RAMAIAH
College of Arts, Science & Commerce - Autonomous

MICROCON - 2026

National Conference on
Smart Microbiology: Artificial Intelligence, Nanotechnology, and Entrepreneurial Innovations Towards Sustainability

25 March 2026 | Bengaluru

Book of Abstracts

Editor
Juliya Rani Francis, Ph. D.

Organized by
Department of Microbiology
In Association with
Microbiologists Society, India

M. S. Ramaiah College of Arts, Science, and Commerce - Autonomous
Bengaluru - 560054, Karnataka, India

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ISBN (Print):
978-81-92756462

Published by:
Department of Microbiology
M. S. Ramaiah College of Arts, Science, and Commerce – Autonomous
Gate Number: 7 And 8, MSR Nagar, MSRIT Post
Bengaluru, Karnataka, India – 560054
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EDITORIAL COMMITTEE

Preface

It is with great honor and deep gratitude that we present the souvenir of MICROCON – 2026, a National Conference organized by the Department of Microbiology, M. S. Ramaiah College of Arts, Science, and Commerce (Autonomous), Bengaluru, in association with Microbiologists Society, India, on 25th March 2026.

The theme, *"Smart Microbiology: Artificial Intelligence, Nanotechnology, and Entrepreneurial Innovations towards Sustainability"*, captures the transformative era in which microbiology is evolving. By integrating microbial sciences with emerging technologies and entrepreneurial vision, MICROCON – 2026 has provided a dynamic platform for academicians, researchers, industry professionals, and students to share knowledge, deliberate on cutting-edge research, and foster collaborations that advance both scientific discovery and societal well-being.

The conference featured a plenary lecture and keynote address, oral and poster presentations, and vibrant discussions across diverse domains including microbial biotechnology, nanobiotechnology, environmental microbiology, bioenergy, diagnostics, and translational research. These sessions highlighted the pivotal role of microbiology in addressing global challenges related to health, environment, and sustainable development.

We extend our sincere appreciation to the college leadership, advisory and organizing committees, distinguished speakers, session chairs, reviewers, authors, and participants whose dedication, and contributions ensured the success of this event. Special recognition is due to the faculty mentors, student volunteers, and partner institutions whose tireless efforts enabled the seamless execution of the conference.

This souvenir, comprising abstracts and proceedings, stands as a testament to collaborative excellence and the shared commitment of the scientific community to advancing microbiological sciences. We hope the ideas and insights documented here will inspire continued inquiry, innovation, and partnerships in the years ahead.

On behalf of the organizing team, we express our heartfelt gratitude to all contributors and participants for enriching MICROCON – 2026 with their presence and scholarship. May this conference serve as a catalyst for future endeavors that strengthen the frontiers of smart and sustainable microbiology.

Dr. Prasanna Srinivas R.
Convenor

Dr. Prashanthi R.
Organizing Secretary

Dr. M. S. Ramaiah, FIAE

1922 – 1997

"A True Karma Yogi"

ABOUT THE COLLEGE

M. S. Ramaiah College of Arts, Science, and Commerce (MSRCASC), Bengaluru, was established in 1994 under the aegis of the Gokula Education Foundation (GEF), founded in 1962 by the visionary philanthropist Dr. M. S. Ramaiah with the mission of advancing education and healthcare for the betterment of society. The college is permanently affiliated with Dr. Manmohan Singh Bengaluru City University (formerly Bengaluru City University), and is recognized by the University Grants Commission (UGC) under Sections 2(f) and 12(B) of the UGC Act, 1956, with approval from AICTE. In recognition of its academic governance and quality standards, MSRCASC was conferred autonomous status by the UGC, the Government of Karnataka, and Bengaluru City University with effect from the academic year 2024 – 25. The institution offers a diverse range of undergraduate, postgraduate, and Ph. D. programmes across Arts, Science, Commerce, and Management, supported by industry-relevant curricula that are periodically updated to align with emerging trends, technological advancements, and societal needs

MSRCASC has earned a reputation for academic excellence, research innovation, and holistic education, reflected in its 'A' Grade accreditation by NAAC (4th Cycle, 2021) and its 67th rank among 4,030 participating institutions in the NIRF – 2025 rankings. The college provides a strong learning ecosystem through modern infrastructure, advanced laboratories, a well-stocked library, and digitally enabled classrooms. Research and innovation are actively promoted, with several departments recognized as research centres by Bengaluru City University and the institution being selected under the DBT – STAR College Scheme by the Department of Biotechnology, Government of India. MSRCASC also serves as a Learning Support Centre for IGNOU and actively participates in national initiatives such as Unnat Bharat Abhiyan, adopting villages and engaging in rural development, community outreach, and experiential learning. With robust placement support, industry collaborations, and emphasis on co-curricular and extracurricular development, MSRCASC nurtures socially responsible, professionally competent, and future-ready graduates, reinforcing its position as one of Karnataka's leading institutions of higher education.

ABOUT THE DEPARTMENT

Established in 1999, the Department of Microbiology has evolved into a distinguished center for higher education and research in the life sciences. The department offers undergraduate (B. Sc.), postgraduate (M. Sc.), and doctoral (Ph. D.) programmes, designed to provide comprehensive academic training and foster advanced research competencies. Guided by a team of highly qualified and experienced faculty members, the department encompasses diverse specializations within microbiology. Faculty actively contribute to scholarly publications, present at national and international conferences, and engage in collaborative research initiatives, thereby enriching the academic and scientific community.

The department is equipped with state-of-the-art laboratories, modern instrumentation, and well-established research facilities, creating an enabling environment for innovation, skill development, and interdisciplinary exploration. Strong collaborations with industry and research organizations further enhance opportunities for students and scholars, bridging academic knowledge with practical applications. With its commitment to academic excellence, professional development, and scientific inquiry, the Department of Microbiology continues to nurture competent graduates and researchers who contribute meaningfully to the advancement of microbiological sciences and allied disciplines.

ABOUT THE CONFERENCE

The national conference on *"Smart Microbiology: Artificial Intelligence, Nanotechnology, and Entrepreneurial Innovations Towards Sustainability"* is designed to convene researchers, academicians, industry professionals, and students on a unified platform. This event highlights the transformative integration of artificial intelligence (AI) and nanotechnology with core microbiological research and applications.

The conference emphasizes the pursuit of sustainable solutions in medical, environmental, and industrial microbiology, while fostering the translation of scientific insights into innovative products and entrepreneurial ventures. By encouraging collaboration and knowledge exchange, the event aims to inspire future-ready research and strengthen interdisciplinary networks.

Scheduled to be held on 25th March 2026 at M. S. Ramaiah College of Arts, Science, and Commerce – Autonomous, Bengaluru, India, the conference seeks to bring together a diverse community of active researchers from across India. It aspires to create a professional environment conducive to learning, collaboration, and networking, thereby facilitating the exchange of ideas and exploration of cutting-edge developments across scientific disciplines.

OUR PATRONS

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Dr. Prasanna Srinivas R., Head, Department of Microbiology, MSRCASC

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Dr. Yashaswini M. S., Assistant Professor, MSRCASC

Messages

Dr. M. R. Seetharam

Chairman

Gokula Education Foundation (Engg. & GS)

Member of Legislative Council &

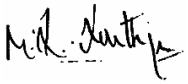
Ex-Minister, Government of Karnataka

Message

It gives me immense pleasure to extend my warm greetings on Microcon 2026, a National Conference organized by the Department of Microbiology, M. S. Ramaiah College of Arts, Science, and Commerce, on the theme *"Smart Microbiology: Artificial Intelligence, Nanotechnology, and Entrepreneurial Innovations Towards Sustainability."*

The integration of emerging technologies such as Artificial Intelligence and Nanotechnology with Microbiology represents a transformative shift in scientific research and innovation. This conference provides an excellent platform for knowledge exchange, fostering interdisciplinary collaboration, and addressing global challenges through sustainable solutions.

I congratulate the organizers for their commendable efforts and extend my best wishes for the grand success of the conference.



Dr. M. R. Seetharam

Sri. M. R. Janakiram

Vice-Chairman

Gokula Education Foundation (Engg. & GS)

& Director, M. S. Ramaiah College of Arts,

Science, and Commerce – Autonomous

Message

I am delighted to know that the Department of Microbiology, M. S. Ramaiah College of Arts, Science, and Commerce, is organizing Microcon 2026, a National Conference centered on a highly contemporary and impactful theme.

The integration of Artificial Intelligence and Nanotechnology with Microbiology represents a paradigm shift in scientific inquiry and application. Such interdisciplinary platforms are essential for fostering innovation, encouraging critical thinking, and nurturing the next generation of scientists and entrepreneurs.

The theme of sustainability embedded within the conference reflects a responsible and forward-thinking approach to science, ensuring that technological advancements contribute meaningfully to environmental conservation and societal well-being.

I appreciate the efforts of the organizing team in bringing together experts from diverse domains and creating an environment conducive to intellectual exchange and collaboration.

I extend my best wishes for the grand success of the conference.

Sri. M. R. Janakiram

Sri. M. R. Anandram

Secretary

Gokula Education Foundation (Engg. & GS)

Message

It is a matter of great pride and satisfaction that the Department of Microbiology is organizing *Microcon 2026* on a theme that resonates with the current global scientific landscape.

The fusion of Microbiology with cutting-edge technologies such as Artificial Intelligence and Nanotechnology is opening new avenues for innovation and discovery. These advancements are playing a crucial role in addressing complex challenges related to health, environment, and sustainable development.

This conference provides a valuable opportunity for researchers, academicians, and students to engage in meaningful discussions, and gain insights into emerging trends and technologies. The focus on entrepreneurial innovations is particularly noteworthy, as it encourages the translation of research into viable solutions and enterprises.

I congratulate the organizers for their vision and meticulous planning, and I am confident that the conference will be both intellectually enriching and highly impactful.

Sri. M. R. Anandram

Sri. M. R. Ramaiah

Director, M. S. Ramaiah College of Arts, Science, and Commerce – Autonomous

Message

I am pleased to note that the Department of Microbiology, M. S. Ramaiah College of Arts, Science, and Commerce, is hosting Microcon 2026 with a forward-looking and interdisciplinary theme.

The rapid evolution of technologies such as Artificial Intelligence and Nanotechnology is transforming the field of Microbiology, enabling more precise, efficient, and innovative approaches to research and application. The integration of these domains is paving the way for groundbreaking discoveries and sustainable solutions.

This conference will serve as a vibrant platform for knowledge sharing, collaboration, and exploration of new ideas. It will also provide participants with an opportunity to interact with experts, gain exposure to the latest advancements, and contribute to the growing body of scientific knowledge.

I commend the organizing committee for their initiative and dedication, and I wish the conference every success in achieving its objectives.

Sri. M. R. Ramaiah

Dr. Parswanath H. V.

Chief Executive

Gokula Education Foundation (Engg. & GS)

Message

It is indeed encouraging to witness the organization of Microcon 2026, which highlights the significance of innovation and interdisciplinary collaboration in the field of Microbiology.

The theme of the conference aptly captures the essence of modern scientific research, where Artificial Intelligence and Nanotechnology are playing pivotal roles in advancing our understanding and application of Microbiological processes. The inclusion of entrepreneurial innovations further emphasizes the importance of bridging the gap between academia and industry.

Such initiatives are instrumental in fostering a culture of innovation, creativity, and problem-solving among students and researchers. They also contribute to the development of sustainable solutions that address real-world challenges.

I extend my heartfelt appreciation to the organizers and wish all participants a productive, insightful, and rewarding conference experience.

Dr. Parswanath H. V.

Dr. Karisiddappa

Chief Academic Advisor

Gokula Education Foundation (Engg. & GS)

Message

It gives me immense pleasure to extend my warm greetings on Microcon 2026, a National Conference organized by the Department of Microbiology, M. S. Ramaiah College of Arts, Science, and Commerce, on the theme "Smart Microbiology: Artificial Intelligence, Nanotechnology, and Entrepreneurial Innovations Towards Sustainability."

The integration of Artificial Intelligence and Nanotechnology with Microbiology is transforming the landscape of scientific research, enabling innovative solutions to global challenges in healthcare, environment, and industry. The focus on entrepreneurial innovations further strengthens the connection between academic research and real-world applications, fostering sustainable development, and technological advancement.

Conferences such as Microcon 2026 provide a valuable platform for knowledge exchange, collaboration, and intellectual growth. I commend the Department of Microbiology for this excellent initiative and extend my best wishes for the grand success of the conference.

Dr. Karisiddappa

Sri. G. Ramachandra

Chief of Finance

Gokula Education Foundation (Engg. & GS)

Message

I am delighted to be associated with Microcon 2026, a National Conference that brings together diverse disciplines under a unified theme of innovation and sustainability.

The integration of advanced technologies such as Artificial Intelligence and Nanotechnology with Microbiology represents a significant step towards achieving sustainable development goals. This conference not only promotes academic excellence but also encourages the practical application of research findings.

The emphasis on entrepreneurial innovations is particularly commendable, as it fosters the development of solutions that are both economically viable and socially beneficial. Events like these play a crucial role in shaping the students as future leaders and innovators.

I appreciate the efforts of the organizing committee in planning and executing this conference and wish it a grand success.

Sri. G. Ramachandra

KARNATAKA SCIENCE AND TECHNOLOGY ACADEMY
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Prof. Rajasab A H
Chairman, KSTA
Former Vice Chancellor, Tumkur University
Chief Research Advisor, Gokula Education Foundation (Engg. & GS)

MESSAGE

It gives me immense pleasure to extend my greetings on the occasion of **Microcon 2026,** a National Conference organized by the Department of Microbiology, M. S. Ramaiah College of Arts, Science and Commerce, on the theme **"Smart Microbiology: Artificial Intelligence, Nanotechnology and Entrepreneurial Innovations Towards Sustainability."**

The integration of advanced technologies such as Artificial intelligence and Nanotechnology is revolutionizing Microbiological research, enabling deeper insights, precision-driven methodologies, and innovative solutions to complex scientific challenges. The emphasis on entrepreneurial innovations further encourages the translation of research outcomes into practical applications that contribute to sustainable development.

Microcon 2026 will serve as an excellent platform for researchers, academicians, and students to share knowledge, foster collaborations, and explore emerging trends in interdisciplinary research.

I commend the organizing team for their initiative and dedication, and I extend my best wishes for the success of this conference.

[Rajasab A H]

Address: Prof. U R Rao Vijnana Bhavan, Major Sandeep Unnikrishnan Road, Vidyaranyapura Post, Bengaluru - 560097

Dr. Pushpa H.
Principal and Professor
M. S. Ramaiah College of Arts, Science,
and Commerce – Autonomous

Message

It gives me immense pleasure to know that the Department of Microbiology is organizing Microcon 2026 on a theme that is both relevant and forward-looking.

As an institution committed to academic excellence and holistic development, we strongly encourage initiatives that promote interdisciplinary learning, research, and innovation. This conference reflects our dedication to fostering a culture of inquiry, creativity, and collaboration.

The focus on Artificial Intelligence, Nanotechnology, and Entrepreneurial Innovations underscores the importance of equipping students and researchers with the skills and knowledge required to address contemporary challenges. The emphasis on sustainability further reinforces our commitment to responsible and impactful science.

I congratulate the Department of Microbiology and the organizing committee for their commendable efforts and wish the conference a grand success.

Dr. Pushpa. H

Dr. Channarayappa

Professor and R & D Head,

M. S. Ramaiah College of Arts, Science,

and Commerce – Autonomous

Message

It gives me immense pleasure to extend a warm welcome to all participants, presenters, academicians, and industry professionals to MICROCON 2026, our National Conference on the theme "*Smart Microbiology, Artificial Intelligence, Nanotechnology, and Entrepreneurial Innovations towards Sustainability".*

In today's rapidly evolving scientific landscape, microbiology stands at the intersection of transformative technologies. The integration of artificial intelligence and nanotechnology is revolutionizing how we understand, analyze, and harness microbial systems. At the same time, entrepreneurship is driving these advancements beyond the laboratory, translating knowledge into sustainable solutions that address pressing global challenges.

This conference aims to provide a dynamic platform for intellectual exchange, collaboration, and innovation. By combining diverse scientific perspectives, we now assert microbiological approaches can be blueprints for sustainable development in healthcare, agriculture, environmental management, and industry.

As the Head of Research & Development, I strongly believe that fostering interdisciplinary dialogue and encouraging innovation-driven research will pave the way for impactful scientific progress. I encourage all participants to actively engage, share insights, and build meaningful collaborations during this event.

I wish MICROCON 2026 great success and hope it inspires new ideas, partnerships, and pathways toward a sustainable future.

Dr. Channarayappa

Dr. Prasanna Srinivas R.

Convenor

HOD, Department of Microbiology,

M. S. Ramaiah College of Arts, Science,

and Commerce – Autonomous

Message

It is with immense pride and enthusiasm that the Department of Microbiology, M. S. Ramaiah College of Arts, Science, and Commerce – Autonomous, presents Microcon 2026.

The theme, *"Smart Microbiology: Artificial Intelligence, Nanotechnology, and Entrepreneurial Innovations Towards Sustainability"*, has been thoughtfully chosen to reflect the dynamic evolution of microbiological sciences and the growing significance of interdisciplinary approaches.

This conference aspires to serve as a vibrant platform for academicians, researchers, industry professionals, and students to exchange knowledge, foster collaboration, and explore pioneering ideas. By encouraging entrepreneurial thinking and translational research, Microcon 2026 seeks to inspire sustainable solutions that bridge scientific discovery with societal impact.

We extend our heartfelt gratitude to all speakers, participants, and supporters for their invaluable contributions. I also sincerely acknowledge the dedication and tireless efforts of the organizing committee in bringing this event to fruition.

