varieties indigenous to Jammu, Ranbir Basmati and Basmati 129, during the reproductive stage. Using metawrap pipeline, we successfully assembled a total of 127 genomes from the rhizospheric compartments of Ranbir Basmati and Basmati 129. In addition to genome reconstruction, we conducted taxonomic identification to elucidate the phylogenetic affiliations of these microbial genomes. Furthermore, functional annotation was performed to decipher the metabolic potential and ecological roles of the identified taxa within the Basmati rice rhizospheres. Our results reveal a myriad of complete genomes, some exhibiting high completeness levels, which may represent novel strains and organisms previously uncharacterized through conventional culturable approaches. In Ranbir Basmati, we identified 11 genomes surpassing 90% completeness and 21 genomes exceeding 95% completeness. Similarly, in Basmati 129, 24 genomes displayed completeness levels above 95%, with 6 genomes surpassing 90% completeness. Leveraging metagenomic analyses coupled with taxonomic identification and functional annotation, we aim to unravel novel insights into the microbial communities associated with these rice varieties.

Evaluation of soil health on the basis of microbial diversity and enzymatic activity in soil of *Pranmati* basin, Himalayan critical zone

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Abstract

Bacterial community plays a major role in soil health thereby balances the ecosystem. Microbes are one of the key and determining components of the soil in the critical zone. The present study deals with the diversity and functional profile of the microbial communities and their enzyme activities in an unexplored region of Himalaya to elucidate the significance of landscape connectivity and its soil health. Bacterial diversity has been explored using Illumina sequencing platform. Three different landforms (forest cover land, agricultural land and flood zone land) have been compared by predicting the relationship between biotic and abiotic factors. The soil belongs to the class sandy soil with pH slightly acidic (6.39 - 6.87) across the three landforms. Acid phosphatase and Beta- glucosidase (Phosphorous and Carbon cycling enzymes) were the most consistent enzymes with high soil activity in all the landforms. Actinobacteriota were dominant in agriculture land (28.97%) and flood zone lands (34.37%) whereas Proteobacteria (29.44%) was predominant in forest cover land. The highest species richness and diversity were observed in forest cover land on the basis of Chao1 and shannon index. The beta diversity analysis indicated the closeness of forest cover land and agricultural land based on Bray-curtis matrix. Differential abundance analysis Lefse showed forest cover land was the most enriched with maximum species abundance. Functional analysis based on 16s rRNA gene showed that the biosynthesis of lipopolysaccharide (LPS) was the major metabolic function in gram negative bacteria found in all the landforms. This biosynthesis is essential for soil bacteria to survive, adapt, and interact with one another, as well as with the complex and dynamic soil ecology. The study documented residential microbial diversity of sensitive ecological niche and generated the baseline information which needs to be further studied.

Key words: Critical zone, Landforms, Soil health, Microbial diversity, Enzyme activity.

Exploring India's Parasitic Ciliates (Phylum Ciliophora): Their Host Preferences and Habitat Diversity

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Abstract

Protozoa represents a significant taxonomic category as a sub kingdom comprising various parasitic members. Globally, there are approximately 50,000 described species of protozoa, with only 11,000 exhibiting parasitic behavior. Parasitic protozoa (PP) owing to their immense potential, cause harm to living organisms, and thus have emerged as an important research group both in science and economics today. In India, a total of 242 species of parasitic ciliates have been studied. This study delves into comparing the spatial distribution pattern of Phylum Ciliophora: their species richness and abundance across Indian states and union territories, along with their preferred habitats, and the type of hosts (vertebrate or invertebrate) they commonly associate with. The study comprehended that Phylum Ciliophora is primarily associated with ectoparasitism, accounting for 75% of the associations, while it also exhibits a minor proportion of endoparasitic associations (25%). They predominantly inhabit freshwater and marine environments. Among the studied species, 156 showed a preference for vertebrate hosts, while 86 exhibited a preference for invertebrate hosts. The Phylum was notably prevalent in West Bengal, constituting 51% of the total distribution, followed by Andhra Pradesh at 25%. This research reviews and reveals the diversity and distribution patterns of parasitic ciliates in India, with a focus on their preferences for hosts and habitats.

Keywords: parasitic protozoa, freshwater, ectoparasitism, spatial distribution, vertebrate, invertebrate

Insight into the possible role of microbes in male infertility

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Abstract

Infertility has been a long-standing global issue, with the male factor alone accounting for more than 24% of infertility. It can be caused by a variety of causes, such as lifestyle choices, environmental influences, health, medical resources and pathogenic microorganism infections. Numerous reproductive disorders can be brought on by bacterial infections of the male reproductive system. Recent years have witnessed a peaked interest in the male reproductive microbes, notably in semen and the prostate, because of its possible effects on male reproductive health, female partners, and the offspring. Male infertility has been linked to bacterial infections, yet the precise processes are still unknown. Moreover, oxidative stress can be induced by bacterial infections via a variety of signaling mechanisms. Chronic infections in the male urogenital tract may influence the parameters of the semen assessment (count or motility) or possibly cause apoptosis, which can have a deleterious effect on fertility. While additional reasons of male infertility are still being investigated, bacterial infections or colonization could be a probable reason for male infertility. However, limited research has been done till date to fully explore the origins, roles, and relationships between the semen microbiome and the prostate microbiome. In this connection, our study aims to unravel the complex interactions between microbiomes and infertility.

Keywords: Infertility, Microbes, Oxidative stress, Apoptosis

The exploration of microbial resistance mechanisms against antibiotics

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Abstract

Today, in our world, multi-purpose uses of antibiotics are often practiced for humans infected with microorganism in order to cure their disease besides the production of animals and agriculture. At the individual patient level, antibiotics are important in the management of severe infections by controlling invading pathogens. Resistance to antibiotics, especially the overuse and misuse of antibiotics create new strains of pathogens at population level and the dissemination of resistant strains is accelerated. The people and the patients are victims of antibiotic resistance effects in every healthcare organization and in almost every home. Infections resistant to drugs bring more pain and ravage animal agriculture and food production. As time goes and farming becomes more difficult, this will consequently affect the living standard of the people. Firstly, the effect of the cause on the life span of meat animals and how it can also pass from one organism to another in the food we take are some of the issues that arise. The spread of resistance genes has an impact not only on clinically relevant human isolates but also on community associated bacteria as well as food-producing animals. Growing threat concerning community-acquired drug resistant's, emergent pathogenic bacteria is one of the major public health issues. As for already, it is known that species of bacteria that can develop resistance can be found in animals, food, meanwhile, is quite often implicated as the source. My paper targets antibiotic use in animal production industry which was the primary cause directly responsible for the development of resistant strains of bacteria. It is true that even resistant bacteria strains exist in nature. Anti-bacterial meds, where the microorganisms are affected, are used to protect plants and animals from the virus, and in humans they are over-consumed by the medicinal dose. The more often a bacterial species is exposed to antibiotics, the more efficient becomes its long-term antibiotic resistance. This especially applies to the case if wide collection of new antibiotics is involved.