I wish each participant an enriching, insightful, and memorable conference experience.

Dr. Prasanna Srinivas R.

MICROBIOLOGISTS SOCIETY, INDIA

(Reg. No. MAH/4814/SAT)

Dr. A. M. Deshmukh
President
Microbiologists Society, India
Contact No: +91 9822079782
Email: mbiosociety@gmail.com
Website: https://microbiosociety.com/

Message

I am happy to inform you about the National Conference – MICROCON 2026, organized by the Department of Microbiology, M. S. Ramaiah College of Arts, Science, and Commerce – Autonomous, Bengaluru, in association with the Microbiologists Society, India. The conference will be held on 25th March 2026.

The theme of the conference is "Smart Microbiology: Artificial Intelligence, Nanotechnology, and Entrepreneurial Innovations Towards Sustainability." The event aims to bring together researchers, academicians, industry experts, and students to share knowledge and discuss recent developments in microbiology and related fields.

The conference will provide a good platform for scientific discussions, presentations, and collaboration. It will help participants learn about new technologies and innovative ideas in microbiology.

I invite researchers and students to participate in this conference and contribute to the exchange of ideas and knowledge. I wish MICROCON 2026 a great success.

Dr. A. M. Deshmukh

MICROBIOLOGISTS SOCIETY, INDIA

(Reg. No. MAH/4814/SAT)

Prof. Praveen T.

State Unit President – Karnataka

Microbiologists Society, India

Contact No: +91 9822079782

Email: mbsikarnatakapresident@gmail.com

Website: https://microbiosociety.com/

Message

I am pleased to announce the National Conference – MICROCON 2026, hosted by the Department of Microbiology, M. S. Ramaiah College of Arts, Science, and Commerce – Autonomous, Bengaluru, in collaboration with the Microbiologists Society, India. The conference is scheduled on 25th March 2026.

The theme, "Smart Microbiology: Artificial Intelligence, Nanotechnology, and Entrepreneurial Innovations Towards Sustainability," highlights the integration of modern technologies with microbiology. The event will unite researchers, academicians, industry leaders, and students to exchange knowledge and deliberate on recent advancements in the field.

This conference will serve as a valuable platform for scientific discussions, presentations, and collaborations, enabling participants to explore emerging technologies and innovative approaches in microbiology.

I warmly invite researchers and students to join this conference and enrich the exchange of ideas and expertise. I extend my best wishes for the grand success of MICROCON 2026.

Prof. Praveen T.

DEPARTMENT OF MICROBIOLOGY

Faculty Members

Dr. Pushpa H.
Principal and Professor
Qualification: M. Sc., M. Phil, Ph. D.
Area of Specialization: Mycology, Biodiversity, Molecular taxonomy, Bioremediation, Bioprospecting

Dr. Prasanna Srinivas R.
Head and Assistant Professor
Qualification: M. Sc., M. Phil, Ph. D.
Area of Specialization:
Medical Microbiology, Immunology, Enzymology

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Associate Professor
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Area of Specialization:
Agriculture Microbiology

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Associate Professor
Qualification: M. Tech., Ph. D.
Area of Specialization:
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Area of Specialization:
Environmental Microbiology

Dr. Juliya Rani Francis
Assistant Professor
Qualification: M. Sc., Ph. D., P. D. F. (UAS-B)
Area of Specialization:
Microbial Ecology, Host-pathogen interaction

Dr. Nimita Venugopal C.
Assistant Professor
Qualification: M. Sc., Ph. D.
Area of Specialization:
Antimicrobial Resistance

Dr. Prashanthi Rajaram
Assistant Professor
Qualification: M. Sc., Ph. D.
Area of Specialization:
Environmental Biotechnology
Phytochemistry

(Continued)

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Area of Specialization:
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Dr. Tejaswini H. K.
Assistant Professor
Qualification: M. Sc., Ph. D.
Area of Specialization:
Mycology, Microbial diversity, Endophytic microbes

Dr. Swetha P.
Assistant Professor
Qualification: M. Sc., Ph. D.
GATE, UGC - NET, ICAR - NET
Area of Specialization:
Agriculture Microbiology, Forest Biotechnology

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Qualification: M. Sc. MBA, B. Ed., Ph. D., ICAR – NET
Area of Specialization:
Food Microbiology, Environmental and Agriculture Microbiology, Pharmacology

Dr. Yashaswini M. S.
Assistant Professor
Qualification: M. Sc. Ph. D., ICAR - NET
Area of Specialization:
Agricultural Microbiology, Bio-preservation, Biocontrol

Ms. Lavanya B. R.
Assistant Professor
Qualification: M. Sc., K S E T
Area of Specialization:
Medical Microbiology, Agricultural Microbiology

Ms. Pooja M. G.
Assistant Professor
Qualification: M. Sc., K S E T
Area of Specialization:
Molecular biology, Immunology, Medical Microbiology

MICROCON – 2026: Souvenir Unveiling

Conference Subtheme:

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Subtheme 1:

Artificial Intelligence & Digital Innovations in Microbiology (AIDIM)

AIDIM-OP-01

AI-enabled probiotic hydrogel platform for smart crop disease detection and sustainable protection

Asfiya Anjum*, Abhilash Kumar Nayak, Kumar Chandu K., S. Anu Kiruthika

Department of Life Sciences, Indian Academy Degree College - Autonomous,
Bengaluru – 560043, Karnataka
***Corresponding author:** dr.anu.lifesciences@iadc.ac.in*

Abstract

The growing incidence of crop diseases, climate fluctuations, and excessive use of chemical pesticides threaten agricultural sustainability and food security. Conventional disease management strategies are often reactive, environmentally harmful, and economically inefficient. This study proposes an AI-integrated probiotic hydrogel system for early crop disease detection and sustainable biological protection. The system combines artificial intelligence, smart sensing, and biodegradable probiotic hydrogels to create an intelligent and eco-friendly plant health management approach. The hydrogel is formulated using water-retentive, biodegradable polymers embedded with beneficial plant growth–promoting microorganisms. These probiotics suppress pathogens through competitive colonization, antimicrobial compound production, and activation of plant defense mechanisms. The hydrogel matrix ensures controlled and sustained microbial release while improving soil moisture retention and nutrient availability, thereby enhancing plant resilience and growth. Artificial intelligence models, trained using crop disease image datasets and environmental parameters such as temperature, humidity and soil moisture, enable early and accurate disease detection. Real-time data collected through imaging devices and IoT-based sensors allow the system to identify stress symptoms before severe damage occurs. Upon detection, targeted hydrogel application provides localized biological intervention, reducing unnecessary chemical pesticide use. By integrating predictive analytics with biological control, this system supports precision agriculture while minimizing environmental contamination and production costs. The adaptive AI model continuously improves through field data, ensuring higher detection accuracy across diverse crops and conditions. Overall, the proposed AI-integrated probiotic hydrogel offers a sustainable, scalable, and environmentally responsible solution for modern crop disease management and improved agricultural productivity.

Keywords: Artificial intelligence, Plant disease detection, Machine learning, Deep learning, Sustainable farming

AIDIM-OP-02

From algorithms to antibiotics: AI driven drug and microbial genomic surveillance

Diya Jain**, Rajani P.

Department of Microbiology, s College for Women (Autonomous), Basvangudi, Bengaluru – 560004, Karnataka

****Corresponding author:*** *diya29330@gmail.com*

Abstract

Over recent decades, the world has not discovered a new class of antibiotics, leading to an increase in antibiotic-resistant pathogens. Growing demand, inadequate research, excessive downstream processing, low molecular success rates, and quick changes in target cells are all contributing an antibiotic crisis. Artificial intelligence's multidimensional capabilities are attracting scientists to accelerate the search for antibiotics, making it faster, cheaper, and broader, leveraging digital tools to uncover or design novel candidates. Artificial Intelligence (AI) is increasingly transforming drug discovery by enabling faster and more efficient identification of therapeutic targets and antimicrobial compounds. AI-driven approaches enable researchers to analyze large-scale biological and genomic datasets available as secondary data, identifying patterns associated with drug resistance and potential treatment strategies. One important application in this field is the use of ResFinder, a bioinformatics tool designed to identify antimicrobial resistance genes from genomic data. By integrating AI algorithms with ResFinder analysis, researchers can rapidly detect resistance determinants in microbial genomes and predict how pathogens may respond to specific antibiotics. Nevertheless, the combination of AI-driven analytics and tools like ResFinder provides a powerful framework for accelerating antimicrobial drug discovery and addressing the growing global threat of antibiotic resistance. The present study focuses on current AI-based technologies used for antibiotic discovery, their successes, drawbacks of AI and economic impact on the industrial domain.

Keywords: Artificial intelligence, Drug discovery, ResFinder, Machine learning, Genomic analysis

AIDIM-OP-03

Computational investigation of α-santalol as a potential natural inhibitor of lung cancer targets using molecular docking

Shree Varsha*, Shreya R., Arkaprabha Deb, Shriya Gejjehalli, Riddhi R. Chandraghatgi, Swetha P.

Department of Microbiology, M. S. Ramaiah College of Arts, Science, and Commerce – Autonomous, Bengaluru – 560054, Karnataka

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Abstract

Santalum album L. (Indian sandalwood) is known for its valuable heartwood oil and has been widely used from time immemorial in traditional Indian medicinal systems as therapeutics. Sesquiterpenols, particularly α-santalol, is the principal bioactive component of sandalwood oil, which has been reported to exhibit anti-inflammatory, antioxidant, and anticancer activities. The present study aimed to investigate the anticancer potential of α-santalol against lung cancer-associated proteins through an *in silico* molecular docking approach. Target protein structures related to lung cancer progression were retrieved from the Protein Data Bank, including 3HS5, 3S7S, 3S79, 4KQ8, 6Y3C, 7MXC, 5KPK, 4NM3, 8TB6, 4NM7, 8BPW, and 4NU1. Ligands were converted from .sdf to .pdb using OpenBabel, proteins were prepared by removing water and unwanted atoms and adding hydrogens and Kollman charges *via* Biopython, and molecular docking was performed using AutoDock Vina, with interactions visualized in BIOVIA Discovery Studio, PyMOL, and RasMol. Docking analysis revealed favorable binding of α-santalol with lung cancer targets, showing binding energies ranging from −6.9 to −8.4 kcal/mol, with strong affinities for 7MXC (−7.2), 5KPK (−7.5), 8TB6 (−7.7), 4NM7 (−7.8), and 8BPW (−8.1 kcal/mol). Notably, the highest binding affinity was observed with the Glycogen Synthase Kinase-3 beta (GSK-3β) related protein structure 4NU1, with a binding energy of −8.4 kcal/mol, indicating a potentially stable ligand–protein complex. Interaction analysis further revealed that the ligand was stabilized within the active sites through hydrophobic interactions, Van der Waals forces, and hydrogen bonding with key amino acid residues, suggesting potential inhibition of signaling pathways associated with lung cancer progression. Structural validation through Ramachandran plot analysis indicated acceptable stereochemical quality of the selected protein structures. Overall, the findings provide computational evidence supporting the potential of α-santalol as a natural inhibitor of lung cancer-associated proteins, particularly targeting GSK-3β, a key regulator of cellular signaling pathways involved in tumor progression. These results highlight the possibility of utilizing α-santalol as a promising lead compound for the development of novel anti-lung cancer therapeutics, either as an adjuvant or as a basis for future drug development.

Keywords: α-Santalol, *Santalum album*, Molecular docking, Lung cancer, AutoDock Vina

AIDIM-OP-04

Integrating protein language models and active learning for scalable virulence prediction

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Abstract

The increase in antibiotic resistance by the microorganisms demands alternative approaches that emphasize on targeting bacterial virulence rather than their survival. Precise analysis and identification of proteins associated with their virulence is therefore critical for pathogen characterization, drug target discovery, and vaccine development. In the present study, we propose a scalable computational framework that uses pre-trained ESM-2 protein language models to predict efficient virulence factor with an uncertainty based active learning strategy. A balanced dataset was constructed from various publicly available database resources and evaluated to intensive preprocessing and stratified partitioning. Using a CLS token representation, three ESM-2 variants (8M, 35M, and 150M parameters) were adapted for binary classification into virulent and non-virulent. Active learning approach was adapted to select iteratively the most informative sequences to address limited labelled data, significantly improving its efficiency. Test accuracies were achieved between 95.34% and 96.01% for all the models. The 150M model gave high accuracy with balanced performance. t-SNE and UMAP techniques revealed clear separation of virulent and non-virulent proteins and predicted high model confidence across most predictions. Streamlit web application was developed to infer real-time sequence. In conclusion, this integrated framework offers an accurate, data efficient, and a practically implementable computational virulence prediction. Source code for the proposed study is publicly available at https://github.com/kssrikar4/AVP-ESM.

Keywords: Virulence prediction, Infectious disease, Protein classification, Computational biology

AIDIM-PP-01

Fragment based design of potential inhibitors against HsrA protein of *Helicobacter pylori*

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Abstract

Helicobacter pylori is a significant gastric pathogen linked to chronic gastritis, peptic ulcers, and gastric cancer. The global rise of antibiotic resistance has diminished the efficacy of standard eradication therapies, necessitating the identification of novel molecular targets. HsrA, an essential orphan response regulator, is a high-value drug target due to its critical role in transcriptional regulation, stress adaptation, and bacterial homeostasis. While prior studies have identified natural inhibitors like flavonoids and Sesamolin *via* high-throughput docking, systematic fragment-based design targeting HsrA remains limited. The objective of this study is to design potential small molecule inhibitors against HsrA protein of *H. pylori* using a fragment-based approach. Eighteen known natural inhibitors were selected based on the review of the literature and were used to generate novel inhibitors. Among them, Sesamolin was selected as the reference compound. Fragment script and BREED of Schrodinger software were used to build novel inhibitor molecules. The resulting 18 novel molecules were docked into the active binding site of HsrA protein and the top 10 compounds were screened based on binding affinity compared to Sesamolin for further study. Among the novel compounds, compound 2, 6, and 7 emerged as the most promising candidates. These molecules exhibited superior binding affinity and stable MM-GBSA binding free energies. Comprehensive pharmacokinetic evaluation using QikProp, SwissADME and ProTox confirmed that these leads meet all essential ADMET criteria, showing favorable oral bioavailability and no toxicity risks. Molecular dynamics simulations will be performed for further validation. These findings aid the development of narrow-spectrum therapeutic agents that bypass existing resistance mechanisms, offering preclinical candidates for experimental validation against *H. pylori's* HsrA.

Keywords: Helicobacter pylori, HsrA, Fragment based design, BREED, ADMET

AIDIM-PP-02

CRISPR spacer-based evidence of cyanophage interactions in *Microcystis aeruginosa*

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Abstract

Cyanobacteria are ecologically significant microorganisms in freshwater ecosystems, often forming large blooms that influence nutrient cycling and water quality. Among them, *Microcystis* species are widely known for producing harmful algal blooms and toxins in freshwater habitats. Understanding the interactions between cyanobacteria and their viruses (Cyanophages) is important for exploring microbial evolution and bloom dynamics. In this study, CRISPR spacer analysis was performed to investigate potential historical virus–host interactions in *Microcystis aeruginosa* NIES-843. The complete genome sequence of this strain was obtained from the National Centre for Biotechnology Information database and analyzed using the tool CRISPRCasFinder to identify CRISPR arrays and associated spacer sequences. A total of 172 spacer sequences were detected within the CRISPR region. Spacer length analysis revealed a range of 32 – 40 bp, with an average spacer length of approximately 35 bp, which is consistent with typical bacterial CRISPR spacer sizes. The spacer sequences were subsequently compared against nucleotide databases using BLAST to identify potential viral matches. Several spacers showed significant similarity to bacteriophage and uncultured phage genomic sequences, indicating possible past viral infection events experienced by *M. aeruginosa.* The presence of these spacers suggests that the CRISPR–Cas system in this cyanobacterium serves as an adaptive immune mechanism that records prior encounters with infecting phages. These findings provide insight into the evolutionary relationship between freshwater cyanobacteria and their viral predators. Overall, the study demonstrates that spacer-based CRISPR analysis is a useful bioinformatics approach for detecting evidence of cyanophage interactions and understanding microbial defense mechanisms in bloom-forming cyanobacteria. Such information may contribute to future studies on cyanobacterial ecology, virus–host coevolution, and the potential role of phages in regulating harmful algal blooms.

Keywords: CRISPR–Cas system, *Microcystis aeruginosa*, Cyanophage, Spacer analysis, Cyanobacteria

AIDIM-PP-03

Structural interaction analysis of glycosylated naphthalimides with the *Pseudomonas aeruginosa* PqsR (MvfR) protein

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Abstract

Molecular docking analysis was performed to evaluate the binding potential of glycosylated naphthalimide derivatives against the target protein (PDB ID: 4JVI) to investigate their structural compatibility and interaction stability within the active site. Docking simulations generated multiple conformational clusters, which were assessed using binding affinity and RMSD parameters to identify energetically favourable and structurally reliable poses. Among the tested ligands, binding affinities ranged from −6.7 to −8.6 kcal/mol, indicating moderate to strong interaction potential. The ligand N1 exhibited the highest binding affinity (−8.6 kcal/mol), suggesting enhanced stabilization within the binding pocket. RMSD analysis demonstrated consistent clustering behaviour, with selected representative poses showing 0 Å deviation, confirming conformational convergence and docking reliability. Two-dimensional interaction analysis revealed that ligand stabilization is primarily mediated through a combination of hydrogen bonding and hydrophobic interactions. Key amino acid residues involved in binding include Arg293, Leu163, Gly164, Tyr165, Lys167, and Leu292. Hydrogen bonding interactions were observed with polar residues, while aromatic stacking and hydrophobic contacts contributed significantly to ligand anchoring within the active site cavity. The glycosyl moiety enhanced interaction versatility by forming additional polar contacts, potentially improving binding specificity. Overall, glycosylated naphthalimides demonstrated favourable docking characteristics against 4JVI, highlighting their potential as scaffold candidates for further structure-guided optimization. The combined evaluation of binding affinity, RMSD stability, and interaction mapping supports the suitability of these compounds for subsequent molecular dynamics simulations and experimental validation studies.

Keywords: Glycosylated naphthalimides, Molecular docking, RMSD analysis, Protein–ligand interaction

AIDIM-PP-04

The emerging role of AI in synthetic microbial therapeutics in cancer treatment

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Abstract

Microbes and their products are engineered to act as potent cancer therapeutic agents and proving its role in cancer immunotherapy. Several molecular manipulation techniques – Cloning, CRISPR, phage modulations, etc. have resulted in engineering mutations and metabolism in weakening the severity of health diseases and enhancing human health. AI is transforming cancer diagnosis, enabling more precise targeted therapies, thereby increasing survival of patients. It is been integrated in cancer research in developing novel microbial drugs and mechanisms that aims in reducing the threats of AMR that the world is currently addressing/witnessing. Need for developing AI algorithms to establish accurate cancer imaging, assisting targeted therapy and drug delivery through assistance of microorganisms, and tracing the metastasis network of tumour's in the body. We must develop ways to check progress monitoring of biomarkers and keep note on optimizing the treatment plans. The gut microbiome profoundly impacts cancer initiation, progression, and therapeutic response. Recent advances are starting to integrate artificial intelligence (AI) into intratumoral microbiota characterization, enabling computational pipelines that map microbe–host interactions and help guide engineered microbial therapeutics. Engineered probiotic strains can locally produce checkpoint inhibition nanobodies and cytokines, using computational modelling of lysis circuits to maximize intratumoral release. CRISPR engineered gut microbes can be further designed to secrete immunomodulatory metabolites, while AI can be employed to ensure strain stability, biocontainment, and safety. Many of microbes are widely used in cancer immunotherapy like *Streptococcus pyogenes* (OK-432) for treating lymphangiomas, *Clostridial* enriched microbiota in breast cancer, *Salmonella,* and *Bifidobacterium* could thrive in hypoxic microenvironments of tumour. Further using AI tools to check the efficacy of new drugs and techniques used to counter the tumour growth and metastasis in lab research conditions.

Keywords: Microbial therapeutics, Cancer immunotherapy, CRISPR engineering, AI in cancer

AIDIM-PP-05

Structure-guided linker engineering for binding affinity optimization of FDA-approved drugs

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Abstract

FDA-approved therapeutics frequently exhibit suboptimal binding kinetics owing to rigid scaffold geometries that preclude maximal energetic complementarity with biological targets. This study aims to develop a computational tool that evaluates the structural compatibility of a diverse panel of established drugs such as Lisinopril, Losartan, Donepezil, and Isoniazid against their primary crystallographic targets (e.g., PDB: 1O86, 4YAY, 5IOK, 2CCA). It is hypothesized that the computational appendage of molecular linkers facilitates better binding, thereby augmenting binding affinity of the derivatives compared to the parent compounds. We developed a parallelized Python workflow which uses RDKit and Auto dock Vina that initially screens over 151,286 linkers using vector-based geometric constraints and a strict distance threshold to filter out candidates with inherent steric clashes. To modify the surviving hits, a novel Python algorithm executes valence-conserving hydrogen substitution, effectively modifying the parent drug's spatial geometry to project binding groups into latent sub-pockets. All derivatives undergo 3D conformational linkage and energy minimization to ensure thermodynamic stability prior to docking through AutoDock Vina. As a primary proof-of-concept, the interaction between Astemizole and the Histamine H1 Receptor (PDB: 8EER) was analyzed. The unmodified parent scaffold exhibited a baseline binding energy of -7.4 kcal/mol. Subsequent automated optimization identified a novel linker-derivatized analog achieving a binding energy of -7.8 kcal/mol. This net improvement of -0.4 kcal/mol corroborates the novel program’s capacity to introduce favorable enthalpic interactions without perturbing the core pharmacophore. This investigation demonstrates that established therapeutics can be systematically re-designed to surpass their original binding profiles. By computationally correcting geometric mismatches through linker derivatization, this methodology presents a scalable pathway for the evolution of high-potency derivative compounds.

Keywords: FDA-approved therapeutics, RDKit, AutoDock Vina, Binding energy, Linker design

AIDIM-PP-06

Artificial intelligence in microbial disease diagnostics: emerging tool for rapid detection

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Abstract

Rapid and accurate diagnosis of microbial diseases is essential for effective treatment and control of infectious diseases. Conventional diagnostic methods such as culture techniques, microscopy, and biochemical tests are reliable but often time-consuming and labor-intensive. In recent years, Artificial Intelligence (AI) has emerged as a powerful tool that enhances the speed and accuracy of microbial disease diagnosis. Al techniques, including machine learning and deep learning algorithms, can analyze large volumes of clinical and genomic data to identify pathogens more efficiently than traditional approaches. These technologies are capable of interpreting complex datasets obtained from medical imaging, genomic sequencing, and laboratory reports, enabling early detection of bacterial, viral, and fungal infections. AI-based diagnostic systems are also being integrated with digital platforms and automated laboratory equipment, allowing faster identification of disease-causing microorganisms and supporting timely medical decision-making. In addition, AI tools assist in monitoring antimicrobial resistance patterns and predicting disease outbreaks, which are crucial for public health management. This review highlights the role of artificial intelligence in microbial disease diagnosis and discusses its potential as an emerging tool for rapid detection. The integration of Al with microbiology is expected to revolutionize diagnostic practices and contribute to improved healthcare outcomes and sustainable disease management strategies.

Keywords: Artificial intelligence, Microbial diagnostics, Machine learning, Infectious diseases

AIDIM-PP-07

Artificial intelligence in microbial diagnostics: accelerating detection from Petri-dishes to processors

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Abstract

Infectious diseases remain a leading global health challenge, with delayed diagnostic results contributing significantly to illness and mortality. Traditional diagnostic methods such as microbial culture, expert image interpretation, and molecular assays, though accurate, are often slow, costly, and difficult to implement in resource-limited settings. The increasing digitization of health records, availability of medical images, affordable sensors, and widespread computing power has created an opportunity for artificial intelligence (AI) and machine learning (ML) to transform microbial diagnostics. AI/ ML technologies excel at recognizing complex patterns that may be overlooked by human experts. They can predict antimicrobial resistance trends, guide treatment selection, and automate processes to reduce human error, thereby improving laboratory efficiency. Beyond diagnostics, AI also plays a role in epidemiology, enabling the prediction of disease outbreaks and supporting public health preparedness. Deep learning approaches applied to microbial genomics, microscopy, and patient clinical data demonstrate high precision and faster processing compared to conventional methods. The integration of AI into microbiology is not merely supplementary but transformative. Properly validated and monitored, these systems can deliver consistent results, timely warnings, and actionable insights. Applications extend across microbiome analysis, taxonomy, pathogen detection, epidemiology, and drug discovery, highlighting the breadth of AI's impact. This review emphasizes that AI is redefining microbial diagnostics by enabling rapid, accurate, and scalable solutions. By harnessing complex datasets and automating workflows, AI offers a pathway to more efficient healthcare delivery, particularly in environments where speed and precision are critical. Ultimately, the digital evolution of microbiology marks a paradigm shift from traditional Petri-dish based methods to processor-driven intelligence.

Keywords: Artificial intelligence, Machine learning, Microbial diagnostic, Drug discovery

AIDIM-PP-08

In silico design and evaluation of a multi-epitope vaccine targeting *Lassa virus* glycoproteins and nucleoprotein

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Abstract

Lassa fever, caused by *Lassa virus* is a zoonotic hemorrhagic fever endemic to West Africa, with around 300,000 – 500,000 annual cases and 5,000 – 10,000 deaths, which is transmitted *via* Mastomys rodents. It presents with fever, headache, sore throat, myalgia, and in severe cases, hemorrhagic manifestations, and multi-organ failure with a case fatality rate of approximately 1 – 15%. This study designs an *in-silico* multi-epitope vaccine targeting LASV glycoproteins and nucleoprotein. A comprehensive immunoinformatics approach was employed, including antigen selection *via* IEDB immunogenicity scoring, CTL, HTL, and B-cell epitope prediction, molecular docking and molecular dynamics simulations using GROMACS to assess immune complex stability, followed by codon optimization using JCat and *in silico* cloning. The vaccine construct demonstrated favourable stability, strong binding interactions, and predicted robust immune responses. *In-silico* analysis suggests that this multi-epitope vaccine is a promising candidate for further experimental validation.

Keywords: *Lassa virus*, Epitope vaccine, GROMACS, IEDB immunogenicity scoring

AIDIM-PP-09

AI in nanomedicine: a new era of intelligent healthcare

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Abstract

Nanotechnology and artificial intelligence (AI) are rapidly converging to reshape modern medicine, offering unprecedented advances in diagnostics, drug delivery, manufacturing, and disease management. This review provides a comprehensive analysis of nanotoxicity, nanoparticle design, and the diverse classes of nanomaterials such as inorganic, lipid-based, and polymeric nanoparticles highlighting how their physicochemical properties govern biological interactions, therapeutic performance, and safety. We examine the molecular mechanisms underlying nanotoxicity, such as oxidative stress, inflammation, genotoxicity, and physicochemical triggers like particle size, charge, dissolution, and aggregation. The review further explores the emerging role of AI in predicting nanotoxicity, optimizing nanomaterial synthesis, and streamlining high-throughput toxicological data integration. Special emphasis is placed on magnetic nanoparticles (MNPs), whose superparamagnetic behavior enables targeted drug delivery, blood–brain barrier (BBB) penetration, magnetic hyperthermia, and advanced imaging modalities such as magnetic particle imaging (MPI). AI-driven modeling enhances nanoparticle formulation, biodistribution prediction, BBB permeability assessment, and image reconstruction, significantly accelerating translation to clinical applications. We also review AI-integrated nanomedicine for Alzheimer's disease, where nanoparticles improve BBB transport, enable early detection of amyloid-β and tau pathology, and support gene therapy and theranostic platforms. Finally, we discuss the transformative emergence of AI-assisted nanomedicine in oncology, including early cancer detection, nanocarrier design, photothermal and photodynamic therapy optimization, and adaptive treatment systems. Overall, the synergistic integration of nanotechnology and AI marks a pivotal shift toward personalized, precise, and data-driven medicine. Despite major advances, challenges remain in toxicity management, large-scale manufacturing, regulatory alignment, and ethical AI deployment. Continued interdisciplinary efforts will be crucial for translating AI-enhanced nanomedicine into safe, effective, and widely accessible clinical solutions.

Keywords: Nanomedicine, Healthcare, Blood–brain barrier (BBB), Hyperthermia, Nanotoxicity

AIDIM-PP-10

Evolution of microbiology with artificial intelligence

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Abstract

Artificial Intelligence (AI) has transformed microbiology by enabling machines to simulate human reasoning, learning, and decision-making. In microbial diagnostics, AI enhances precision and speed through advanced data analysis, pattern recognition, and rapid diagnostic processes. Integrated with techniques such as matrix-assisted laser desorption/ ionization time-of-flight mass spectrometry (MALDI-TOF MS), AI can swiftly identify microorganisms based on spectral signatures. Machine learning (ML) and deep learning (DL) approaches further strengthen predictive modeling, particularly in anticipating antimicrobial resistance by analyzing genomic datasets of bacterial isolates. This capability is crucial in addressing the global challenge of resistant pathogens. Beyond traditional organism-level studies, AI facilitates exploration of entire microbial communities, advancing personalized medicine through individualized treatment strategies and epidemic surveillance. In environmental microbiology, AI-driven image datasets such as EMDS-6 support classification and diagnosis of novel microorganisms. In microbial forensics, AI contributes to source detection, postmortem interval estimation, tissue identification, and crime scene analysis, thereby aiding investigations into cause of death. Collectively, AI applications across diverse branches of microbiology from diagnostics and therapeutics to environmental and forensic studies are enhancing accuracy, efficiency, and innovation. This review highlights recent advances in AI-driven microbiology, emphasizing its role in disease identification, treatment customization, resistance prediction, and microbial community analysis, underscoring its potential as a cornerstone of modern microbiological research.

Keywords: Artificial intelligence, Deep learning, Machine learning, Microbial diagnostics

Subtheme 2:

Nanotechnology & Advanced Microbial Applications (NAMA)

NAMA-OP-01

Characterization and evaluation of biological activity of silver nanoparticles synthesized from selected fungal isolates

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Abstract

In this study, mycelia filtrate of *Aspergillus niger* and *Trichoderma* was used to reduce $AgNO_3$ to form silver nanoparticles (AgNPs). The effect of variable concentration of $AgNO_3$ on the diameter of AgNPs was analyzed. Under optimal conditions, the diameter of AgNPs was reduced considerably compared to the basal culture condition and $AgNO_3$ concentration was found to be most significant factor affecting the diameter of AgNPs. *A. niger* nano-Ag was characterized using UV-Visible spectroscopy, Transmission electron microscopy, Scanning electron microscopy, and X-ray diffraction (XRD). The minimum UV absorption was obtained at 420 nm and the microscopic results showed particles with narrow size distribution ranging from 100 to 500 nm. XRD pattern of AgNPs revealed four diffraction peaks of metallic silver. *A. niger* showed potent minimum inhibitory concentration (MIC) against four reference microorganisms. The MIC values of AgNPs were 5.25 to 10 g/mL. Nevertheless, *Trichoderma* AgNPs did not demonstrate any antagonistic activity against any of the bacterial pathogens. The *in-vitro* assays of the *Aspergillus* AgNPs showed potential antioxidant (62.9%) and antidiabetic activity of 73.2% of alpha-amylase and (65.5%) of alpha glucosidase enzyme while that for *Trichoderma* AgNPs were insignificant.

Keywords: Nanoparticles, XRD, Amylase, Antibacterial activity, Minimum inhibitory concentration (MIC)

NAMA-OP-02

Green synthesis and characterization of silver nanoparticles using endophytic fungus *Pestalotiopsis cruenta* and their anticancer activity against MCF-7 cell line

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Abstract

The development of eco-friendly nanomaterials for cancer therapy has gained significant attention in recent years. In this study, the endophytic fungus *Pestalotiopsis cruenta*, isolated from healthy plant leaves, was utilized for the green synthesis of silver nanoparticles (AgNPs). The formation of AgNPs was confirmed by a visible color change, indicating the reduction of silver ions. The synthesized nanoparticles were characterized using UV–Visible spectroscopy, Fourier Transform Infrared (FTIR) analysis, X-ray Diffraction (XRD), and Scanning Electron Microscopy (SEM), confirming their formation, stability, crystalline nature, and morphology. The cytotoxicity study of the AgNPs was tested against the human breast cancer cell line (MCF-7) using the MTT assay. The results showed a concentration-dependent decrease in cell viability, indicating significant cytotoxic effects. The IC_{50} value further confirmed the efficiency of the nanoparticles in inhibiting cancer cell proliferation. This study highlights the potential of *P. cruenta* mediated silver nanoparticles as an eco-friendly and promising approach for cancer therapy, contributing to the advancement of sustainable nanomedicine.

Keywords: *Pestalotiopsis cruenta*, AgNPs, UV-Vis, XRD, FTIR, MCF-7

NAMA-OP-03

Silver nanoparticles produced by *Artocarpus gomezianus* for antifungal and antibacterial activity: a sustainable combustion synthesis

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Abstract

As nanotechnology continues to expand at a rapid pace, new possibilities for novel biomedical and therapeutic uses of silver nanoparticles are opening in the field of nanomedicine. The present study describes the synthesis and characterization of silver nanoparticles, as well as their antifungal and antibacterial properties. Spherical silver nanoparticles (AgNPs) were produced *via* an environmentally benign green combustion process using citrate from *Artocarpus gomezianus* fruit as a fuel source. The structural, morphological, and compositions of the synthesized Ag NPs were systematically investigated using Powder X-ray Diffraction (PXRD), Scanning Electron Microscopy (SEM), and Fourier Transform Infrared (FTIR) spectroscopy. PXRD analysis confirmed the formation of crystalline silver nanoparticles with a face-centered cubic (fcc) crystal structure. SEM micrographs show that the particles are uniform with well distributed elliptical/spherical particles with a size range from 5 to 50 nm with inter-particle distance. The average crystallite size of the synthesized silver nanoparticles was determined using Scherrer's equation and was found to be approximately 50 nm for samples prepared with varying volumes (10, 15, 20, and 25 mL) of 10% *A. gomezianus* fruit extract, indicating that the crystallite size remained relatively consistent across different extract concentrations. The antimicrobial activity of the synthesized silver nanoparticles was assessed using the zone of inhibition method, which revealed pronounced antifungal effects against *Aspergillus niger*, indicating their strong potential to inhibit fungal growth. The observed activity is attributed to the small particle size and increased surface-to-volume ratio. Overall, the results demonstrate that green-synthesized AgNPs derived from *A. gomezianus* fruit extract hold significant potential for future nanomedical, antimicrobial, and biological applications.

Keywords: Green combustion, Silver-nanoparticles, Antimicrobial activity, Zone inhibition.