Key words: Antibiotics, microorganisms, pathogens, healthcare, food chain.

A Pedagogical Approach to STEM Education using Mixed Reality

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Abstract

The key to India becoming a developed nation in the next twenty-five years is through technological innovations. These innovations shall lead to product/services development that provide solution to various societal problems indigenously. Technology always fascinate students and it is necessary that they are exposed to it at the right stage. Virtual Reality (VR) and Augmented Reality (AR) are two of the well-known industry 4.0 technologies that have potential to transform the world. Their amalgamation with IoT, 3D printing, AI, Data Analytics etc. will take innovation to a new level. Mixed reality is a technology that encompasses the best of VR and AR and creates a space for learning where digital and physical objects can co-exist and interact immersively. Mixed reality applications are more effective in visualizations of complex 3D structures that are otherwise difficult to illustrate in 2D environments and phenomena that are invisible to the naked eye. The present work highlights an immersive approach through the use of various open domain visualization and designing applications such as ShapesXR and Gravity Sketch which are deployed on Meta Quest 3 headset to design 3D models and visualize various topics under STEM. An online library with basic templates for STEM models has been developed to facilitate beginners incorporate mixed reality into STEM learning. The efforts showcase the transformative potential of mixed reality technology in STEM education by enhancing the cognitive perceivance of learners.

Key words: Mixed reality, Virtual Reality, Augmented Reality, STEM learning

Intelligent micro-irrigation system

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Abstract

India is an agriculture dominant country where farmers are dependent on rains as well as on natural/ artificial water reservoirs for irrigation. The water reservoirs have a limited irrigation capacity which is further depleted by over irrigating the fields beyond the plant/crop requirement. Thus, it is very crucial to design an automated irrigation system to not only conserve water but save onto the unnecessary farmer expenses besides evading environmental damage, soil degradation and hence, proliferating suboptimal plant growth. The present work addresses this issue by designing a methodical water conservation framework based on Internet of Things (IoT) and Artificial Intelligence (AI). This innovative intelligent micro-irrigation system, that uses pipes deep-rooted into the soil to deliver water directly to the root zone, will solve the farmers' concerns pertaining to water conservation, soil degradation and optimum plant growth. The proposed system comprises sensor nodes deployed across the agricultural field near the plant roots to monitor real time soil moisture levels**.** The data from these sensor nodes is collected on IoT based server. The data collected is processed using AI algorithms to determine precise irrigation requirements for different areas of the field and accordingly control the water flow. It is further envisaged to integrate machine learning techniques as well as camera to continuously adapt and optimize irrigation schedules to meet the specific needs of crops, thereby reducing water wastage and contributing towards the Sustainable Development goals (SDG 6**).**

Key words: Internet of Things, Artificial Intelligence, micro-irrigation, real-time soil moisture levels, machine learning, SDG 6

AMR crisis: An overlooked upcoming disaster for India

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Abstract

Antimicrobial resistance (AMR) has become a global public health crisis, and India, as a densely populated country with limited access to quality healthcare, is no exception. This poster presentation focuses on the varying factors that contribute to the rise of AMR in India. It also examines major challenges that can be anticipated in fields such as agriculture, animal farming, aquaculture, and climate change as a result of this crisis. The epidemiological impact of AMR on the spread, diagnosis, and treatment of infectious diseases like malaria, gonorrhea, cholera, etc. is also analysed.
The molecular mechanisms of drug resistance development are also discussed, including the role of gene transfer and transposable elements. Currently, several measures to curb AMR are being implemented in India. Some of them, including Antimicrobial Stewardship Program, National Action Plan on Antimicrobial Resistance (NAP-AMR), and the Red-Line campaign, are also highlighted here. While these measures have shown some success in reducing the use of antibiotics in some states and union territories, there is still a long way to go in preventing the emergence and spread of resistant strains.
Finally, some recommendations are presented, including the need for microbial literacy, surveillance of AMR, and vaccination strategies. With the continued efforts of healthcare professionals, policymakers, and researchers, it is hoped that the AMR crisis in India can be addressed and controlled.

Key words: Drug Resistance, Infectious Diseases, Public Health

Identification and i*n-silico* analysis of HUB genes in active and latent tuberculosis Gene expression profiles

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Abstract

India accounts for the highest burden (28%), of global incidence of Tuberculosis (TB). Tuberculosis is a chronic infectious disease caused by ***Mycobacterium*** **tuberculosis.** The disease is characterised by widespread pulmonary infection with high mortality if not treated properly. The long treatment regimen often makes the afflicted person to drop treatment midway, leading to the problem of MDR and XDR Tuberculosis. Additionally, many times the infection stays asymptomatic leading to occurrence of latent TB. Globally, latent TB burden is one-fourth of world's population. People with latent infection can progress to active TB or undergo reactivation at any time. Management of latent TB can prevent progression to active disease. There is an urgent requirement to determine biomarkers for early diagnosis and correct treatment. The objective of our present study was to explore and analyse available gene expression datasets for differentially expressed genes amongst latent, active and under- treatment TB. Dataset namely, GSE19491 with 498 arrays was selected after exploring datasets on GEO (Gene Expression Omnibus). We got significant ($p<0.01$) gene-expression profiles on comparing 54 active and 69 latent TB samples with 38 healthy-controls: latent with active TB and 14 post-treatment along with 7 before treatment TB samples. About 8386 genes were downregulated and four were upregulated in latent TB. Similarly, we compared expression among Active TB, latent TB, after and before treatment samples to obtain comparative expression profiles. Gene Ontology analysis using DAVID (Database for Annotation, Visualization, and Integrated Discovery), software enriched many significant terms such as "T-cell activation" and "Regulation of type I interferon production" were selected for network analysis. Based on our analysis on STRING (Search Tool for the Retrieval for Interacting Genes/Proteins), we could establish the hub-genes RIPK2, NFKB1, TRAS6 and MYD88. Hub genes could be studied further as potential drug targets for future therapeutic or prognostic purposes.

Key words: Tuberculosis, Differentially Expressed Genes, Bioinformatics, GEO2R

Influenza Virus: A Study of its Virology and Future Prospects of its Treatment

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Abstract

Influenza virus from the Orthomyxoviridae family remains to be a major health concern for the human population resulting in yearly epidemics and pandemics occasionally. The virus is categorized into four subtypes; A, B, C and D out of which influenza A and B are in circulation among humans. According to the WHO, influenza virus causes nearly 500,000 deaths annually. The respiratory droplets from an infected person results in the transmission of the virus and the symptoms might resemble that of other respiratory viruses making its diagnosis difficult. The novel pandemic strains are mainly a result of the point mutations and the genetic reassortments resulting in high morbidity. Owing to the high evolutionary rates of the virus, the antiviral treatments have to be revised regularly thus it becomes necessary to trace the evolutionary dynamics of the virus to produce efficient treatments. This can be done using various meta omics studies like genomics, proteomics, transcriptomics and epigenetics. The useful targets can thus be identified for the formulation of drugs and vaccines with high efficacy. In-silico studies can help in identification of CpG dinucleotides and conserved epitopes of the virus which are necessary for the pathogenicity and replication of the virus. This can be useful for the production of a broad spectrum or universal vaccine against existing strains of influenza virus.