NAMA-OP-04

Biosynthesis of chitosan nanoparticles and evaluation of their antimicrobial and cytotoxic activity against the human cancer cell line

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Abstract

The growing demand for eco-friendly and sustainable approaches in nanotechnology has led to the exploration of bio synthesis methods for producing nanoparticles with enhanced biomedical applications. In this study, chitosan nanoparticles (CNPs) were synthesized using a biocompatible approach that avoids the use of toxic chemicals, employing natural reducing and stabilizing agents. The physicochemical properties of the synthesized CNPs, including particle size, surface morphology, were characterized using techniques such as scanning electron microscopy (SEM), transmission electron microscopy (TEM), dynamic light scattering (DLS), and Fourier-transform infrared spectroscopy (FTIR). The antimicrobial potential of the nanoparticles was evaluated against a panel of Gram-positive and Gram-negative bacterial strains to determine their inhibitory efficacy and minimum inhibitory concentrations (MICs). Furthermore, the cytotoxic activity of the CNPs was assessed *in vitro* against the human cancer cell line using standard assays, such as MTT and apoptosis analysis, to determine their potential as an anticancer agent. The results revealed that the bio synthesized CNPs exhibited uniform nanoscale morphology, high stability, and significant surface functionalization conducive to biological interactions. The nanoparticles demonstrated notable antimicrobial activity, with pronounced effects against both Gram positive and Gram-negative bacteria, indicating their potential as broad-spectrum antimicrobial agents. Moreover, the CNPs displayed dose dependent cytotoxicity against cancerous cells, inducing apoptosis and reducing cell viability significantly, suggesting their promise as a complementary therapeutic strategy in cancer treatment. This study highlights the potential of bio-synthesized chitosan nanoparticles as multifunctional biomaterials, combining antimicrobial and anticancer activities while adhering to environmentally sustainable synthesis practices, offering a promising platform for future biomedical applications.

Keywords: Chitosan nanoparticles (CNPs), UV, FTIR, XRD, SEM, TEM, Apoptosis

NAMA-OP-05

Enhancing regenerative medicine and the role of nanotechnology in shaping stem cell therapy

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Abstract

Stem cells have emerged as a transformative tool in regenerative medicine due to their unique ability to self-renew and differentiate into specialized cell types. These properties make them highly promising for repairing or replacing damaged tissues and organs caused by injury, degenerative diseases, or aging. However, several challenges such as low survival rate after transplantation, poor targeting efficiency, and limited control over differentiation continue to hinder the full clinical translation of stem cell–based therapies. Recent advancements in nanotechnology offer innovative solutions to overcome these limitations and significantly enhance the therapeutic potential of stem cells. Nanotechnology provides a versatile platform for improving stem cell delivery, tracking, and functionality. Nanomaterials such as nanoparticles, nanofibers, and nanotopographical scaffolds can mimic the natural cellular microenvironment, thereby promoting stem cell adhesion, proliferation, and directed differentiation. Additionally, nano-based carriers enable the controlled delivery of growth factors, genes, and drugs to stem cells, improving their regenerative efficiency. For example, nanoparticle-mediated gene delivery systems can modulate stem cell behavior and enhance tissue regeneration while minimizing systemic side effects. Furthermore, nanotechnology plays a crucial role in stem cell diagnostics and monitoring. Nanoprobes and nanosensors allow real-time imaging and tracking of transplanted stem cells within the body, providing valuable insights into cell migration, viability, and therapeutic outcomes. Such nano-enabled diagnostic tools enhance the precision and safety of stem cell therapies. The integration of nanotechnology with stem cell research is paving the way for advanced regenerative strategies capable of addressing complex medical conditions, including neurodegenerative disorders, cardiovascular diseases, and tissue injuries. By improving delivery efficiency, cellular control, and therapeutic monitoring, nanotechnology-based approaches are expected to accelerate the development of next-generation regenerative treatments. This paper highlights the synergistic role of nanotechnology in enhancing stem cell therapy, with a focus on nano-based diagnostic tools and targeted drug delivery systems. The convergence of these interdisciplinary fields holds immense potential for developing safer, more effective, and personalized regenerative medicine therapies in the future.

Keywords: Stem cells, Nanotechnology, Regenerative medicine, Targeted drug delivery, Gene delivery systems

NAMA-OP-06

Combinatorial approach using *Piper nigrum* extracts and nanoparticles: a novel strategy against MDR *Pseudomonas aeruginosa*

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Abstract

Globally and particularly in India, antimicrobial resistance (AMR) poses a major danger to public health. Over the past few years, MDR and XDR strains of *Pseudomonas aeruginosa* have become common with rates ranging from 15% to 30%. The antibacterial activity of *Piper nigrum* phytochemicals and nanocomposites, both separately and in combination, was investigated for its ability to block the efflux pump in MDR strains whose Multiple Antibiotic Resistance Index (MAR) ranged between 0.13 to 0.8. Using polymyxin as a positive control, the antibacterial activity of Mg-V, Fe-V, and Mg-Fe nanoparticles as well as n-hexane, chloroform, methanol, and aqueous extracts of black pepper seeds were evaluated using the agar well diffusion method. The synergistic effect of Mg-V NPs and black pepper seed methanol extract was examined. Levofloxacin's MIC variation was examined using *P. nigrum* seed methanol extract as a possible efflux pump inhibitor. Results indicated that all the *P. nigrum* seed solvent extracts had antibacterial efficacy against MAR strains of *P. aeruginosa*. Mg-V NPs had the highest antipseudomonal activity, followed by Fe-V and Fe-Mg NPs. Mg-V NPs had a synergistic impact against the five MAR strains assessed when combined with n-hexane, chloroform, methanol, and aqueous extracts of *P. nigrum* seeds. When compared to the positive control, isolate 10 displayed a noticeable zone of 24.6 ± 4.50 mm with a concentration of 400 µg/mL and n-hexane extract and 31 ± 6.92 mm with a concentration of 400 µg/mL and chloroform extract. The minimum inhibitory concentration (MIC) against levofloxacin with and without methanol extract, increased antibacterial activity ranging from two to thirty-two times. The results demonstrated a decrease in MIC, suggesting that phytochemicals and levofloxacin work in concert. This investigation showed that a resistance-modifying compound could be used as a novel inhibitor for the alternative treatment of *P. aeruginosa* that is resistant to drugs.

Keywords: Antibacterial, *Pseudomonas aeruginosa*, *Piper nigrum,* Nanoparticles

NAMA-OP-07

Nano-based diagnostics and drug delivery

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Abstract

Nanotechnology has become a significant asset in contemporary medicine, particularly in disease diagnosis and targeted drug delivery. Diagnostics based on nanotechnology utilize nanoparticles, such as gold nanoparticles, quantum dots, liposomes, and magnetic nanoparticles, to detect diseases early with increased sensitivity and specificity. These nanomaterials improve imaging methods, biosensors, and molecular detection techniques, allowing for quick and precise recognition of biomarkers linked to a range of illnesses, including cancer and infectious diseases. Beyond diagnostics, nanotechnology significantly impacts drug delivery systems. Nanocarriers such as polymeric nanoparticles, dendrimers, and nano-liposomes enhance the effectiveness of medications by improving their stability, solubility, and bioavailability. These nanoscale delivery mechanisms facilitate targeted drug administration to specific tissues or cells, thereby reducing side effects and minimizing harm to healthy tissues. Additionally, nanotechnology-enabled carriers can achieve controlled and sustained drug release, resulting in better treatment outcomes.

Keywords: Nanotechnology, Nanomedicine, Nanoparticles, Drug delivery systems, Targeted drug delivery

NAMA-OP-08

Marine actinomycetes as a promising resource for nanomaterials and advanced microbial innovations

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Abstract

Synthesis of Nanoparticles through biological agents is a promising approach which is ecofriendly and comparatively cost effective. Among different microorganisms actinomycetes are found to be efficient in synthesis of Nanomaterials. Marine actinomycetes are diverse group of filamentous Gram-positive bacteria with high G+C content (>70%) widely distributed in sediments, mangroves, and sponges. They are distinct from terrestrial counterparts due to their unique adaptation to high salt, low nutrient, and high-pressure marine environments. They have gained significant attention as a source of novel secondary metabolites. More than 500 various species are included in actinomycetes among which *Streptomyces* holds the greatest position as producers of bioactive metabolites of industrial significance. In recent years, marine actinomycetes have emerged as promising biological resources in the field of nanotechnology and advanced microbial applications. The nanoparticles are produced through intracellular as well as extracellular synthesis processes. The characterization of nanoparticles involves techniques such as UV-Vis, SEM, TEM, XRD, EDX, and FTIR. Due to their high surface area- to-volume ratio, nanoparticles exhibit unique physicochemical properties, leading to enhanced catalytic, magnetic, mechanical, and optical activities. The nanoparticles synthesized by marine actinomycetes find their application as anticancer, antioxidant, and anti-biofilm properties, making them valuable in biomedical, pharmaceutical, and agricultural sectors. They play an important role in the development of nano-biosensors, drug delivery systems, and nanocatalysts. The unique enzymes and metabolites produced by marine actinomycetes facilitate controlled nanoparticle synthesis with enhanced stability and functionality. Their metabolic versatility enables the eco-friendly synthesis of metal nanoparticles such as silver, gold, zinc oxide, and copper nanoparticles through biological reduction processes. They also contribute towards bioremediation of marine pollutants, degradation of complex organic compounds. Therefore, the exploration of marine actinomycetes represents a promising frontier for sustainable nanomaterial production and innovative microbial technologies. Continued research integrating microbiology, nanoscience, and biotechnology will further unlock their potential for developing next- generation therapeutic agents, environmental solutions, and advanced industrial products.

Keywords: Marine actinomycetes, Secondary metabolites, Nanoparticles, Characterization, Bioremediation

NAMA-OP-09

In vitro ROS scavenging, AMPK activation, and *in silico* validation of eugenol as a potent antioxidant from wild *Cymbopogon flexuosus*

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Abstract

The present study investigates the antioxidant potential of secondary metabolites from the leaves of wild *Cymbopogon flexuosus* (Lemongrass) through a combination of *in vitro*, *ex vivo*, and *in silico* approaches. Crude extracts prepared using solvents of varying polarity (methanol, chloroform, aqueous, ethyl acetate, diethyl ether, hexane, butanol) were evaluated for antioxidant activity using DPPH radical scavenging, nitric oxide scavenging, and phosphomolybdenum assays. The methanol extract consistently exhibited the strongest free radical scavenging capacity and was selected for further investigation. In HepG2 liver carcinoma cells, the methanol extract exhibited potent inhibition of intracellular ROS (H_2DCFDA assay) and significantly upregulated α-AMPK expression (flow cytometry), surpassing ascorbic acid in AMPK induction while showing no cytotoxicity (MTT assay). Column chromatography of the methanol extract yielded multiple fractions, with fraction 14 exhibiting superior ROS suppression and negligible toxicity, thereby selecting it for detailed phytochemical characterization. FT-IR analysis indicated the presence of phenolic/alcoholic –OH, alkene/aldehyde C–H, and other oxygen-containing functional groups. GC-MS profiling of fraction 14 identified eugenol as the predominant compound, accompanied by 2-methoxy-4-vinylphenol, geraniol, 2, 5-furandione, triacontanoic acid, and hexacontane. Eugenol was subsequently isolated and purified (~95% purity) by GC-FID and structurally confirmed by ^{1}H and ^{13}C NMR. Drug-likeness evaluation (Lipinski's rule of five, Swiss ADME) revealed that eugenol, 2-methoxy-4-vinylphenol, and geraniol possess favorable physicochemical properties, high gastrointestinal absorption, BBB permeability, and no significant toxicity flags. Molecular docking demonstrated that eugenol exhibited strong binding affinity to key antioxidant enzymes, particularly xanthine oxidase. The stability of the eugenol–xanthine oxidase complex was further validated by a 100 ns molecular dynamics simulation, which showed low RMSD/RMSF values and persistent hydrogen bonding/hydrophobic interactions. Collectively, these findings establish eugenol as the major bioactive antioxidant metabolite in wild *C. flexuosus* leaves, supporting its potential as a natural, non-toxic therapeutic candidate for oxidative stress-related conditions.

Keywords: *Cymbopogon flexuosus,* Eugenol, Antioxidant activity, Molecular docking, ROS, Xanthine oxidase

NAMA-OP-10

Phytochemical, nutritional, mineral, and antioxidant profiling of different solvent extract of *Malpighia emarginata* DC. fruits

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Abstract

Malpighia emarginata DC. (Acerola), a tropical fruit rich in vitamin C and bioactive phytochemicals, has garnered attention for its potential nutritional and antioxidant properties. This study aimed to evaluate the phytochemical composition, nutritional and mineral content, and *in vitro* antioxidant potential of different solvent extracts of acerola fruits collected from the Western Ghats region of Karnataka, India. Successive solvent extraction was performed using petroleum ether, ethyl acetate, and ethanol, followed by proximate and elemental analysis to determine macronutrient and mineral profiles. The ethanol extract (AEE) exhibited the highest content of phenolics, flavonoids, and other bioactive compounds. Antioxidant activities were assessed using DPPH, ABTS, superoxide anion, nitric oxide, hydroxyl radical scavenging assays, ferrous ion chelation, and reducing power methods. Among the extracts, AEE consistently demonstrated superior radical scavenging and metal-chelating activities, with lower IC_{50} values compared to ethyl acetate (AEAE) and petroleum ether (APEE) extracts, though the standard BHT showed stronger overall activity. Proximate analysis revealed a high carbohydrate content (14.08 ± 0.62%), moderate protein (1.16 ± 0.36%) and fiber (2.12 ± 0.28%), and low fat (0.2 ± 0.48%), while elemental analysis confirmed the presence of essential minerals including sodium, potassium, calcium, magnesium, and iron. These findings highlight acerola as a functional fruit combining nutritional richness, mineral content, and potent antioxidant capacity, suggesting its potential applications in dietary supplementation, functional foods, and nutraceutical development.

Keywords: *Malpighia emarginata*, Acerola, Phytochemicals, Antioxidants, Nutritional profile, Mineral content

NAMA-OP-11

Label-free electrochemical sensing of Hg^{2+} using a Bi_2WO_6-DNA nanocomposite interface

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Abstract

Heavy metal ion detection is important for ensuring public health and protecting the environment. To address this issue, DNA-mediated bismuth tungstate (BW) was developed towards electrochemical detection of mercury ions (Hg^{2+}). In the composite, Bi^{3+} interacts with the oxygen atoms of tungstate anion WO_4^{2-} while sugar and phosphate groups of DNA gets attracted to positively charged Bi^{3+} ions in BW. The BW-DNA modified electrode surface demonstrates excellent electrochemical oxidation of mercury ions with good reaction kinetics in a diffusion-controlled process. The Hg^{2+} ions selectively bind to these thymine bases of DNA, such as thymine–Hg^{2+}–thymine base pair, a metal-mediated mismatch formation instead of the standard Watson-Crick base pairs formation. The results show an excellent linear concentration of 10 µM - 1 mM and the LOD is 1.3 µM. Finally, a sensing approach has been effectively applied in real time analysis of Hg^{2+} ions in tap and lake water, with acceptable recovery results.

Keywords: BW, BW-DNA, Hg^{2+} ion, High selectivity, Electrochemical

NAMA-OP-12

Enhanced acetaminophen detection in Dolo-650 tablets using electrocatalyst $SnWO_4$-DNA composite and its antibacterial efficacy

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Abstract

Important aspects of this research include the development of a very sensitive electrochemical sensor for acetaminophen (AMP) in D-650 tablets using $SnWO_4$-DNA as the sensing material. The surface area and porosity of the material were investigated using the Brunauer−Emmett−Teller (BET) instrument. Furthermore, a TEM study was performed to observe the presence of DNA in $SnWO_4$, and X-ray photoelectron spectroscopy (XPS) was executed to record the chemical composition. The sensor is based on the chemical interaction between Sn^{2+} and WO_4^{2-} ions, which enhances the catalytic activity and the active sites for AMP interaction created by the DNA's nitrogen bases, promoting efficient electron transfer with high sensitivity. The developed sensor performs over AMP detection in D-650 with a much wider linear detection range (200 nM–1 mM), a much lower limit of detection (55 nM), and excellent reversibility. Furthermore, the sensor provides fast detection, suitable for real-time monitoring. In addition, the antibacterial properties of the $SnWO_4$-DNA composite are demonstrated by the effective inhibition growth of *Klebsiella pneumoniae* and *Staphylococcus aureus,* making this a multifunctional tool in both AMP and antibacterial applications. Being able to provide simultaneous chemical detection and antibacterial responses allows this material to have dual capability in medical diagnostics. The high sensitivity and multifunctionality of the proposed sensor make it an innovative and promising approach that would have wide application in the medical industry for AMP monitoring, pathogen control, and potentially in personalized medicine for determining the appropriate treatment regimen for patients.

Keywords: $SnWO_4$, $SnWO_4$-DNA, Acetaminophen, Sensitivity, Stability

NAMA-OP-13

Guar gum supported ZIF-8 as an effective catalyst for electrochemical sensing of gallic acid in liquid food samples

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Abstract

Monitoring of food-based products is mandatory in recent days because of increasing health-related issues and to produce ready to-eat foods. Generally, in the food industry, the antioxidant property of phenolic compounds is utilized to improvise human health. Gallic acid (GA) is a widely known and abundant phenolic acid found used in numerous foods because of its huge health benefits. So far, many methods have been developed for the detection of GA using diverse nanocomposites. Likewise in the view of providing a simple and inexpensive material, we propose a zeolitic imidazolate framework (ZIF-8) functionalized with guar gum (GG) towards GA sensing. Here, the composite is prepared in a very easy and time-efficient manner using biocompatible GG. The physiochemical properties confirm the material formation due to the electrostatic interaction between the zinc ion of ZIF-8 and GG's hydroxyl or carboxyl groups. Morphological studies confirm the nanostructured rhombic dodecahedral ZIF-8 particles embellished on the surface of GG's microlayers. Further, electrochemical studies reveal the composite excellent behaviour towards the GA sensing with a wide linear range of 200 nM – 2.5 mM and a detection limit (LOD) of 60 nM. In addition to this, the composite offers significant selectivity, and good stability of up to 84% for 100 cycles along with acceptable repeatability and reproducibility. Finally, the investigation of the practical utility of unspiked wine, grape juice, and tea samples also profound the composite's exceptional sensing with remarkable recovery. Considering all these results, the proposed ZIF-8@GG composite can be fit for the fabrication of sensor devices towards food product testing in industries.