Keywords: Influenza virus, meta omics, in-silico studies

Breaking trails in diagnosis: Unravelling MTB challenges

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Abstract

The diagnosis of *Mycobacterium tuberculosis,* the causative agent of tuberculosis, is crucial for effective management and control of this infectious disease. Various diagnostic methods have been developed to detect and confirm tuberculosis infections. Accurate identification of Mycobacterium tuberculosis is crucial for managing tuberculosis.

Traditional methods like acid-fast staining and culture, with sensitivity levels of 20-70%, are foundational. Molecular tests, such as nucleic acid amplification, offer rapid and direct detection, improving precision. Serological tests show potential, especially with a high negative predictive value.

Immunodiagnostic assays detecting specific antibodies provide simpler, faster, and cost-effective diagnostics. Challenges in paediatric diagnosis emphasize the need for advanced technologies. Rapid sputum tests amplifying M. tuberculosis RNA or DNA show promise.

Integrating traditional and modern methods is essential for precise diagnosis and effective treatment decisions, enhancing patient outcomes and global disease control.

In conclusion, the current solutions available like TrueNAT and Genexpert, used for diagnosis of drug resistance tuberculosis are not very cost effective as the initial cost of machine installation is very high, also as these tests can be run only on specific machines, they cannot be used in every diagnostic centre resulting in restricted usage and testing.

So we propose the use of RT PCR based diagnostic testing which is fast, affordable and can be used in every diagnostic centre since it can run in any RT PCR machine.

Profiling xenobiotic degrading microbial biodiversity from Bhalswa sanitary landfill, Delhi: A metagenomic approach

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Abstract

Landfill and open dumping of municipal solid waste (MSW) is a common method of solid waste disposal globally (more than 70%). India is a developing country and is also facing this issue due to rapid industrialization, urbanization and population explosion. Presence of toxic xenobiotic compounds in landfills such as pesticides, polycyclic aromatic hydrocarbons (PAHs), personal care products (PCPs), active pharmaceutical compounds, heavy metals, etc., pose a significant threat to both the environment and human well- being. Present challenges in degradation of xenobiotic compounds are due to their complex chemical compositions and their potential for bioaccumulation and biomagnification. Physical and chemical techniques like coagulation, filtration, adsorption and ozonation can degrade these xenobiotic compounds, but there are various challenges such as cost effective, lack of space, complex procedures, regulations, and toxic by-products. In recent years, microbe-based bioremediation of xenobiotic pollutants, has emerged as the most efficient, eco-friendly, and cost-effective approach for eliminating these harmful compounds. Metagenomics, over conventional culture-based methods, is a powerful tool to explore the microbial diversity of landfill. This study aimed to identify xenobiotic-degrading bacterial genera in Bhalswa landfill, North Delhi using metagenomics approach. Soil samples from diverse microhabitats within the landfill were collected and using 16S rRNA gene (v3-v4 region) sequencing, coupled with bioinformatics analysis tools like QIIME2, DADA2, etc., the taxonomic classification and diversity of bacteria was assessed. These results will help in determining the most efficient microbe for biodegradation and bioremediation of xenobiotic compounds in landfills.

Keywords: Xenobiotic compounds, xenobiotic degradation, municipal waste landfill, metagenomics

Synthesis of magnetic nanoparticles and their role in enzyme catalysis

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Abstract

In recent years, Nanoparticles have gained more attention in the field of research due to their unique properties, high surface area and small size. Among these, the magnetic nanoparticles with unique magnetic properties have been widely used in different fields such as biomedicine, agriculture, Energy, catalyst etc.

Enzymes play a crucial role in biological systems by catalysing chemical reaction necessary for cellular processes like catalysis, specificity, regulations etc. Nanoparticles can alter enzyme activity in a variety of ways, depending on their composition, size, shape, surface charge, and interaction with the enzyme. Nanoparticles can have a variety of effects on working of the enzymes. They can interact directly with enzymes' reaction sites or alter how enzymes interact with their targets. This can cause enzymes to work quicker or slower, or even alter the types of processes that they can do.

Iron oxide magnetic nanoparticles (MNPs) with smaller sizes are the best choices to analyse the enzymatic applications. MNPs can enhance the enzymes activity via immobilization, enhancement in mass transfer, protection of enzymes, targeted drug delivery. Especially, the superparamagnetic magnetite, Fe_3O_4, is the most commonly used iron oxide because of its high biocompatibility and low toxicity.

In this presentation, the various routes of synthesis of magnetic nanoparticles, their role in enzyme catalysis by the researchers in last ten years has been discussed.

Decoding the monkeypox virus: Unraveling phylogenomics, host-pathogen interactions, and mutational landscapes

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Abstract

Monkeypox virus (MPXV) poses a significant threat as a potential global outbreak, underscoring the need for accelerated genomic research to develop effective prevention and treatment strategies. This study investigates the evolutionary lineage of MPXV using whole-genome-based SNP phylogeny and core-genome phylogeny, involving high-quality isolates primarily from Europe and North America. Four major clusters were identified among 628 MPXV isolates through SNP-based analysis, revealing distinct evolutionary lineages, complex epidemiology, and diverse geographical distributions. Core-genome phylogeny further elucidated the conservation of genomic regions and highlighted unique subclades with specific regional dominance. Evolutionary dynamics analysis revealed positively selected genes, including L5, A22, DUT, E8L, E7, CrmB, and a putative FAD-linked protein, potentially contributing to immune evasion and enhanced viral replication. The host-pathogen interaction network unveiled key viral proteins like E3, SPI-2, K7, and CrmB as regulatory hubs inhibiting the host's innate immune response. Structural analysis of E3 and CrmB proteins revealed potential stability disruptions due to specific mutations. While identifying numerous mutations in the newly emerged clade, this study emphasizes the urgency of expediting genomic analyses of recently detected strains worldwide to develop improved preventive and therapeutic measures against MPXV.

Exploring Antiphage Potential of Medicinal Plant Extracts : A Promising Strategy for Phage Control in Dairy Industry

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Abstract

Bacteriophages possess significant threat to commercial dairy manufacturing facilities by infecting probiotic starter cultures and deteriorating the product quality causing great economic losses in the dairy industry. Despite routine phage control measures, these phages exhibit resistance to conventional methods, including pasteurization. This study investigates the effectiveness of two medicinal plants viz *Withania somnifera* and *Aegle marmelos* against bacteriophages of *Lactococcus lactis,* a probiotic culture used in cheese making. Solvent-guided fractionation of *Withania somnifera* root sample and *Aegle marmelos* leaf sample in different solvents identified methanol to be the best solvent for extracting bioactive compounds exhibiting most pronounced inhibition of the phage infection compared to petroleum ether, diethyl ether, ethyl acetate, and acetone. Preliminary phytochemical tests detected the presence of major secondary metabolites like alkaloids, phenols, tannins in *Withania somnifera* roots while alkaloids, phenols, saponins, and flavonoids were detected in *Aegle marmelos* leaf. Antiphage assay using crude methanolic extract of *Withania somnifera* showed a significant reduction in phage titre with a log reduction of 0.713 ± 0.08 after 20 min of exposure and 0.736 ± 0.18 after 90 min of exposure. However, for *Aegle marmelos*, a log reduction of 0.0846 ± 0.083 after 20 min of exposure and 0.708 ± 0.081 after 90 min of exposure was reported. Notably, this reduction in the phage titre was seen without any observed inhibition of the host. LC-MS analysis of *Withania somnifera* identified key compounds like Withaferin A, and Withasomnine while *Aegle marmelos* exhibited prominent compounds like Carnegine and Piperine. Additionally, GC-MS analysis for both the plants revealed the presence of several volatile compounds. The presence of these compounds in these plants suggests their potential application in addressing phage related challenges in the dairy industry.

Key words: Dairy phage, Antiphage, Medicinal Plants, *Lactococcus lactis*

Effect Of Paraquat-Based-Herbicide (Pbh) On Anti-Microbial Immune Response In Human Monocytic Macrophage Cell Line

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Abstract

The escalating global population and the demand for food have triggered a surge in the usage of chemical-based compounds in agriculture, notably herbicides and pesticides. While these chemicals offer rapid results at low costs, their widespread application poses significant environmental and health risks. This study examines the impact of Paraquat-Based-Herbicide (PBH) on antibacterial immunity, employing the THP-1 cell line as a model for human monocytic leukemia cells. The study evaluated the macrophage-mediated bactericidal activity against *Pseudomonas aeruginosa* in the presence and absence of herbicides and focused on the cytotoxic impact of PBH dose-dependent on THP1 cells on cellular viability and reactive oxygen species (ROS) formation. In this study, we investigated the cytotoxic effects of PBH on THP1 cells using the MTT assay, the antibacterial ability by assessing macrophage-mediated bactericidal activity, and the phagocytic capability of THP-1 cells through CFU counting. ROS production in the presence of PBH concentration was measured using the NBT assay. Our findings revealed that PBH exhibited deleterious effects on macrophages, compromising their morphology and functionality. Evaluation of its antibacterial activity and assessment of phagocytic activity in THP-1-derived macrophages indicated suppression of immunological function induced by the herbicide. The data demonstrated a significantly higher bactericidal activity in treated cells, suggesting suppression of phagocytosis capability by the herbicide. Additionally, the cytotoxic effect of PBH led to a decrease in ROS levels. Suggesting the necessity for exploration of the adverse effects of herbicides, shedding light on their potential implications for human health and the environment.

Keywords: ROS, Cytotoxicity, PBH, Macrophage

SARS CoV2 wild type *vs*. mutants induced cytokine production in A549 cells

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Abstract

Multiple variants of SARS CoV2 have emerged throughout different parts of the world since its appearance in Dec, 2019. These variants, especially variants of concern, have an impact on transmission ability, pathogenic potential, diagnosis and vaccine effectiveness. SARS CoV-2 gets internalized into a susceptible host cell through its spike protein interaction with the cell surface ACE-2 receptor, potentially correlating with the disease severity. Five SARS CoV-2 variants of concern: alpha, Beta, Gamma, Delta and Omicron have been identified based on epidemiological update by the WHO. Of which, Delta variant that was initially identified in India was responsible qfor second wave of COVID-19 infections in India. In the current study, we sought to understand the immunopathogenesis induced by the interaction of spike protein mutants with ACE-2 receptor binding and understand their role in causing pathogenesis. We had chosen five mutations: E484K, K417N, D614G, P681R, and P681H including delta variants, as these were reported to have a link with higher pathogenicity in the literature. All five mutants were generated by site-directed mutagenesis using full length wild type spike protein encoding gene construct. The expression of all the mutants were confirmed by IFA staining. The interaction of ACE2-spike protein mutant vs. wild-type driven cytokine production was measured by real-time PCR. The binding affinity of spike protein and its mutants with host cell surface ACE-2 receptor is being evaluated. Results will be presented.

Effect of different carrier material and delivery methods on in field efficacy of already evaluated bacillus based bioformulation

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Abstract

Bioformulation is defined as the biologically active substance that contains active microbes or their metabolites formulated in an inert material known as carrier materials. The microbes that have been used to prepare bioformulation have plant growth promoting properties that help plants to promote growth, increase soil fertility, nutrient acquisition, and control disease. Various organic and inorganic carrier materials have been used to prepare bioformulation for plant growth promoting microbes depending on their shelf life, stability of the inoculant, and ecofriendly nature. Now a days, bioformulation has been extensively used to enhance the yield of crops as it can be utilized as substitute for chemical fertilizers. Bacillus sp. strain D5 (BarD5) native to saffron, isolated from cormosphere has various plant growth promoting (PGP) activities like Indole-3-acetic acid activity, phosphate solubilization, protease production, amylase production, siderophore production. Previously Bar D5 based bioformulation has been prepared using calcium carbonate as carrier material along with corm dip delivery method and laid down field trials at different traditional and non-traditional locations of saffron cultivation of Jammu and Kashmir UT. Bar D5 treated samples have shown increase in morphological characteristics along with yield of saffron. Till now only calcium carbonate based Bar D5 bioformulation has been used for cultivation of saffron. So, there is need to evaluate different carrier materials along with suitable delivery method to cultivate other economically important crops.

Keywords: Bioformulation, Carrier materials, Bar D5, shelf life.