Keywords: ZIF-8, Guar gum, Electrochemical sensor, High sensitivity, Food sample monitoring

NAMA-OP-14

Bio-modified NiAl–LDH for high-performance electrochemical sensing and degradation of Bisphenol-A

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Abstract

Bisphenol A (BPA) is a chemical of increasing concern because of its widespread harmful impacts on environment and aquatic system. To address this issue, we synthesized the stearic acid modified Nickel-Aluminium layered double hydroxide with rutin intercalated (Ru@SA-NiAl LDH) for the electrochemical detection of BPA. The excellent reduction in band gap lowers the energy required for electron excitation, thereby improving conductivity and charge transfer at the electrode surface. In the same way, increased roughness in the composite indicates successful Ru loading and provides more active sites, improved surface heterogeneity, and enhanced interaction capability for BPA detection. The $[Fe(CN)_6]^{3-/4-}$ redox probe validated the electrochemical activity of Ru@SA–NiAl LDH and its suitability for BPA sensing by demonstrating efficient interfacial charge transport, high stability, successful surface modification, enhanced electroactive surface area, and rapid electron-transfer kinetics. In SWV analysis, Rutin (Ru) act as the electron mediator to shuttle the electrons to BPA hence it improves the sensitivity of the Ru@SA-NiAl LDH with linear range 10 nM - 600 µM and its LOD is 1.29 nM, as a reliable platform of BPA in real time environmental monitoring. Interestingly, we also analyse the degradation study of the BPA through different metal ions such as Fe, Cu and Cr interacting with •OH radicals, oxidatively break BPA into phenoxyl radicals reducing the amount of electroactive BPA available for oxidation at the electrode. Also, from the analysis of degradation ability with different buffers, demonstrated that BPA is deprotonated the phenolate ions which are nucleophilic and more reactivity to degrade the BPA in NaOH buffer. Overall, the Ru@SA-NiAl LDH exhibited outstanding electrochemical sensing and degradation ability.

Keywords: NiAl-LDH, Rutin, Bisphenol-A, Degradation, Electrochemical sensor

NAMA-OP-15

Phyto-mediated synthesis, characterization, and biological assessment of CuO nanoparticles using *Caralluma fimbriata* tea-infusions

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Abstract

Nanotechnology has emerged as a breakthrough field in contemporary medicine due its increasing use in targeted drug administration and diagnostic applications. This work investigates the use of beneficial herbal tea infusions from *Caralluma fimbriata* in the sustainable production of copper oxide (CuO) nanoparticles. Tea bags with four different formulations: C1, C2, G1 and G2 were used to prepare the tea extract. This polyphenol-rich extract functioned as both stabilizing and reducing agents. The best formulation was determined by UV-visible screening to be C2, which showed a distinctive surface plasmon resonance peak at 247 nm. X-ray diffraction (XRD) structural characterization verified a crystalline nature. Scanning Electron Microscopy analysis showed a block-like form thereby confirming the size of the particles and elemental purity was confirmed by energy-dispersive X-ray spectroscopy (EDX). FTIR spectrum confirmed CuO stretching vibrations below 600 cm^{-1}. Antioxidant assays (ABTS, DPPH, FRAP) and antidiabetic assays (α-amylase and α-glucosidase inhibition) were used to evaluate the therapeutic potential. These findings provide an insight on green technology applications and indicate that the tea-infused CuO nanoparticles exhibit promising potential for therapeutic agents to combat oxidative stress and diabetes.

Keywords: Green biosynthesis, *Caralluma fimbriata*, CuO nanoparticles, Nanotherapeutic agents, Tea-infusions

NAMA-OP-16

Sustainable green synthesis of cadmium nitrate nanoparticles using vanillin and ascorbic acid and their potential therapeutic applications

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Abstract

Nanotechnology has emerged as a rapidly advancing interdisciplinary field with significant applications in medicine, biotechnology, and environmental sustainability. Among various nanomaterials, metal-based nanoparticles have gained considerable attention due to their unique physicochemical and biological properties. In recent years, green synthesis approaches have been widely explored as eco-friendly alternatives to conventional chemical methods for nanoparticle production. It is considered sustainable because the nanoparticles are synthesized using eco-friendly natural compounds (vanillin and ascorbic acid) instead of toxic chemical reducing agents, minimizing environmental impact, and promoting green nanotechnology. The present study focuses on the green synthesis of cadmium nitrate nanoparticles (CdNPs) using vanillin and ascorbic acid as natural reducing and stabilizing agents. The synthesis was carried out using a microwave-assisted method, which provides rapid and uniform heating, facilitating efficient nucleation and formation of nanoparticles within a short reaction time. Characterization of the nanoparticles was performed using UV–Visible spectroscopy, X-ray diffraction (XRD), scanning electron microscopy (SEM), transmission electron microscopy (TEM), and energy dispersive X-ray analysis (EDAX) to determine their structural, morphological, and elemental properties. To evaluate their biomedical potential, several biological assays were conducted. A hemolytic assay was performed to assess cytocompatibility with human red blood cells, while a sedimentation assay evaluated nanoparticle stability in biological media. The antimicrobial activity of CdNPs was tested against *Escherichia coli* and *Streptococcus aureus*, demonstrating notable antibacterial effects. Furthermore, antidiabetic activity was assessed through α-amylase inhibition, α-glucosidase inhibition, and glucose uptake by yeast assays, indicating the potential role of CdNPs in regulating glucose metabolism. Overall, the study demonstrates that green-synthesized cadmium nitrate nanoparticles exhibit promising antimicrobial and antidiabetic properties along with good cytocompatibility, highlighting their potential application in sustainable nanomedicine and therapeutic development.

Keywords: Green synthesis, Nanoparticles, Vanillin, Ascorbic acid, Antimicrobial activity, Antidiabetic activity

NAMA-OP-17

Bridging nanotechnology and the microbiome for advanced drug delivery and diagnostics

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Abstract

Traditional drug delivery approaches often face several limitations such as poor drug solubility, low bioavailability, rapid degradation, and off target effects. To overcome these limitations, nanotechnology-based drug delivery systems have been extensively researched in recent years. Nanoparticles, usually ranging from 1 - 100 nm in size possess high surface to volume ratio and allow easy surface modifications, enabling efficient drug loading, targeted delivery, and controlled release of drugs inside the body. Some of the widely used nanocarriers include liposomes, polymeric nanoparticles, dendrimers, SLNs, NLCs and metallic nanoparticles from different sources such as biological synthesis, chemical engineering, and physical processes. The integration of nanotechnology with microbiome facilitates the selective targeting of pathogenic microbes, to restore beneficial microbial balance, interact with microbial metabolites and enhance treatment efficiency. In addition to nanocarriers, nanoscale sensors, drug delivery devices and microbial biomarkers are being used for early disease diagnostics and personalized treatment strategies. However, challenges such as long-term safety, potential toxicity, collateral damage, regulatory approval, and the complex host-microbiome interactions remain as important obstacles that still need to be resolved. This review highlights the development and application of nanotechnology and microbiome intervention in disease diagnosis, targeted drug delivery, and development of precision medicine in various fields like cancer therapy, gut microbiota, drug delivery to lungs, small intestine, control of microbial biofilms, and treatment of IBD, give an overview of the current works and discuss future research opportunities.

Keywords: Nanoparticles, Drug delivery, Microbiome, Nano carriers, Biomarkers, Disease diagnosis

NAMA-OP-18

Isolation, screening, and characterization of microbial derived antibacterial compounds for therapeutic applications

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Abstract

The rise of antibiotic-resistant pathogens has increased the demand for the identification of new antimicrobial agents from natural origins. This research emphasizes the methodical extraction, evaluation, and analysis of bioactive antibacterial substances obtained from microorganisms. Environmental samples were gathered and processed to isolate microbes to acquire pure cultures, which were subsequently characterized according to their cultural and biochemical traits. Initial screening of isolates was conducted to assess their antibacterial properties, and effective strains were chosen for additional examination. Molecular identification using sequencing methods was conducted to verify the identity of potent isolates. The chosen microorganisms were subsequently grown to produce secondary metabolites, which were then extracted and analyzed using primary screening tests like Minimum Inhibitory Concentration (MIC) and Minimum Bactericidal Concentration (MBC). Additional refinement of bioactive compounds was accomplished through column chromatography, succeeded by fractionation and screening to pinpoint active fractions. The strong fractions were analyzed with sophisticated analytical methods such as Fourier Transform Infrared Spectroscopy (FTIR), Gas Chromatography–Mass Spectrometry (GC-MS), and Nuclear Magnetic Resonance (NMR) spectroscopy to identify their structural and functional characteristics. Following this, *in vivo* research involving animal experiments, immunochemical evaluations, and toxicity assessments were performed to assess the safety and effectiveness of the discovered compounds. The results of this research aid in creating possible therapeutic agents and offer a thorough process for discovering antimicrobial compounds from microbial origins.

Keywords: Bioactive, Secondary metabolites, Toxicity, Therapeutic agents

NAMA-OP-19

Biofunctional evaluation of leaf and flower extracts of *Nyctanthes arbor-tristis* and their green synthesized copper oxide nanoparticles

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Abstract

Nyctanthes arbor-tristis is a medicinal plant native to South and Southeast Asia and has been extensively used in traditional systems of medicine such as Ayurveda, Siddha, and Unani for the treatment of fever, liver disorders, rheumatism, and skin infections. Indigenous communities of the Indian subcontinent have long recognized the therapeutic potential of various parts of *N. arbor-tristis*. Phytochemical investigations have revealed the presence of diverse bioactive compounds, including terpenoids, steroids, glycosides, flavonoids, alkaloids, and several aliphatic constituents. Plant extracts and microbial components were also explored for their dual role as reducing and stabilizing agents in the green synthesis of metal and metal oxide nanoparticles. Green synthesis approaches, which employ biological entities such as plant extracts, microorganisms, or whole plant systems, have emerged as eco-friendly and cost-effective alternatives to conventional chemical synthesis methods. Antimicrobial activity was evaluated in both the presence and absence of nanoparticle extracts using the agar well diffusion method. Antioxidant activity was evaluated. The antioxidant capacities and total phenolic contents in extracts of *N. arbor-tristis* were determined.

Keywords: *Nyctanthes arbor-tristis*, Antimicrobial activity, Antioxidant, bioactive compounds

NAMA-OP-20

Label-free impedimetric electrochemical apta-sensor for the detection of *Bacillus anthracis* spores using a disposable screen-printed gold nanoparticle

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Abstract

Anthrax is an acute zoonotic disease caused by the bacterium *Bacillus anthracis*. It remains a major global public health and biodefense concern due to recurrent outbreaks and the prolonged persistence of spores in contaminated soils. In India, anthrax continues to pose a significant threat in several states, particularly Karnataka, Andhra Pradesh, Maharashtra, and Tamil Nadu. Between 2018 and 2023, nearly 90 confirmed outbreaks were reported across 14 districts of Karnataka, predominantly affecting sheep and cattle. In the current study, an aptamer-based impedimetric electrochemical biosensor was developed using a disposable screen-printed gold nanoparticle electrode (DEP) as the sensing platform for the detection of *B. anthracis* spores. The electrode surface was functionalized with 11-mercaptoundecanoic acid (MUA) to form a self-assembled monolayer, followed by EDC–NHS coupling chemistry to immobilize a specific aptamer designed to recognize *B. anthracis* spores. The stepwise modification of the sensing interface was characterized using electrochemical impedance spectroscopy (EIS). The charge-transfer resistance (R_{ct}) increased progressively with each modification step, confirming successful surface functionalization and aptamer immobilization. The developed biosensor demonstrated high specificity for *B. anthracis* spores, with minimal electrochemical response to *B. thuringiensis*, used as a negative control. EIS measurements showed a clear concentration-dependent increase in R_{ct} across a spore concentration range of 20 – 500 spores/mL. A strong correlation was observed between R_{ct} and spore concentration, with a well-defined linear response between 20 and 200 spores/mL. These findings indicate that the aptamer-functionalized electrode provides reliable electrochemical detection of *B. anthracis* spores. Overall, the proposed biosensing platform offers a rapid, label-free, and sensitive approach for detecting *B. anthracis.*

Keywords: Biosensor, *Bacillus anthracis*, Aptamer, Spore, Screen-printed electrode, Electrochemistry

NAMA-PP-01

Green synthesis of antifungal carbon dots from *Selaginella* (Pteridophyte) for crop disease management

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Abstract

Fungal diseases pose significant threats to global crop yields, necessitating eco-friendly alternatives to synthetic fungicides. This study presents the green synthesis of antifungal carbon dots (CDs) from *Selaginella bryopteris* (Pteridophyte) extracts *via* a hydrothermal process at 180 °C for 6 hours, yielding fluorescent nanoparticles (2 – 10 nm) with a quantum yield of 18 – 25% and rich surface functional groups (–OH, –COOH, $–NH_2$). CDs were characterized using TEM, FTIR, XRD, and PL spectroscopy, confirming their amorphous graphitic structure and ROS-generating capability under visible light. Antifungal activity was evaluated against major crop pathogens including *Botrytis cinerea*, *Fusarium oxysporum*, and *Phytophthora infestans* through agar diffusion, MIC assays, and confocal microscopy. CDs exhibited potent inhibition (80 – 95% mycelial growth suppression at 200 – 500 µg/mL) *via* membrane permeabilization, hyphal deformation, and oxidative stress induction. *In vivo* foliar applications on tomato plants reduced gray mold incidence by 45% and late blight by 38%, while boosting defense enzymes (β 1-3 Glucanase, Peroxidase, Catalase,) without phytotoxicity or yield impacts. These biocompatible, cost-effective *Selaginella* derived CDs offer a sustainable platform for precision crop protection, minimizing environmental residues and resistance development. This green nanotechnology approach aligns with global sustainable agriculture goals.

Keywords: Carbon dots, Green synthesis, *Selaginella,* Antifungal activity, Crop disease management

NAMA-PP-02

From fish scale waste to functional nanomaterials: green synthesis of copper nanoparticles with XRD and TEM insights

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Abstract

Biowaste is valued for its multiple sustainable applications, one of which is the synthesis of nanomaterials. In this study, biopolymer-rich extracts of *Labeo rohita* (Rohu) fish scale waste were used to synthesis ultra-small metallic copper nanoparticles (CuNPs) using green chemistry technique. The keratin-based biopolymers and natural collagen, fish scales, functioned as both stabilizers and reducers during the synthesis of nanoparticles. Sodium hydroxide (NaOH) and copper sulphate pentahydrate ($CuSO_4.5H_2O$) served as pH-controlling agents and precursors for the synthesis of CuNPs. Interestingly, X-ray diffraction (XRD) investigation verified the synthesis of pure metallic Cu nanoparticles with a face-centered cubic (FCC) crystal structure, despite the reaction being originally intended for the synthesis of CuO nanoparticles. The full reduction of Cu^{2+} ions to Cu^{o} was probably caused by the powerful reducing potential of the biopolymers produced from fish scale. Structural analysis using Scherrer's method (SM), Williamson–Hall (W–H) analysis, and the size–strain plot (SSP) approach confirmed the presence of ultra-small crystallites. The average crystallite sizes were determined as Davg = 6.494 nm (SM), D_{WH} = 4.917 nm (W–H), and D_{SSP} = 6.305 nm (SSP). The W–H analysis further revealed a significant internal micro-strain ($\varepsilon = -0.00087$), indicating lattice distortions that may influence functional properties. These results highlight the nanoscale dimensions and strain effects intrinsic to the synthesized material. Transmission Electron Microscopy (TEM) analysis confirmed the formation of predominantly spherical copper nanoparticles with sizes in the range of 20 – 40 nm. The nanoparticles exhibited slight agglomeration and were uniformly distributed over the matrix. Fast Fourier Transform (FFT) analysis indicated the polycrystalline nature of the synthesized nanoparticles. In addition to turning fish scale waste into a useful asset, this is a sustainable way for creating ultra-small metallic nanoparticles that may find use in conductive materials, catalysis. antimicrobial coatings and wound dressings.

Keywords: Green synthesis, Copper nanoparticles, Fish scale biopolymers, Sustainable nanotechnology

NAMA-PP-03

Biogenic synthesis of silver nanoparticles using actinomycetes: characterization and antimicrobial applications

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Abstract

Nanotechnology is found to be an emerging interdisciplinary science with vast applications in medicine, agriculture, and environmental biotechnology. Among the various methods of synthesizing nanoparticles, the microbial method of green synthesis has been found to be an eco-friendly approach for synthesizing nanoparticles. Actinomycetes are a group of filamentous Gram-positive bacteria commonly found in soil. They are found to be capable of producing a variety of bioactive compounds, enzymes, and antibiotics. The ability of actinomycetes to reduce metal ions is also an important trait for synthesizing nanoparticles. The present study deals with the green synthesis of silver nanoparticles using actinomycetes and their evaluation for their antimicrobial activities against various pathogenic microorganisms. Actinomycetes were isolated from the soil by using selective media. Identification was done based on their shape, structure, and biochemical characteristics. The cell-free liquid from the actinomycetes was treated with silver nitrate, which initiated the synthesis of silver nanoparticles. This synthesis was confirmed by a distinct color change. This synthesis was further confirmed by UV-Visible spectroscopy along with other methods. The antimicrobial activity of the silver nanoparticles was checked against selected bacterial pathogens by using standard methods. In addition, the biosynthesized AgNPs had a strong antimicrobial activity, which further confirmed their potential as effective agents in combating detrimental microorganisms. The study highlights the potential of using actinomycetes as effective natural factories for producing nanoparticles, as well as their potential in antimicrobial therapy and biomedical science. In essence, the synthesis of nanoparticles using a green approach with actinomycetes provides a promising, eco-friendly alternative to conventional chemical synthesis, with a focus on the production of environmentally friendly nanoparticles for future biomedical applications.