Botanical Extracts as Sustainable Catalysts for organic transformations

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Abstract

The principles of sustainable chemistry have become paramount in the field of organic chemistry, driving the exploration of environmentally friendly methods for organic transformations. A significant area of interest lies in the utilization of plant cell cultures and various plant components as biocatalysts, offering a sustainable approach to chemical synthesis. These components, including roots, bark, leaves, fruits, peels and seeds possess a rich repertoire of chemicals such as vitamins, proteins, pectin, starch, sugars, polyphenols, flavonoids, organic acids and bases, which exhibit promising organocatalytic properties. The integration of plant extracts as catalysts and solvents not only aligns with the principles of Green Chemistry but also provides a sustainable alternative to traditional chemical catalysts. Using plant/fruit extracts in organic synthesis promotes sustainable practices, reduces ecological impact and facilitates cleaner production techniques. Biotransformation for bond construction is essential in sustainable chemistry and integrating it into commercial fields can create an eco-friendlier environment. The synthesis of 2-amino-4H-pyrans can be done in the presence of WETS (water extract of tamarind seed ash). Henry reaction can be catalyzed by WEB (water extract of Banana peel). Multicomponent synthesis of Pyrano[2,3-*d*]pyrimidinones and 3,4,5-substituted furan-2(5H)-ones are also catalyzed using Ver fruit juice and watermelon juice respectively. The reduction reactions of urea-ketone and nitro group on aromatic compounds are reported to be catalyzed by tomato juice and grape juice respectively. Citric acid also acts as biocatalyst for deprotection of phenylhydrazones, semicarbazones and oximes to their corresponding carbonyl compounds. The synthesis of tetrahydrobenzo[b]pyrans and 3,4-dihydropyrano[c]chromenes was catalyzed by using alcoholic extract of spinach leaves. This review emphasizes the potential of utilizing natural resources, specifically plant tissues and fruit juices, as stimuli for bond construction, resulting in the synthesis of molecules with notable pharmacological applications.

Keywords: Sustainable Chemistry, Biocatalyst, Plant extracts, Fruit juices, Ash

Extraction and purification of a heat-resistant protease from *Thermus parvatiensis*

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Abstract

The Himalayas are recognized with ecologically extreme diverse such as hot springs, cold deserts, glaciers, grasslands, medicinally important plants, and so forth. Advancement in science and technology revealed a huge and complicated world of these tiny warriors inhabiting extreme high temperature environments and playing key roles in the environmental process. The microorganisms living in these environments possess several structural and functional adaptations to perform normal life processes. These microorganisms have been recognized as the source of thermozymes and novel heat-stable proteases as bioactive compounds of industrial and biotechnological importance. Our group has successfully isolated and cultivated *Thermus parvatiensis* from Manikaran, Himachal Pradesh, India, hot-spring water sample (temperature 96°C) and taxonomically characterized. Further, its complete genome was sequenced, leading to the identification of various industrially important thermostable enzymes such as DNA polymerase enzyme and extracellular proteases. Proteases account for about 60% of the enzyme market in the world, and they are used in various industrial applications, especially in the food, pharmaceutical, detergent, and leather processing industry. In industrial applications, serine protease is largely utilized in detergents as a supplement for cleaning since they promote the detergent efficiency, facilitating the reduction of the leftover protein stain. We aim to clone the gene responsible for the expression of serine protease. Protease gene from genome will be identified, codon optimized and clone in *E. coli* expression vector. The protease so produced will be purified and its activity as a detergent at different temperature enzyme from 28°C-80°C will be tested.

Key words: Thermostable protease, Transformation, Purification

Genetic engineering of *Bacillus subtilis* for secretion of Hexachlorocyclohexane (HCH) catabolic proteins for sustainable bioremediation of HCH contaminated sites

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Abstract

Massive use of Hexachlorocyclohexane (HCH) an organochlorine pesticide in the past decades has become a global concern due to their persistence in all the strata of ecosystems and detrimental effects on non-targeted species. A number of microbial species belonging to the genera, *Sphingobium*, *Sphingomonas*, *Sphingophyxis*, *Streptomyces*, *Microbacterium*, *Pseudomonas* and *Bacillus* have been reported to degrade HCH isomers, including the most recalcitrant β-HCH isomer. However, application of potential degraders at HCH contaminated sites for bioremediation poses many challenges due to the requisites such as adequate microbial biomass, their thriving ability in suboptimal conditions, efficient accessibility to the pollutant and battling indigenous predation. To counter some of these challenges, in this study, we have genetically modified *Bacillus subtilis* bacterial strain to constitutively express and secrete HCH catabolic enzymes. Recombinant DNA molecules (pYS5-LinA and pYS5-LinB) constructed by cloning HCH catabolic genes', *linA* and *linB*, amplicons from *Sphingobium indicum* B90A (a well-known HCH degrader) genome linked with an N-terminal signal sequence in a shuttle vector plasmid pYS5 are introduced into *Bacillus subtilis*. The engineered *Bacillus* strains, Bas-LinA & Bas-LinB showed heterologous expression and secretion of the LinA and LinB proteins, respectively. Bas-LinB demonstrated 100% degradation of 5ppm β-HCH in liquid medium within 18h of incubation, with the production of metabolite, tetracholrocyclohexanol. Bas-LinB also showed 30% reduction of HCH in soil matrix in 15 days. Abilities like rapid multiplication, secretion of the catalytic enzyme and sporulation under unfavourable conditions reveal potential of engineered *Bacillus* strains for reclaiming HCH-polluted sites.

Keywords: *Bacillus subtilis*, hexachlorocyclohexane, genetic engineering, catabolic enzyme, secretion, Bioremediation

Enhancing Antibiotic (Kanamycin) efficacy against *Micrococcus luteus* with *Zingiber officinale*: A Synergistic Approach

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Abstract

The global issue of antimicrobial resistance demands innovative approaches to enhance the effectiveness of antibiotics. Leveraging the rich medicinal properties of plants, particularly *Zingiber officinale*, presents a promising solution. Known for its diverse therapeutic benefits, including addressing ailments like arthritis, digestive disorders, and cancer, it offers a compelling avenue for improving antibiotic performance. The study investigated the potential of powdered extracts from *Zingiber officinale* rhizomes to augment the efficacy of the antibiotic kanamycin against gram-positive bacteria, specifically *Micrococcus luteus*. The study unfolded in two phases, involving the extraction of rhizome compounds using various solvents (petroleum ether, chloroform, methanol, and distilled water), followed by testing for synergistic effects with kanamycin through Disc Diffusion assay.

Among the extracts, the chloroform extract showed the most promising results, demonstrating a 15 mm zone of inhibition when combined with kanamycin, compared to 10 mm with kanamycin alone and 3 mm with chloroform extract alone. While petroleum ether and methanol extracts showed a 2 mm zone of inhibition, synergistic effects with antibiotics were not observed.

The analysis of *Zingiber officinale* rhizome extracts and their concentrations provides valuable insights into enhancing the efficacy of kanamycin against *Micrococcus luteus*. These findings underscore the therapeutic potential of *Zingiber officinale* and other plant extracts in combating the challenge of antibiotic resistance.