Keywords: Actinomycetes, Green synthesis, Silver-nanoparticles, Antimicrobial activity, Nanobiotechnology

NAMA-PP-04

Nano-fertilizers: a modern technology key dimension for sustainable soil management

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Abstract

Major hindrance to agricultural productivity is fungal diseases, which causes significant yield losses and reduced crop quality worldwide. Although conventional fungicides are used and effective, often suffer from drawbacks such as low solubility, poor target specificity, environmental contamination, and the development of fungicide resistance. To overcome these limitations, Nanotechnology has led to the development of Nano-fungicides, which are Nano-scale formulations designed to improve the sustainability and efficacy of fungal disease management. Using metal and metal oxides, Nanoparticles are chemically synthesized and developed using polymer-based nanoparticles, lipid-based carriers, and Nano-encapsulated fungicides. These Nano-formulations enhance antifungal activity by improving solubility, controlled release, stability, and targeted delivery of active ingredients. Due to their small size and high surface area, Nano-fungicides can efficiently interact with fungal cells, disrupt cell membranes, generate reactive oxygen species, and inhibit spore germination and mycelial growth. The application of Nano-fungicides in agriculture offers several advantages including reduced chemical dosage, minimized environmental impact, prolonged protection, and lower risk of resistance development. However, concerns related to toxicity, environmental persistence and regulatory approval need to be addressed before large scale commercialization. Overall, Nano-fungicides represent a promising and innovative approach for sustainable plant disease management offering improved crop protection while supporting environmentally friendly agricultural practices.

Keywords: Nano-fungicides, Plant pathogens, Disease management, Sustainable agriculture

NAMA-PP-05

Nano-enhanced microbial biogas production from waste: a sustainable alternative to LPG

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Abstract

The use of liquefied petroleum gas is going up and there are problems in meeting the demand escalating due to the Iran-Israel conflict. Therefore, an alternative way is using nanoparticles to make biogas from waste. Biogas is a way to turn waste into energy. The anaerobic degradation of waste and addition of metal-based nanoparticles like iron helps make methane gas while boosting process efficiency and overall system stability. This process is good for the environment as it reduces levels of harmful compounds like hydrogen sulfide. The methane yield increases from 46% to more than 150% due to enhanced microbial activity and better electron transfer between microbial species. The use of recycled and bio-based nanoparticle, surface modified and green synthesized nanoparticles supports circular economy, helps in reducing toxicity and maintaining efficiency. Therefore, we can use biogas and nanoparticles to make energy that is sustainable and good for the earth. Even with large scale and cost challenges, it is a great renewable energy solution especially in rural and resource limited areas where it can act as practical alternative to LPG.

Keywords: Biogas, Nanoparticles, Anaerobic digestion, Methane production, Sustainable energy

NAMA-PP-06

Application of natural bio-preservatives to improve shelf life of dairy products

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Abstract

Fresh dairy products such as milk and curd were collected from local markets and dairy outlets in Shivamogga, Karnataka, India. The samples were collected aseptically in sterile containers and stored at 4 °C until further analysis. Natural bio-preservatives were prepared using plant extracts from *Dracaena trifasciata* (snake plant) and *Tridax procumbens*, which were collected from the Shivamogga region. The fresh plant materials were thoroughly washed, shade-dried, and ground into fine powder. Plant extracts were prepared using sterile distilled water or methanol as solvents. The extracts were filtered and stored at 4 °C for further experimental use. In addition to plant-based preservatives, lactic acid bacteria were isolated from curd samples and cultured in MRS broth medium. After incubation, the cultures were centrifuged to obtain cell-free supernatant, which was used as a microbial bio-preservative. The antimicrobial activity of the prepared bio-preservatives was evaluated against common dairy pathogens such as *Escherichia coli* and *Staphylococcus aureus* by agar well diffusion method, and zones of inhibition were measured to determine the effectiveness of the bio-preservatives. Selected concentrations of natural bio-preservatives were then added to dairy products. Treated samples consisted of dairy products with added bio-preservatives, while control samples contained no preservatives. All samples were stored under refrigerated conditions to evaluate shelf-life. Microbial analysis was performed at regular intervals of 0, 3, 7, and 14 days using aerobic plate count to determine total bacterial load. The results indicated that natural bio-preservatives effectively reduced microbial growth and improved the shelf life and safety of dairy products.

Keywords: Bio-preservatives, Dairy products, Antimicrobial activity, Lactic acid bacteria, Shelf-life evaluation

NAMA-PP-07

Clinical efficacy of endophytic fungus *Cladosporium cladosporioides* derived silver nanoparticles on microbial pathogens and cancer cell lines

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Abstract

The endophytic fungus *Cladosporium cladosporioides* from the medicinal plant *Opuntia dillenii* was used in this research to synthesize bio-nanoparticles (Cla-AgNPs). Secondary metabolites from *C. cladosporioides* submerged fermentation ethyl acetate extract was studied. Bioanalytical methods characterized Cla-AgNPs. According to the UV-visible spectrophotometer, Cla-AgNPs were synthesized at 410 nm. Cla-AgNPs exhibited functional groups based on Fourier Transform Infrared Spectroscopy (FTIR) peaks at 3732, 3266, 2916, 2845, 2100, 1614, 1530, 1394, 1206, and 1031 cm^{-1}, confirming Cla-AgNPs capping. Scanning Electron Microscopy-Energy Dispersive Analysis of X-ray (SEM-EDAX) and High-Resolution Transmission Electron Microscopy (HR-TEM) showed spherical Cla-AgNPs, and 3 keV EDAX showed silver atoms. X-ray diffraction (XRD) study showed Cla-AgNPs crystalline structure with peaks at (111), (200), (220), (311), and (222). Synthesized Cla AgNPs were 84.90 nm using Dynamic Light Scattering (DLS). GC-MS and FTIR were used to analyze secondary metabolites in the ethyl acetate extract. Cla-AgNPs had significant antimicrobial properties against *Pseudomonas aeruginosa*, with a maximal inhibition zone of 16.06 ± 0.11 mm. The minimum inhibitory concentration (MIC) of 0.5 mg/ mL inhibited *Escherichia coli, Staphylococcus aureus, Pseudomonas aeruginosa* and *Klebsiella pneumoniae*. Cla-AgNPs exhibited significant antifungal activity, with a maximum zone of inhibition against *Aspergillus brasiliensis* (13.13 ± 0.2 mm). Furthermore, the study showed that the synthesized Cla-AgNPs inhibited DPPH and ABTS with IC_{50} values of 84.1 and 139.4 µg/mL, respectively. Cla-AgNPs showed cytotoxicity against HepG2 cell lines in the MTT study, with maximum cytotoxicity of 33.63% at 200 µg/mL.

Keywords: *Cladosporium cladosporioides*, Bio-nanoparticles, Cla-AgNPs, *Opuntia dillenii*, Cytotoxicity

NAMA-PP-08

Synthesis and characterization of carbon-based quantum dots using *Actiniopteris radiate*

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Abstract

This study focuses on the production of Carbon Dots (CD) using *Actiniopteris radiata* (Mayurshikha) plant. Carbon dots are zero dimensional, fluorescent carbon-based nanomaterials with diameters below 10 nm, recognized for their low toxicity, high biocompatibility and excellent photostability. Mayurshikha is a commonly employed medicinal plant in Ayurveda commonly identified as peacock tail fern, with bioactive compounds that may have anti-inflammatory activities. The aim of this investigation was to assess the therapeutic value of bioactive fractions used in traditional Ayurveda. Here, we synthesize the CDs using Mayurshikha plant *via* bottom-up method (Microwave synthesis) and they are characterized by SEM, XRD and FTIR. These CDs are used in bioimaging, drug delivery system and environmental remediation. In the field of nanotechnology, CDs offer a low-cost versatile platform.

Keywords: Carbon dots, *Actinopteris radiata*, SEM, XRD, FTIR

NAMA-PP-09

Ecofriendly fabrication of carbon quantum dots using *Hemidesmus indicus*

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Abstract

Hemidesmus indicus is a medicinal plant, belonging to the Apocyanaceae family, widely used as traditional medicine, which possesses anti-inflammatory, antidiabetic, antimicrobial, and antifungal properties. Aqueous extract of *H. indicus* was used to produce carbon dots. Carbon dots are zero-dimensional nanomaterials that have emerged due to their excellent properties. Carbon dots from natural sources can be produced *via* a hydrothermal approach, offering a sustainable alternative to chemical methods. In this study, fluorescent carbon dots were synthesized through a bottom-up approach and characterized by UV-visible spectroscopy to analyse absorption property, zeta potential analysis to measure particle stability, FTIR to identify functional group and XRD to study their morphology. The produced carbon dots exhibited green fluorescence under a UV source at an excitation wavelength of 365 nm. Further studies on biostimulants, including their antimicrobial activity and phytotoxicity, will be carried out to evaluate their effectiveness.

Keywords: *Hemidesmus indicus*, Carbon dots, Hydrothermal approach, Bottom-up approach, Spectroscopy

NAMA-PP-10

Isolation and antibiotic susceptibility pattern of bacterial pathogens from clinical samples

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Abstract

Bacterial infections remain a major global health challenge, causing significant morbidity and mortality worldwide. The increasing emergence of antimicrobial resistance has reduced the effectiveness of commonly used antibiotics. This situation makes treatment more difficult, costly, and time-consuming, highlighting the urgent need for continuous monitoring of bacterial pathogens and antibiotic susceptibility patterns. In the present study, clinical samples including burn wound, blood sore, and pus were collected from Sarji Super Speciality Hospital, Shivamogga, Karnataka, India. The collected samples were transported to the microbiology laboratory in sterile containers or appropriate transport media for immediate processing. Serial dilution of the samples was performed, followed by inoculation onto selective and differential culture media such as Nutrient Agar, Blood Agar, and MacConkey Agar. The inoculated plates were incubated at 37 °C for 18 – 24 h to allow bacterial growth. Distinct colonies were selected and sub-cultured to obtain pure bacterial isolates. Gram staining was carried out to differentiate the bacteria into Gram-positive and Gram-negative groups. Further identification was performed using standard biochemical tests including Catalase, Indole, Methyl Red, Voges–Proskauer, and Citrate utilization tests. Selected bacterial isolates were subjected to molecular identification through 16S rRNA gene sequencing. Antibiotic susceptibility testing was conducted using the Kirby–Bauer disc diffusion method on Mueller–Hinton agar. The findings of this study contribute to local antimicrobial resistance surveillance, assist clinicians in selecting appropriate antibiotics, promote rational antibiotic use, and strengthen infection control strategies to improve patient management and protect public health.

Keywords: Bacterial infections, Antimicrobial resistance, Clinical isolates, 16S rRNA sequencing

NAMA-PP-11

Engineered silver–carbon quantum dot nanobioconjugates for enhanced immunophenotyping of immune responses to *Staphylococcus aureus* extracellular vesicles

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Abstract

Extracellular vesicles (EVs) released by pathogenic bacteria play an important role in host–pathogen interactions by delivering bioactive molecules that modulate immune responses. *Staphylococcus aureus*, an opportunistic pathogen associated with chronic infections such as diabetic foot ulcers, secretes EVs capable of influencing host immune cell activity. In the present study, extracellular vesicles derived from *S. aureus* strains were isolated and characterized to investigate their immunomodulatory effects on neutrophils obtained from diabetic and non-diabetic individuals. Fluorescence microscopy-based assays revealed EV-induced neutrophil extracellular trap (NET) formation, demonstrating differential NETosis responses under varying EV concentrations. To further understand immune activation patterns, immunophenotyping approaches targeting key immune markers were considered to assess cellular responses following EV exposure. In parallel, the study explores the potential application of engineered silver–carbon quantum dot nanobioconjugates as next-generation fluorescent probes for enhanced detection sensitivity during immune cell profiling. These nanobioconjugates enhances photostability and signal amplification compared to conventional fluorophores, thereby providing opportunities for advanced immunological investigations. Overall, this integrated approach highlights the immunomodulatory role of *S. aureus* extracellular vesicles and proposes nanobioconjugate-assisted immunophenotyping as a promising strategy for studying host immune responses during microbial interactions. The findings contribute to a deeper understanding of pathogen-mediated immune modulation and may support the development of improved diagnostic and analytical tools in infection biology.

Keywords: Extracellular vesicles, Immune response, Nanobioconjugates, Silver–carbon quantum dots

NAMA-PP-12

Antibacterial efficacy of chebulagic acid–encapsulated chitosan nanoparticles against biofilms

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Abstract

In the current medical field, biofilms have emerged as a major global public health concern, posing significant threats to human health. The formation of microbial biofilms has led to numerous complications, particularly in patients with underlying diseases. Increasing antimicrobial resistance associated with biofilms has begun to reduce the effectiveness of current diagnostic methods and negatively impact the success of critical medical procedures such as surgical care, organ transplantation, and cancer therapy. Although biofilms are commonly linked with healthcare-associated infections, they are also increasingly observed in community settings, thereby raising the overall risk of infection. Nanomedicine offers a promising platform with wide applications in medical science, including diagnostics, targeted drug delivery, biosensing, and cancer therapy. The extensive use of antibiotics in clinical practice has contributed to the emergence of resistant pathogens capable of surviving antimicrobial treatments. Biofilms further enhance resistance through mechanisms such as the accumulation of resistance genes within microbial cells often mediated by plasmids and the increased expression of multidrug efflux pumps that expel various antibiotics. Therefore, the present study aims to evaluate the bioinspired synthesis of chebulagic acid-encapsulated chitosan nanoparticles and assess their antibiofilm activity. This approach may help establish chitosan-based nanocarriers as effective therapeutic agents for the management of biofilm-associated infections.

Keywords: Biofilms, Antimicrobial resistance, Chitosan nanoparticles, Chebulagic acid, Antibiofilm activity

NAMA-PP-13

Citric acid production by *Aspergillus niger* using low-cost substrates

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Abstract

Low-cost agricultural substrates such as Kaffir lime (*Citrus hystrix*) and *Phyllanthus emblica* were collected from local markets and agro-processing units to produce citric acid through microbial fermentation. The solid substrates were thoroughly washed, shade-dried, powdered, and sieved to obtain uniform particle size. Prior to use, the prepared substrates were sterilized to eliminate microbial contamination. A high-yielding strain of *Aspergillus niger* was obtained from a laboratory culture collection and maintained under controlled conditions. The culture was sub-cultured on Potato Dextrose Agar plates and incubated at 28 – 30 °C for optimal fungal growth. Spores from a 5 – 7 days old culture were harvested using sterile distilled water containing a mild surfactant to ensure proper suspension. The spore suspension was standardized to an appropriate concentration and used as inoculum for fermentation. A basal fermentation medium containing the selected low-cost substrates as the primary carbon source along with essential mineral salts was prepared. The pH of the medium was adjusted to the required level before sterilization. Citric acid production was carried out using submerged fermentation (SmF). The sterile production medium was inoculated with the prepared *A. niger* spore suspension and incubated at 28 – 30 °C for 7 – 10 days under controlled conditions. At the end of fermentation, the broth was filtered to separate fungal biomass from the fermentation medium. Citric acid concentration was determined using the titrimetric method with standardized NaOH and a suitable indicator. The obtained citric acid was also evaluated for antimicrobial activity using the agar well diffusion method.

Keywords: Citric acid production, *Aspergillus niger*, Submerged fermentation, Low-cost substrates

NAMA-PP-14

Use of nanoparticles in food preservation

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Abstract

Food spoilage caused by microorganisms, oxidation and enzymatic reactions leads to significant food losses worldwide. Nanotechnology has emerged as an innovative approach to improve food preservation and safety. Nanoparticles, which range in size from 1 – 100 nanometers have a large surface area and enhanced reactivity, making them effective in protecting food from contamination and deterioration. In the food industry, nanoparticles are widely used in active packaging, antimicrobial coatings, and nano-encapsulation systems to extend the shelf life of food products. Nanoparticles preserve food through antimicrobial activity, antioxidant properties, improved barrier characteristics, and controlled release of preservatives. Commonly used nanoparticles include silver, zinc oxide, titanium dioxide, and chitosan nanoparticles, which inhibit the growth of food-spoilage microorganisms and help maintain food freshness and nutritional quality. They are also applied in edible coatings and food quality monitoring systems. However, potential toxicity, environmental concerns and limited long-term safety data highlight the need for proper regulations and further research.

Keywords: Nanotechnology, Food preservation, Nanoparticles, Antimicrobial activity, Shelf-life extension

NAMA-PP-15

Smart nano-innovations for sustainable agriculture: evaluating the efficacy of activated carbon nanoparticles in alleviating drought stress in *Vigna radiata* L.

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Abstract

Drought stress is a primary factor limiting the growth and yield of essential food crops like mung bean (*Vigna radiata* L.). This study investigates the potential of Activated Carbon Nanoparticles (ACNPs) as a sustainable nano-technological intervention to alleviate drought-induced stress. ACNPs were characterized using UV-Vis Spectrophotometry (λ_{max} 380.5 nm), XRD, SEM, and EDS to confirm their structural and functional properties. Mung bean plants were grown in a hydroponic system using Hoagland's medium and subjected to drought stress induced by 5% polyethylene glycol (PEG 6000). Five concentrations of ACNPs such as 10, 20, 30, 40, and 50 mg/L were evaluated for their impact on physiological and biochemical parameters after seven days of treatment. The results demonstrated that ACNP application significantly improved plant resilience in a concentration-dependent manner. The 40 mg/L concentration was identified as optimal, showing a 26% increase in shoot length, a 50% increase in root length, and a 45% increase in fresh biomass compared to the stressed control. Furthermore, biochemical analysis revealed a significant elevation in antioxidant enzyme activities, including superoxide dismutase, catalase, and peroxidase, at the 40 mg/L dosage. These findings suggest that ACNPs effectively mitigate oxidative damage and enhance growth under water-deficit conditions. This research highlights the promising role of nanotechnology in developing smart, sustainable agricultural practices to ensure food security in drought-prone regions

Keywords: Carbon nanoparticles, Drought stress, *Vigna radiata,* Sustainable agriculture

Subtheme 3:

Microbial Entrepreneurship & Sustainable Solutions (MESS)

MESS-OP-01

Bioactive constituents of *Cissus quadrangularis* and their therapeutic role in tissue repair

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Abstract

Cissus quadrangularis, belonging to the family Vitaceae is majorly distributed across India, Sri Lanka and Bangladesh. The plant is well known for its therapeutic potential, over the centuries it has been widely used to treat various illness such as indigestion, irregular menstruation, asthma, as an analgesic in eye and ear diseases, antiparasitic and most importantly strengthen the bones and in healing fracture. In this study the aqueous and methanolic extract of the whole plant was subjected to qualitative assays such as phytochemical screening revealed the presence of tannins, terpenoids, saponins, flavonoids and other secondary metabolites. The antimicrobial studies were conducted against *Escherichia coli* and *Bacillus subtilis* the methanolic extract showed significant zone of inhibition against gram positive *B. subtilis.* The antioxidant assay revealed a notable dose dependent free radical scavenging activity. The extracts were further purified and analyzed through GC-MS and the bioactive components were investigated for toxicity prediction. Even though studies have been conducted on treating various ailments there are limited information on mechanistic pathway involved in the treatment. Henceforth, the subsequent research of this work focuses on the mechanistic pathways in therapeutic practice.

Keywords: Vitaceae, GC-MS, Antioxidant assay, Therapeutic role

MESS-OP-02

Multidrug resistance and virulence factors in *Staphylococcus aureus* and coagulase negative *Staphylococci* isolated from raw meat

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Abstract

Methicillin-resistant *Staphylococcus aureus* (MRSA) and methicillin-resistant coagulase-negative staphylococci (MRCoNS) associated with meat-producing animals and retail meat products are a growing public health concern due to their role in the spread of antimicrobial resistance (AMR) through the food chain. In this context, the present study aimed to characterize *S. aureus*, *S. epidermidis*, and *S. saprophyticus* isolated from raw meat samples with respect to their antimicrobial susceptibility patterns, biofilm-forming ability, virulence factors, and resistance to last-resort antibiotics such as vancomycin, linezolid, and daptomycin. A total of 52 raw meat samples, including chicken, goat, pork, beef, and sheep meat, were collected from retail markets and supermarkets in Mathikere, Bengaluru. The samples were enriched in brain heart infusion (BHI) broth and subsequently cultured on Baird Parker agar for the isolation of *Staphylococcus* species. Antimicrobial susceptibility testing was performed using the Kirby–Bauer disc diffusion method. Methicillin resistance was screened phenotypically using cefoxitin discs and further confirmed through PCR by detection of *mecA* gene. Additionally, the isolates were assessed for biofilm production and enzymatic virulence factors using phenotypic assays. Resistance to vancomycin was evaluated using vancomycin agar screening, E-test, and broth macrodilution techniques. Of the 52 meat samples analyzed, 48 (92%) yielded *Staphylococcus* species, with *S. aureus* being the most predominant isolate. A high proportion of the isolates (87.5%) exhibited phenotypic methicillin resistance, with MRSA predominating. The isolates showed considerable resistance to β-lactam antibiotics, and multidrug resistance was commonly observed. Although vancomycin agar screening initially suggested resistance, MIC confirmation did not demonstrate true vancomycin resistance. However, two *mecA* positive MRSA isolates displayed phenotypic resistance to vancomycin, linezolid, and daptomycin. Overall, the study highlights widespread contamination of retail meat with multidrug-resistant and potentially virulent staphylococcus species, emphasizing important food safety and public health concerns.

Keywords: MRSA, MRCoNS, *MecA* gene, Disc diffusion, Multidrug resistance

MESS-OP-03

Comparative phytochemical, biochemical, antioxidant, antibacterial, cytotoxic and *in silico* evaluation of *Leucas aspera*

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Abstract

The present study is designed to systematically evaluate the phytochemical composition, biochemical characteristics, antioxidant potential, antibacterial activity, cytotoxic effects, and *in silico* interactions of *Leucas aspera* to assess its possible therapeutic significance. Aqueous and methanolic extracts of *L. aspera* have been prepared and subjected to preliminary phytochemical screening using standard qualitative techniques. Biochemical analysis will be conducted for cholesterol estimation to examine its potential lipid-lowering activity. Antioxidant activity will be determined using the hydrogen peroxide scavenging assay. The bioactive constituents present in the extracts will be partially purified through column chromatography and subsequently identified using GC–MS analysis. Cytotoxic activity will be evaluated by the MTT assay. Furthermore, molecular docking studies will be conducted targeting HMG-CoA reductase to investigate potential inhibitory interactions. The study is expected to identify important bioactive compounds in *L. aspera* that may demonstrate significant antioxidant activity, cytotoxic properties, and cholesterol-modulating effects. The findings of this research may provide scientific validation for the medicinal value of *L. aspera* and indicate its potential for future therapeutic and pharmacological applications. The antimicrobial assay of extracts has been conducted and the results are awaited

Keywords: *Leucas aspera*, Phytochemical screening, Antioxidant activity, Cytotoxicity, GC–MS analysis

MESS-OP-04

The interplay between Mpox and miRNA: implications for virus replication and disease

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Abstract

The orthopoxvirus known as Mpox (MPV) is native to western and central Africa. First discovered in 1958 in captivity, the virus was discovered in a human in the Democratic Republic of the Congo (DRC) in 1970. In contrast to the variola virus, which only infected humans, MPV can infect a variety of animals, including rodents, which may be a reservoir. The virus was once thought to be exclusively zoonotic, but it has recently demonstrated the ability to spread from person to person through direct contact with lesions, bodily fluids, respiratory droplets, and contaminated objects. MPV was only discovered outside of Africa prior to the current outbreak in cases that had travelled to Nigeria (Israel in 2018, Singapore in 2019, the UK in 2018, 2019, and 2021), the United States of America in 2021, or cases that resulted from contact with infected pet animals (Prairie dogs) that contracted the infection from Gambian pouched rats imported from Ghana to the United States. As of July 12, 2023, 112 countries across all WHO regions have been impacted by the current Mpox outbreak, which has resulted in 148 deaths and 88,288 laboratory-confirmed cases. Several biomolecules were involved in host pathogen interactions during pathogenesis. Recent studies showed the important role of miRNA in this process. The identification of a class of non-coding RNAs known as microRNAs (miRNAs), which are about 22 nt long. A variety of essential cellular functions are modulated by the distinct degree of post-transcriptional gene regulation that these regulatory RNAs offer. Several viruses, particularly herpesviruses, also encode miRNAs; to date, over 200 viral miRNAs have been found. According to available data, viruses can modify the expression of their genes in cells as well as in themselves. Moreover, several RNA viruses have been shown to directly interact with cellular miRNAs and/or utilize these miRNAs to increase their replication potential. This indicates that viral infection can have a significant effect on the profile of cellular miRNA expression. Therefore, in the current study, the interactions of miR-19b-3p were analyzed using the RNAenrich tool.

Keywords: Mpox (MPV), MicroRNAs, Democratic Republic of the Congo (DRC), virus replication

MESS-OP-05

Role of siderophore-producing marine bacteria in improving *Solanum lycopersicum* performance under salinity stress

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Abstract

Salinity stress remains a significant constraint on global tomato production as it disrupts ionic balance and hinders nutrient uptake. This study investigates the potential of halotolerant siderophore-producing marine bacteria as a sustainable solution to mitigate these adverse effects. Marine environments host unique microbial communities that have evolved specialized mechanisms to thrive in high salinity while facilitating iron acquisition through the secretion of siderophores. By inoculating tomato plants with these beneficial microbes, we observed a substantial enhancement in plant growth parameters including shoot length and biomass. The bacteria effectively sequestered iron and made it available to the plants even in saline conditions where iron solubility is typically low. Furthermore, the application of these halotolerant strains resulted in improved chlorophyll content and enhanced antioxidant enzyme activities which helped the plants manage oxidative stress. The findings demonstrate that marine-derived bacteria can act as potent biofertilizers by regulating sodium and potassium ratios within plant tissues. This microbial intervention not only bolsters the resilience of tomato crops against salt toxicity but also promotes overall soil health. Our results suggest that utilizing marine microbial resources offers a promising strategy for reclaiming salt-affected agricultural lands and ensuring food security. This research highlights the critical role of siderophore production in the complex interaction between marine microbes and terrestrial crops under environmental pressure.

Keywords: Biofertilizers, Halotolerant bacteria, Salinity stress, Siderophores, *Solanum lycopersicum*

MESS-OP-06

Recycling agricultural residues as mushroom substrate: a circular bioeconomy model for rural women's entrepreneurship and organic farming in Karnataka

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Abstract

Karnataka generates millions of tonnes of agricultural residues annually, predominantly paddy straw and sugarcane trash which are routinely disposed of through open-field burning, releasing PM2.5, carbon dioxide, methane, and nitrous oxide, thereby degrading rural air quality and accelerating greenhouse gas emissions. This study proposes a village-level circular bioeconomy model in which these lignocellulosic residues are recycled as substrates for oyster mushroom (*Pleurotus ostreatus*) cultivation, offering a dual solution to environmental pollution and rural economic vulnerability. Substrate preparation involves residue chopping (3 – 5 cm), moisture conditioning to 65 – 70%, heat pasteurisation at 80 – 90 °C for one hour, cooling, and inoculation with certified spawn at 2 – 3% w/w. Inoculated polypropylene bags are incubated at 25 – 30 °C for mycelial colonisation (12 – 18 days), followed by a fruiting phase at 85 – 90% relative humidity, yielding two to three flushes over 45 – 60 days. The model is managed by women's self-help groups (SHGs), enabling consistent household income. Small units achieve biological efficiencies of 80 – 120% and net profit margins of 40 – 60%, with market linkages to local vegetable markets, hotel supply chains, and online agri-platforms. Spent mushroom substrate (SMS) is valorised through controlled aerobic composting (55 – 65 °C, weekly turning, four to six weeks), yielding nutrient enriched organic compost rich in nitrogen (1.5 – 2.5%), phosphorus, potassium, and micronutrients. SMS compost can replace 25 – 40% of synthetic fertilisers, improving soil structure, water-holding capacity, and microbial activity, thereby closing the nutrient loop from residue to mushroom to soil. This integrated model reduces residue burning, empowers rural women entrepreneurs, and promotes organic farming - contributing to SDG 1, 2, 5, 8, 12 and 13, demonstrating a scalable, replicable pathway for inclusive and environmentally sustainable rural development in Karnataka.

Keywords: Mushroom cultivation, Agricultural waste recycling, Women entrepreneurship, Organic farming, SDG

MESS-OP-07

Harnessing paraquat-degrading *Bacillus* species for sustainable bioremediation and biofertilizer innovation

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Abstract

Paraquat dichloride is a widely used non-selective herbicide that poses significant environmental and health risks due to its high persistence and toxicity in soil ecosystems. The present study aimed to isolate and characterize bacterial strains capable of degrading paraquat from pesticide-contaminated agricultural soils. Two bacterial isolates were obtained and screened for their paraquat degradation potential under optimized culture conditions. The isolates were subjected to morphological and biochemical characterization, followed by molecular identification using 16S rRNA gene sequencing. Genomic DNA extraction was performed using a spin column method, and PCR amplification of the 16S rRNA gene was carried out using universal primers. Sequence analysis and BLAST comparison revealed that the potent isolate showed ≥99.8% similarity with *Bacillus* species. The degradation capability of the isolate was further confirmed using Gas Chromatography–Mass Spectrometry (GC-MS). The chromatographic profile demonstrated a significant reduction in the parent paraquat peak along with the appearance of lower molecular weight metabolites and pyridine-related intermediates, indicating stepwise degradation involving N-demethylation and bipyridyl ring cleavage. The absence of intact paraquat during later incubation stages confirmed effective microbial degradation rather than simple adsorption. These findings highlight the potential of the identified *Bacillus* species as a promising candidate for the bioremediation of paraquat-contaminated soils. Furthermore, the isolate may serve as a potential bioresource for the development of microbial biofertilizers that simultaneously promote sustainable agriculture and environmental detoxification.

Keywords: Paraquat degradation, *Bacillus* species, Bioremediation, GC–MS analysis, Sustainable agriculture

MESS-OP-08

Augmentation of chitinase production by *Bacillus proteolyticus* using solid-state fermentation

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Abstract

Chitin is a natural polysaccharide composed of β-1,4-linked N-acetyl-D-glucosamine units, which can be hydrolyzed by chitinase enzymes into chitosan oligosaccharides or N-acetyl-D-glucosamine. Plant growth-promoting rhizobacteria (PGPR) play an important role in enhancing plant growth by improving nutrient availability, regulating plant hormones, and functioning as biocontrol agents against plant pathogens. The present study focuses on the screening, production, partial purification, characterization, and application of chitinase enzyme from *Bacillus proteolyticus*, a promising bacterial isolate obtained from a severely depleted arecanut plantation. Chitinase production was optimized using the solid-state fermentation (SSF) method. The results revealed that SSF produced a chitinase activity of 25.03 U/mL/min. Two substrates, rice bran and wheat bran, were evaluated for fermentation. Among them, wheat bran showed greater efficiency in supporting chitinase production compared to rice bran. The chitinase produced from wheat bran was subsequently subjected to partial purification, which resulted in a 2.5-fold increase in enzyme purity. The enzyme exhibited maximum activity at pH 7 and a temperature of 30 °C, with dextrose serving as the optimal carbon source and beef extract as the preferred nitrogen source. SDS-PAGE analysis revealed that the partially purified chitinase had a molecular weight of approximately 25 kDa. Furthermore, the enzyme demonstrated significant antifungal activity against the phytopathogenic fungus *Colletotrichum gloeosporioides*.

Keywords: Chitinase enzyme*, Bacillus proteolyticus,* Phytopathogens, Solid-state fermentation

MESS-OP-09

Harnessing endophytic fungi from *Acorus calamus* for sustainable microbial solutions in agriculture and healthcare

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Abstract

Endophytic fungi associated with medicinal plants are valuable sources of bioactive metabolites with potential applications in agriculture, medicine, and biotechnology. This study investigated the multifunctional potential of two endophytic fungal isolates, *ACR12* and *ACR15* obtained from the rhizome of *Acorus calamus,* focusing on their plant growth–promoting, biocontrol, antimicrobial, antioxidant, and cytotoxic properties. Both isolates exhibited important plant growth–promoting traits, including indole-3-acetic acid (IAA) production, phosphate solubilization, ammonia production, and siderophore secretion, indicating their ability to enhance nutrient availability and plant development. In maize seed germination assays, *ACR15*-treated seeds showed improved germination and seedling vigor compared with *ACR12* and control treatments. Dual culture assays against the phytopathogens *Colletotrichum sp*. and *Fusarium* sp. revealed antagonistic activity, with *ACR15* demonstrating stronger inhibition of mycelial growth. Ethyl acetate crude extracts of the isolates were further evaluated for antimicrobial, antibiofilm, antioxidant, and cytotoxic activities. The extracts exhibited inhibitory effects against several pathogens, including *Escherichia coli, Staphylococcus aureus, Pseudomonas aeruginosa, Bacillus subtilis,* and *Candida albicans*. Antioxidant activity and cytotoxic effects against MCF-7 breast cancer cell lines were also observed, with *ACR15* showing higher activity. Overall, the findings highlight the multifunctional bioactivity of endophytic fungi from *Acorus calamus*, particularly *ACR15*, demonstrating their potential for sustainable agricultural applications and development of novel antimicrobial and pharmaceutical bioproducts.

Keywords: Endophytic Fungi, *Acorus calamus*, Plant growth promoting traits, Biocontrol, Bioactive metabolites

MESS-OP-10

In silico and *in vitro* analysis of a novel, lantibiotic preserved MUFA enriched probiotic supplement for adult nutrition

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Abstract

The development of affordable microbial products that support gut health and nutritional balance has become an important focus in functional food biotechnology. In this study, a cost-effective probiotic protein supplement was developed using beneficial probiotic microorganisms combined with locally sourced natural ingredients. Probiotic strains were isolated from commercial probiotic products and characterized through morphological and biochemical analyses, followed by molecular identification using 16S rRNA sequencing. The isolates were confirmed as *Lactobacillus acidophilus*, *L. casei*, and *L. delbrueckii* subsp. *bulgaricus*, well-recognized lactic acid bacteria with probiotic potential. The probiotic cultures were cultivated under optimized laboratory conditions and preserved through freeze-drying to obtain stable lyophilized probiotic biomass. Approximately 5 g of probiotic powder containing viable counts in the range of 10^9 – 10^{10} CFU g^{-1} was incorporated into each formulation batch to ensure adequate probiotic delivery. The microbial component was integrated with nutritionally rich ingredients including milky mushroom (*Calocybe indica*) as a protein source, flaxseed as a source of monounsaturated fatty acids and dietary fibre, and palm jaggery as a natural mineral-rich sweetener. To enhance product stability and microbial safety, lantibiotics such as nisin derived from *Lactobacillus* spp. were incorporated as natural antimicrobial preservatives. Five formulations incorporating lyophilized probiotic cultures were developed and evaluated through proximate analysis, antioxidant profiling, protein digestibility assessment, and cytotoxicity studies. Among them, formulation FMP-2 exhibited superior nutritional composition, containing 17.2% protein, 9.5% crude fibre, 47.3% carbohydrates, and an energy value of 444.45 kcal/100 g, along with the highest total phenolic content (39.6 mg/100 g) and total flavonoid content (31.8 mg/100 g). Cytotoxicity evaluation using the MTT assay confirmed high cell viability, indicating the safety of the probiotic-fortified formulation. These findings highlight the potential of probiotic-enriched functional foods as sustainable microbial innovations supporting adult nutrition and gut health.