Keywords: Synergism, *Zingiber officinale*, Zone of inhibition, Antibiotic resistance, Disc Diffusion assay

Identification of hydrolytic gene in potential biocontrol agent for the management of wilt disease in pigeonpea

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Abstract

Cajanus cajan (L.) Millsp. wilt disease of pigeonpea infected by *Fusarium udum* causes crop losses worldwide, including India. To identify the potential biocontrol agent against wilt disease, forty-seven isolates were evaluated for their antagonistic activity against *F. udum* on a potato dextrose Agar (PDA) medium using the dual culture method. The interaction of *F. udum* and antagonistic bacteria was studied in PDA under *in vitro* conditions, and lysis fungal hyphae were observed using a scanning electron microscope (SEM). Hydrolytic enzymes such as cellulase, pectinase, amylase, lipase, protease assay of *in vitro* conditions and primer based on hydrolytic genes like chitinase and 1,3-glucanase genes, amplified at 402 and 750 bp, respectively, were used. Out of forty-seven bacterial isolates, only eight isolates, viz., *Bacillus amyloliquefaciens* CFLB 31, *B. velezensis* CFLB 24, *B. subtilis* CFLB 11, *Stenophomonas rhizophila* CFLB 26, *S. matalophil* CFLB 47, *Microbacterium* sp. CFLB 28, *Glumibactor nicotiana* CFLB 18 and *Pseudoarthrobacter* sp. CFLB 36 showed promising antagonistic activity against *F. udum* with 70 to 84% inhibition in a dual culture method assay. Among them, three *Bacillus* species (*B. amyloliquefaciens*, *B. velezensis*, *B. subtilis)* and *S. maltophilia* CFLB 47 were the most effective biocontrol agents against *F. udum* under *in vitro* conditions**.** The fungal hyphae lysis was recorded during fungus and bacteria interaction on PDA. These isolates were screened for the production of hydrolytic enzyme activities, and they showed positive for the production of enzymes such as pectinase, amylase, lipase, protease, and cellulase under *in vitro* conditions. These isolates were PCR amplified with chitinase and β-1,3-glucanase-related genes at 402 and 750 bp, respectively. The results propose that the eight potential strains and their hydrolytic enzymatic properties made them promise to manage the wilt disease of pigeon peas.

Fabrication of polymeric nanoparticle formulations of triphala "nanotriphala"- as an efficient antimicrobial agent

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Abstract

Increased use and misuse of antibiotics over a period of time has led to the development of anti microbial resistance to many drugs. Livestock feed has been a major contributing factor in the spread of AMR from antimicrobials. According to a study published in january2022,it has been observed that approximate 1.2 million deaths were the cause of antimicrobial resistance infections in 2019 so the World Health Organization [WHO] developed SDG3 which indicates proper guidelines to all countries to deal with the antimicrobial resistance .Therefore, polymeric nano nanoparticles were fabricated to encapsulate the drug as a strategy to deliver pharmaceutical agents or drugs to the targeted tissue precisely hence, demonstrating better efficiency and safety. Nanoformulations help to reduce overall dose thereby reducing the related toxic side effects. Nanoparticles resolve the drug solubility problem as found in conventional Drug Delivery System [DDS]. Triphala [Tri- three, phala- fruit] is a traditional ayurvedic polyherbal formulation which consist of three medicinal plants: *Terminalia chebula* [Haritaki]; chemical constituents: chebulic acid and gallic acid, *Terminalia bellericca* [Bibhitaki]; chemical constituents: tannic acid and *Emblica officinalis* [Amalki] - Rich in vitamin C and some oil. It is classified as Tridoshic rasayana in ayurvedic medicine as it promotes longevity and rejuvenating effects on three doshas Vata, Pitta and Kapha. Triphala encapsulated polymeric nanoparticle formulations are characterised for their size in nm. Synthesis of polymeric nanoparticle formulation of Triphala - using micellar aggregates of copolymers of N-isopropylacrylamide [NIPAAM] and N-vinyl-2-pyrrolidone [VP]. Alcoholic extraction using a Soxhlet apparatus was performed to extract the pure form of Triphala. Antimicrobial efficacy of the formulation was evaluated by disc diffusion methods on different microbes. A comparison of nanoformulation is done with marketed available kanamycine and extract of triphala. Result is showing the efficient antimicrobial activity of nanoformulation as compared to ampicillin and triphala.

Keywords: Triphala, Nanopraticles, AMR, SDG3, Ayurveda, NIPAAM

Probiotic characterization of lactic acid bacteria (LAB) isolated from arrowroot *(Maranta arundinacea* L.) powder

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Abstract

Arrowroot (*Maranta arundinacea* L.) is a significant tuber primary recognized for its high quality of starch, fibre and long history of use. The soluble dietary fibres present in arrowroot can act as prebiotics and helps in increasing the biomass of probiotics. Sample of Arrowroot powder was collected from the Palakkad district, Kerala, India. Lactic acid bacteria (LAB) were isolated from enriched arrowroot powder at the dilutions of 10^{-4} and 10^{-6}, using MRS (de Mann, Rogosa, and Sharpe) medium. Five isolates (ARP-1 to ARP-5) were selected, and characterized for their probiotic properties. ARP-1 and ARP-5 found to utilize all five sugars (dextrose, sucrose, maltose, lactose, and fructose) without any gas formation. Isolates, ARP-2, 4, and 5 recorded consistent increase in growth at elevated concentrations of bile salts (3% and 5%), lower pH levels (2, 3, and 4), various temperatures (4°C and 37°C), and NaCl concentrations (8% and 10%) after 4 hours of incubation. All the five isolates were tested for its antibiotic resistance, where ARP-1 and ARP-4 exhibited high resistance to penicillin, gentamicin, and vancomycin. ARP-5 was found to be the most promising isolate, and selected for the development of probiotic drinks.

"AMR and food borne pathogens"

Phylogenomic analysis of Campylobacter: Perspectives on pathogenic potential

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Abstract

The disease known as campylobacteriosis is brought on by a number of species of the genus *Campylobacter* that are common in both people and animals. It is known that a protracted *Campylobacter* infection raises the possibility that healthy cells could develop into malignant ones. Many medical conditions, including colon cancer and mucosa-associated lymphoid tissue lymphoma, have been related to *Campylobacter.* Thirteen species of Campylobacter including, *C. jejuni, C. coli, C. fetus, C. lari, C. hyointestinalis, C. rectus, C. insulanigrae, C. sputorum, C. helveticus, C. upsaliensis, C. mucosalis* and *C. ureolyticus* are considered as pathogenic species according to a number of previous studies. However, the pathogenic potential of other species has not been investigated. Therefore, in this study, the phylogenomic position of the *Campylobacter* spp. was elucidated by using the 16s rRNA gene, 31 bacterial marker genes, and whole genome based ANI analysis and tetra nucleotide frequency analysis to recognize how other species of *Campylobacter* are related to the pathogenic spp. of the genus. According to this study, major pathogenic species including *C. jejuni, C. coli, and C. fetus* are phylogenetically related to non-pathogenic or minor pathogenic species like *C. hepaticus, C. taniopygae, C. estrildidarum, C. aviculae, C. iguaniorum, C. hyointestinalis,* and *C. laninae*. Further, comparing the Cdt toxin genes of *C. jejuni* to the Cdt genes of other species of the genus that allowed to further explore the pathogenicity potential. The results of this investigation showed that the Cdt toxin genes of *C. jejuni* are more identical to those of *C. vulpis, C. upsaliensis, C. helveticus, and C. pleoridis* species. Based on our findings, we suggest that there is a possibility that some non-pathogenic species may eventually turn pathogenic. Additionally, comparative analysis of the Cdt genes of *C. jejuni* to the Cdt genes of the other species of the genus indicates that *C. vulpis, C. upsaliensis*, *C. helveticus*, and *C. pleoridis* species may exhibit oncogenic potential. Further other virulence factor identified and compared among the genus which strength the presence of pathogenic potential in species of *Campylobacter* genus.

Key words: *Campylobacter*, cytolethal distending toxin, cancer, gastrointestinal infection.

SeqCode – Origin and its Unsung Heroes

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Abstract

SeqCode is a Novel Nomenclatural Code used to designate the valid names of Prokaryotes based on their Genetic Information. Due to the inaccessibility of the majority of prokaryotes in their pure cultures, they do not meet the criteria for nomenclature under the International Code of Nomenclature of Prokaryotes (ICNP). To tackle this predicament, the **Code of Nomenclature of Prokaryotes Described from Sequence Data** (**SeqCode**) was introduced in 2022, which is a code of nomenclature that employs whole genome sequences as the fundamental basis for bestowing names upon prokaryotes. The SeqCode offers a framework that ensures the replicability and objectivity of nomenclature for all prokaryotes, irrespective of their ability to be cultured. It also enhances communication across various microbiological disciplines. The development of the SeqCode represents a significant stride in the investigation of uncultivated prokaryotes. By establishing a standardized system for the nomenclature and classification of these microorganisms based on their genetic information, the SeqCode will facilitate the exploration, comprehension, and comparison of these microorganisms, thereby enabling a better understanding of their environmental role and their contribution to the Earth's overall functioning.

While SeqCode was officially established in 2022, the foundation for its creation has been underway for the past decade. During this time, numerous scientists worldwide began recognizing the significance of genomic data in taxonomy. Here, we aim to uncover the origins of SeqCode and highlight the numerous contributions made by scientists from around the globe. Their collective efforts have played a crucial role in transforming the initially abstract concept into a tangible reality.

Key Words: SeqCode, Nomenclature, Uncultivated, Prokaryotes

Navigating the landscape of haloalkane dehalogenase engineering: From discovery to optimization

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Abstract

In recent years, enzyme technology has seen remarkable advancements, particularly in optimising haloalkane dehalogenases (HLDs). HLDs are versatile biocatalysts with applications ranging from environmental remediation to industrial processes. Here, a comprehensive review of strategies for optimizing HLDs performance and discovery, including bioinformatics, structural modification, enzyme discovery and rational design are presented. Through a detailed examination of these methodologies, their practical application in enhancing HLDs catalytic efficiency, substrate specificity, and stability, addressing challenges such as low catalytic efficiency, substrate promiscuity, and limited stability under varying environmental conditions are showcased. Optimized HLDs offer sustainable alternatives to conventional chemical methods and enhance the potential for scalability, ensuring long-term viability and efficiency in various applications. The effectiveness of optimization strategies in HLD research highlighted in this paper aims to guide researchers in selecting and applying specific methods to address key challenges and unlock the full potential of HLDs.

Keywords: Haloalkane Dehalogenases, Enzyme Engineering, Bioremediation, Biocatalysis

Re-integration of *Hypericum perforatum* L. with its root-associated and non-associated beneficial bacteria distinctively sculpts rhizosphere bacterial community structure and produces differential amounts of secondary metabolites

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Abstract

Hypericum perforatum L. (St. John's Wort) is a medicinal plant, globally consumed with an average annual sales exceeding 6 billion USD to treat depression. Plant flowering tops, considered the primary medicinal material, contain pharmacologically active secondary metabolites, hypericin and hyperforin. Deliveries of raw materials to the international market are primarily fulfilled through unrestrained plant harvesting from the wild stands. However, relying on wild collection cannot guarantee a steady supply of raw materials due to inherent phytochemical variability and deliberate adulteration. Plant domestication can support natural supplies and ensure supply of consistent quality raw materials. However, previous investigations suggest that medicinal plant domestication is frequently associated with a significant decline in secondary metabolites. The rhizosphere microorganisms can directly influence the contents of secondary metabolites. Hence, the re-integration of beneficial rhizosphere microorganisms selected from plants' wild stands is expected to uptick the production of secondary metabolites. However, no such efforts have been made; nevertheless, previous investigations demonstrated that plant-beneficial microorganisms augment the amount of secondary metabolites irrespective of the plant specificity. Albeit, comparisons of host-plant-associated and non-associated beneficial rhizobacteria in augmenting secondary metabolite contents are still obscure. To address these gaps, here we re-integrated *H. perforatum* plants with host-plant-associated and non-associated beneficial rhizobacteria at field scale. Established a comprehensive microbe-plant-metabolite regulation pattern for hypericin and hyperforin biosynthesis at rhizosphere bacteriome, metabolome, and transcriptional abundance levels. Notably, complete ammonia-oxidizing bacteria (Comammox *Nitrospira*), *Gemmatimonas*, and Vicinamibacteraceae associated with the highest hypericin and hyperforin accumulation, corroborating with higher expression of pivotal genes, *PKS2*, *POCP1*, *BBE*, *HPPKS2*, and *HPMT2* regulating their biosynthesis were found in the rhizosphere of plants treated with host-plant-associated beneficial rhizobacteria. This study enhances our understanding of how the host-plant-associated and non-associated beneficial rhizobacteria distinctively shape the rhizosphere bacterial communities and impact the biosynthesis of specialized metabolites, guiding future cultivation of *H. perforatum*.

Keywords: Rhizosphere, Plant beneficial rhizobacteria, Secondary metabolite biosynthesis, Bacterial community structure

Assessment of Diversity in Microbial Community through Metagenomic Analysis of an Integrated Constructed Wetland used for treatment of Sewage

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Abstract

The microbial community diversity in Constructed Wetlands (CWs) plays a key role in the removal of pollutants from waste water. The integrated functional CW, which showed 75-95%, removal efficiency of different pollutants, was selected to understand and assess the extent of similarity in the microbial community diversity of the sludge of stabilizing pond and rhizospheric sediment of vegetated CW, using metagenomic approach. This is first report of the microbial community diversity of an integrated CW system used for in situ bioremediation of sewage.

The sludge samples (N1, N2, and N3) and sediment samples (N4, N5 and N6) were collected from stabilizing pond and vegetated CW, respectively of the integrated CW System (CWS) located at DDA Neela Hauz Biodiversity Park, Delhi, India. The DNA extracted and the raw samples were transported to Bionivid (Genomic Company in Bangalore, India) for sequencing of amplicons of 16S rRNA gene generated through PCR amplification processes using specific primerson Illumina Miseq. About 851109 filtered sequences (Reads) were generated. Using the statistical programmes, these reads are clustered into 6732 OTUs which are identified and classified into taxa ranging from species to plant kingdom through blasting off against Greengene database; α –diversity was also estimated using diversity indices and OTUs were clustered using Bray-Curtis distance Coefficient.

The sediment showed higher diversity than sludge and both formed distinct clusters. The OTUs are distributed among 2 kingdoms, 103 phyla, 227 classes, 337 orders, 320 families, 295 genera and 84 identified species. This taxonomic structure of microbial community is more diversified than the diversity reported by other workers. Both the sludge and sediment share some common taxa and some unique taxa specific to the sludge or sediment except at the phylum level. Most of these unique taxa are either rare or very rare with low abundance values. Further, relative abundance of different taxa at each taxonomic rank are markedly different between sludge and sediment and the top 5 dominant taxa at each taxonomic category are also different between sludge and sediment suggesting that the composition and structure of microbial communities are markedly diverse between sludge and sediment and contribute to richness of microbial diversity that makes integrated CWS perform better in pollutant removal than other CWs. Another unique structure of microbial communities of integrated CW system is that the number of abundant taxa decreases in descending order of taxonomic hierarchy i.e. phylum to species, while the number of rare and very rare taxa increases. Such structural organization in microbial communities of CWs might have evolved to sustain the diversity under limiting resources in CW environment.

The outcome of the present studies are that (i) the integrated CW has much higher microbial community diversity than the diversity reported for other CWs and the rich diversity can be used for optimizing the performance efficiency of CWs in the removal of pollutants from waste water and (ii) and the unique community structure observed might enable to sustain diversity under limiting environmental conditions.



Unveiling environmental effects on ground water and soil health - An Indian case study

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Abstract

Increasing industrialization driven by aggressive economic factors, intense agricultural activities and rampant population growth, have caused environmental hazards in terms of degrading ecosystems. Widespread contamination, arising from both natural origins and human activities poses significant risks to human health and water security due to movement of pollutants into soil and groundwater. Uncontrolled release of pollutants that take place through disposals of wastes as well as discharge of effluent or chemicals from industries and agricultural activities, contaminates the soil and groundwater causing environmental and human health problems. This has lead to increasing vulnerability of groundwater and soil resulting into which has become an important and worrisome global environmental issue. The leaching of pollutants into soil is a rather complex phenomenon influenced by variables such as soil properties (particle size distribution, inherent carbon content), meteorological parameters (e.g., rainfall, vapor pressure and temperature) besides a host of local factors. India, known for its dense population, soil variability and pronounced groundwater challenges, serves as a prominent case study. In this study we present an analysis of contamination disparities across various Indian states of semi-arid and cold regions, encompassing diverse assessment methods. The studies conducted reveal the consistent presence of fluorides and nitrates majorly, more often than not exceeding the permissible limits mandated by both the Bureau of Indian Standards (BIS) and the World Health Organization (WHO). The permissible limits recommended by BIS for fluoride and nitrate are 1.0 mg/L and 45 mg/L respectively, while WHO guidelines indicate 1.5 mg/L and 50 mg/L respectively. These contaminants pose skeletal and dental threats, methemoglobinemia, and even cancer. Similarly, in cold regions, nitrate exposure and pesticide residues exceeding BIS and WHO parameters, lead to gastrointestinal and other waterborne health concerns. The findings also indicated that the recommended limits of several quality parameters established by both BIS and WHO, including pH (8.5), Electrical Conductivity (EC) (1500 µS/cm), Total Dissolved Solids (TDS) (1000 mg/L), total hardness (500 mg/L), and total alkalinity (500 mg/L) majorly surpassed.

Key words: Leaching, Nitrate, Fluoride, Contamination, Environment

The potential of neonatal capsaicin with Cocos nucifera L. in Eczema treatment: A promising therapeutic approach

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Abstract

Eczema represents a prevalent chronic inflammatory skin disorder, characterized by multifaceted etiology and intricate pathogenesis. Conventional treatment modalities, though utilized extensively, often yield suboptimal long-term outcomes and may induce adverse effects. In response, the exploration of alternative therapeutic avenues, particularly those rooted in natural remedies, has garnered attention. This abstract investigates the potential of integrating neonatal capsaicin, derived from chili peppers, with *Cocos nucifera* L. (coconut) for the management of eczema. A comprehensive review of existing literature was conducted to evaluate the individual pharmacological properties of neonatal capsaicin and *Cocos nucifera* L. Relevant studies examining their efficacy in eczema management, both independently and in combination, were identified and analyzed. The focus was placed on outcomes related to symptom alleviation, including pruritus, erythema, and skin dryness, as well as any reported adverse effects. Neonatal capsaicin exhibits potent analgesic, anti-inflammatory, and antioxidant characteristics, effectively modulating sensory nerve function, attenuating neurogenic inflammation, and diminishing pruritus. Similarly, *Cocos nucifera* L. is renowned for its emollient, moisturizing, and anti-inflammatory properties, facilitating skin barrier repair and ameliorating inflammation. Combined application of these agents has shown promising synergistic effects in alleviating eczema symptoms, with studies reporting enhanced efficacy and reduced adverse effects compared to conventional therapies. The integration of neonatal capsaicin with *Cocos nucifera* L. presents a compelling therapeutic approach for eczema management. Their complementary actions offer a multifaceted strategy targeting key aspects of eczema pathophysiology, potentially leading to improved symptom control and enhanced patient satisfaction. Further research, including randomized controlled trials and mechanistic investigations, is imperative to validate and optimize this novel therapeutic modality. Nevertheless, this innovative approach holds significant promise in reshaping eczema care, offering new dimensions in holistic and sustainable dermatological treatment.

The β-lactam (Penicillin) resistant protein, Penicillin-Binding protein 1C showing cross resistance with non β-lactam antibiotic

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Abstract

Antibiotics are used in medical practices to treat the bacterial infections. They show bactericidal or bacteriostatic actions but sometime, antibiotics fail to work and create a problem of resistance. Currently, Antibiotic resistance is a serious global concern for the human population as well as animals. It started after the discovery of first commercial antibiotic, Penicillin. Initially, bacterial population was sensitive to penicillin but later on bacteria developed mechanisms for resistance. Penicillin-Binding protein 1C showing resistance against the β-lactam antibiotic, Penicillin and hence surviving in the contaminated toxic environmental matrices (antibiotic contamination in soil and water). Due to overuse of antibiotics, bacterial population encounters mutation at genomic level and get adapted against the toxic environment and hence become resistant against multiple antibiotics. Our study showed the interaction of Penicillin-Binding protein 1C with the β-lactam its cross resistance with the non β-lactam antibiotic through molecular docking. Study suggests the multidrug resistance property of Penicillin-Binding protein 1C in bacterial system.

Key words: Bacteria, Antibiotic, Antibiotic resistance, Cross resistance

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