Keywords: Probiotics, *Lactobacillus*, Food biotechnology, Lyophilization, Lantibiotics, Microbial innovation

MESS-OP-11

Bactoplast: a microbial based innovation for sustainable plastics

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Abstract

Plastic pollution has become a major environmental problem due to the non-biodegradable nature, persistence in the environment, and the toxic chemicals released during its lifecycle. The accumulation of plastics in marine and terrestrial environments has led to several species ingesting plastics, resulting in developmental, reproductive, neurological, and immune disorders. Bio-plastics have emerged as a sustainable, biodegradable, and eco-friendly alternative to conventional plastics. This venture focuses on the production of natural biodegradable plastic using the bacterium *Ralstonia eutropha*, a facultative chemolithotroph, which is capable of synthesizing Polyhydroxyalkanoates (PHA), inside its cells under nutrient-limited conditions. In this process, the bacterium is cultured in a nutrient medium under controlled temperature and pH conditions in a fermentation system. Carbon sources such as glucose, molasses, or vegetable oils are supplied in excess while limiting nitrogen to stimulate the accumulation of PHA granules within the bacterial cells. After fermentation, the cells are harvested by centrifugation, and PHA is extracted using chemical or mechanical methods. The purified PHA is then dried and processed to form biodegradable plastic materials. Exploring PHA metabolism can unlock new avenues for eco-friendly bioplastic production, driving sustainable development.

Keywords: *Ralstonia eutropha,* Polyhydroxyalkanoates, Biodegradable plastic, Nitrogen limitation

MESS-OP-12

Development and evaluation of spiced millet-based ice cream with functional properties

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Abstract

Millets are a group of climate-resilient cereals known for their high nutritional benefits and potential to improve food and nutritional security. These are rich in micronutrients, dietary fibres, and bioactive compounds. Therefore, millets are increasingly being considered as an important functional food ingredient. However, the use of millets for developing innovative food products with acceptable sensory properties is still limited. The aim of this study was to develop a new ice cream with a sweet and spicy taste by incorporating spices such as cinnamon, ginger, and white pepper, which are known for their flavour, aroma, and medicinal properties. The ice cream was prepared by using milk obtained from various millets available in the market, fresh cream, sugar, ice cream stabilizer, and spices. The prepared ice cream was evaluated for its physicochemical properties such as pH and melting rate. Phytochemical screening tests were conducted to detect the presence of phytochemicals such as proteins, amino acids, flavonoids, phenols, tannins, saponins, terpenoids, fats, and carbohydrates. The estimation of the amount of protein and carbohydrate content in the product was also done. The sensory evaluation tests were conducted to check the colour, taste, aroma, texture, and acceptability of the product. The results revealed that the millet-based spicy ice cream had favourable physicochemical characteristics like those of normal ice cream. The phytochemicals present in the product are also favourable. The results revealed that the product had favourable sensory attributes. The results revealed that millet milk can be used to produce nutritious spicy ice cream with favourable sensory attributes. The product has the potential to be used as a non-dairy product to encourage the consumption of millet.

Keywords: Millet, Functional food, Spices, Physicochemical analysis, Sensory analysis

MESS-OP-13

Microbial entrepreneurship and sustainable solutions: role of biofuels and biofertilizers

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Abstract

Microbial entrepreneurship is gaining increasing importance as a sustainable approach to address global challenges such as food security, environmental pollution, and the growing demand for renewable energy. Microorganisms possess diverse metabolic capabilities that can be utilized for the development of eco-friendly technologies and commercially valuable products. Among these innovations, biofertilizers and biofuels represent two significant microbial solutions that contribute to sustainable agriculture and renewable energy production. Biofertilizers are preparations containing beneficial microorganisms such as *Rhizobium*, *Azotobacter*, *Azospirillum*, and phosphate-solubilizing bacteria that enhance soil fertility and promote plant growth. These microorganisms improve nutrient availability by fixing atmospheric nitrogen, solubilizing phosphorus, and producing growth-promoting substances. The application of biofertilizers reduces the dependence on chemical fertilizers, improves soil health, and supports environmentally sustainable agricultural practices while maintaining crop productivity. Microorganisms also play a crucial role in the production of renewable biofuels. Various microbes including bacteria, yeast, and microalgae can convert organic biomass into bioethanol, biodiesel, and biogas through fermentation and other metabolic processes. Microbial biofuel production provides a promising alternative to fossil fuels and contributes to the reduction of greenhouse gas emissions. Additionally, the use of agricultural and industrial waste materials for microbial fermentation supports effective waste management and resource utilization. The integration of microbial biotechnology with entrepreneurial initiatives creates opportunities for innovative and sustainable biotechnological enterprises. Startups focusing on microbial biofertilizers and biofuel production can promote green technology, sustainable agriculture, and renewable energy development. Therefore, microbial entrepreneurship represents a promising pathway for translating microbiological research into practical and environmentally responsible solutions for a sustainable future.

Keywords: Microbial entrepreneurship, Biofertilizers, Biofuels, Sustainable agriculture, Renewable energy

MESS-OP-14

Biodegradation of thiourea by microbial isolates for sustainable environmental solutions

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Abstract

Thiourea, a thiocarbonyl-containing compound widely used in pharmaceuticals, agriculture, metal extraction, and electronics, poses significant toxicity risks to humans and animals and can persist in soil and water, leading to environmental pollution. The present study investigates the potential of microbial isolates for the sustainable biodegradation of thiourea from contaminated environments. Sewage samples were collected as a source of pollutant-adapted microorganisms and subjected to enrichment and isolation using thiourea-amended culture media. Serial dilution followed by plating enabled the isolation of bacterial and fungal strains, which were morphologically and microscopically characterized as *Bacillus, Trichoderma*, and *Fusarium* species. Screening of isolates using minimum inhibitory concentration (MIC) assays and the gradient plate technique revealed their tolerance and adaptability under thiourea stress. Organic acid production assays indicated strong acid synthesis by *Trichoderma*, moderate activity by *Fusarium*, and comparatively lower production by *Bacillus*, suggesting their role in thiourea transformation. Further studies focused on the optimization of physicochemical parameters such as pH, temperature, incubation time, and nutrient sources to enhance microbial growth and degradation efficiency. Evaluation of different carbon, nitrogen, mineral, and salinity sources indicated that optimized nutritional conditions improved microbial biomass and metabolic activity. Biodegradation experiments were carried out by incubating microbial cultures in thiourea-containing media. Samples collected during incubation were centrifuged to obtain cell-free supernatants for FTIR and HPLC analysis to monitor structural changes and degradation products. The study also explored possible bioaccumulation and metabolic transformation mechanisms**,** indicating that microbial biomass may contribute to thiourea removal through intracellular accumulation and enzymatic degradation. The findings highlight the potential of microbial isolates such as *Bacillus*, *Trichoderma*, and *Fusarium* species for eco-friendly bioremediation of thiourea-contaminated environments.

Keywords: *Bacillus, Trichoderma, Fusarium,* Gradient plate method, Microbial bioremediation

MESS-OP-15

Development of tri-microbial biopolymer pellets for biofertilizer delivery

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Abstract

Beneficial microorganisms are widely used as biofertilizers due to their ability to improve soil fertility, promote plant growth and reduce dependence on chemical fertilizers. However, conventional microbial formulations often suffer from low shelf life, poor soil survival, and rapid loss of microbial activity after application. Encapsulation using biodegradable polymer matrices provides protection to microbial cells, improves stability, and enables controlled release in soil. This study aims to develop a tri-microbial biopolymer pellet containing *Rhizobium* spp., phosphate-solubilizing fungi (*Trichoderma* spp./ *Aspergillus niger*), and *Streptomyces* spp. for biofertilizer delivery. *Rhizobium* was isolated from leguminous plant root-nodules and cultured on Yeast Extract Mannitol Agar. *Trichoderma* spp., *Aspergillus niger*, and *Streptomyces* spp. were isolated from organic-rich soil using pure culture techniques on Potato Dextrose Agar and Starch Casein Agar. Microbial density analysis showed approximately 3×10^7 CFU/mL for *Rhizobium* and 4×10^7 SFU/mL for *A. niger* and *Trichoderma*. Based on compatibility testing, single and dual microbial pellets (*A. niger* + *Rhizobium*; *Trichoderma* + *Rhizobium*) were fabricated. Encapsulation was performed using a sodium alginate–starch matrix with glycerol as plasticizer through calcium chloride ion cross-linking. Swelling studies at pH 5, 7, and 9 showed stability with slight swelling in acidic conditions and dissolution in neutral and alkaline buffers except at 0.02 M concentration, indicating potential for controlled microbial release in soil. The ongoing study is expected to provide insights into the effectiveness of encapsulated biofertilizers for controlled microbial release, contributing to improved soil management strategies.

Keywords: Biofertilizer, Microbial encapsulation, Sodium alginate, *Rhizobium*, *Trichoderma*

MESS-OP-16

Bioactive fractions from *Curcuma angustifolia* Roxb. rhizomes as natural anti-microbial and anti-biofilm agents against *Enterococcus faecalis* for sustainable microbial control

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Abstract

The increasing prevalence of antimicrobial resistance and biofilm-associated infections highlights the need for sustainable antimicrobial alternatives. *Enterococcus faecalis*, a clinically significant pathogen, is well known for its ability to form persistent biofilms and cause chronic infections. In this study, rhizomes of *Curcuma angustifolia* Roxb. were investigated as a potential source of natural antimicrobial compounds targeting *E. faecalis*. The powdered rhizomes were subjected to successive Soxhlet extraction using petroleum ether, chloroform, and ethyl acetate. Among the extracts obtained, the ethyl acetate fraction enriched with polar bioactive constituents was selected for further investigation. The extract was fractionated using column chromatography, and the resulting fractions were evaluated for antimicrobial and anti-biofilm activities against *E. faecalis*. Several fractions exhibited notable inhibition of bacterial growth and biofilm formation. Structural characterization of the active fractions was performed using HPLC, LC-MS, NMR, and FTIR analyses. These findings indicate that bioactive fractions derived from *C. angustifolia* rhizomes possess promising antimicrobial potential against *E. faecalis* and may serve as candidates for developing sustainable antimicrobial formulations.

Keywords: *Curcuma angustifolia*, *Enterococcus faecalis*, Anti-Biofilm, Phytochemicals, Microbial control

MESS-OP-17

Fungal bioremediation of textile dye effluents: biosorption potential of *Aspergillus* and *Penicillium* species

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Abstract

Bioremediation is an eco-friendly approach that utilizes microorganisms, such as fungi and bacteria, to clean the environment by removing pollutants. These microorganisms employ mechanisms like biosorption and bioaccumulation to remediate various contaminants. Textile dye effluents are a significant source of aquatic pollution, contributing to elevated chemical oxygen demand (COD) in water bodies, which negatively impacts the growth, development, and reproductive potential of aquatic organisms. Moreover, these dyes can induce oxidative stress and cause multi-organ injuries in humans. In addition to dyes, heavy metals such as cadmium, copper, lead, nickel, and zinc are naturally occurring elements that have been exacerbated by uncontrolled human activities. The excessive presence of these metals in soil and aquatic environments has disrupted geochemical cycles and biological equilibria, further stressing the need for bioremediation strategies to restore balance. This study investigates the bioremediation potential for the removal of dyes and heavy metals from wastewater by *Aspergillus* and *Penicillium* species. The bioremediation potential was assessed by evaluating the biosorption capacity of these fungi on Sabouraud's Dextrose Broth (SDB) containing the given dye Malachite Green and Rose Bengal. Both dyes are frequently utilized in the textile industry and are known for their environmental persistence and toxicity. The assessment involved analyzing the absorbance of dyes using spectroscopic and colorimetric techniques. Consecutive optical density (OD) measurements revealed that *Penicillium* sp. exhibited the highest absorbance across both dyes, highlighting its superior biosorption capacity. *Aspergillus* sp. also demonstrated appreciable absorbance, indicating notable biosorption potential. Overall, the study underscores the effectiveness of fungal species, particularly *Penicillium* sp. in the biosorption of harmful dyes from wastewater. Bioremediation presents a promising solution for mitigating environmental contamination caused by textile dyes and heavy metals, offering an efficient and sustainable method to protect aquatic ecosystems and human health.

Keywords: Biosorption, Bioaccumulation, Malachite Green, Rose Bengal

MESS-OP-18

Decolorization of Reactive Black 5 dye using *Penicillium citrinum* SC6

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Abstract

Reactive Black 5 (RB5), an anthraquinone dye widely used in the textile industry, is a hazardous and persistent organic pollutant associated with carcinogenic, teratogenic, and genotoxic effects. The present study investigated the bioremediation potential of 15 filamentous fungi isolated from dye containing sediment. Among these fungi, isolate SC6 demonstrated the highest decolorization (30.47%) of RB5. Following molecular sequencing by ITS method, isolate SC6 was identified as *Penicillium citrinum* (GenBank Acc. No: PZ097208). Various physical and nutritional parameters, including pH, temperature, nitrogen source, salt concentration, and inoculum size, were evaluated to determine the optimal conditions for efficient dye degradation. Dye degradation experiments were carried out at initial RB5 concentration of 50 mg/L using starch solution (0.5% w/v) and NH_4Cl (0.25% w/v) as co-substrate and nitrogen source, respectively. The optimized mineral salt media (containing % w/v: K_2HPO_4, 0.025; KH_2PO_4, 0.04; NaCl, 0.1; and $CaCl_2$, 0.005) enhanced fungal dye degradation efficiency. Maximum dye removal (97.54%) was observed at pH 6.0, 30 °C under shaking conditions with an inoculum concentration of 0.025% v/v. Enzymatic analysis indicated that extracellular laccase played a predominant role in the biodegradation process, while peroxidase contributed to a lesser extent. Under these optimized conditions, *P. citrinum* SC6 achieved significant RB5 removal efficiency (3.2-fold increase compared to unoptimized condition). Detoxification of the treated dye solution was evaluated through phytotoxicity assays using *Vigna radiata* L. seeds. The results demonstrated improved seed germination and growth compared to untreated dye solutions, indicating the formation of less toxic metabolites after fungal treatment. These findings highlight the potential of *P. citrinum* SC6 as an effective and eco-friendly biological agent for the remediation of RB5-contaminated industrial wastewater.

Keywords: *P. citrinum* SC6, Reactive Black 5, Dye biodegradation, Laccase, Phytotoxicity, *Vigna radiata*

MESS-OP-19

Waste to wealth: vermibioconversion of *Eichhornia crassipes* into nutrient-rich compost by *Perionyx excavatus*

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Abstract

The rapid proliferation of the invasive aquatic weed, *Eichhornia crassipes* has created serious ecological and environmental challenges in freshwater ecosystems worldwide. Its uncontrolled growth leads to blockage of waterways, depletion of dissolved oxygen, and disruption of aquatic biodiversity. Effective and sustainable management strategies are therefore required to utilize this abundant biomass in an environmentally beneficial manner. Vermibioconversion, an eco-friendly biotechnology that employs earthworms to transform organic wastes into nutrient-rich compost, offers a promising solution. The present study explores the potential of converting *E. crassipes* biomass into valuable organic fertilizer through vermicomposting using the earthworm species *Perionyx excavatus*. Freshly collected water hyacinth biomass was washed, chopped, and subjected to pre-decomposition before being mixed with cow dung as a supplementary substrate. The prepared mixture was then inoculated with *P. excavatus* and maintained under controlled moisture and aeration conditions. Over the course of the vermicomposting process, significant physicochemical changes were observed in the substrate. The resulting vermicompost exhibited improved nutrient composition, including increased levels of nitrogen, phosphorus, and potassium, along with a reduction in the carbon-to-nitrogen ratio. The findings demonstrate that vermibioconversion effectively transforms problematic aquatic weed biomass into a stable and nutrient-enriched organic compost suitable for agricultural applications. This approach not only provides a sustainable strategy for managing invasive aquatic weeds but also contributes to the production of eco-friendly biofertilizers that support soil fertility and sustainable agriculture. Thus, vermicomposting of *E. crassipes* using *P. excavatus* represents a viable waste-to-wealth strategy with significant environmental and economic benefits.

Keywords: Vermicomposting, *Eichhornia crassipes*, *Perionyx excavatus*, Weed management, Biofertilizer

MESS-OP-20

Polyhydroxybutyrate production by *Burkholder aenigmatica* using coconut husk hydrolysate as a low-cost carbon feedstock

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Abstract

The sustainable production of biodegradable plastics from renewable resources is gaining significant attention as an alternative to petroleum-based plastics. In the present study, *Burkholderia aenigmatica* was identified as a novel polyhydroxyalkanoate (PHA)-producing bacterium and evaluated for its ability to produce PHA using both refined sugars and low-cost lignocellulosic substrates. Primarily, six refined sugars were screened for PHA production, among which xylose supported the highest PHA yield of 0.77 ± 0.05 g/L, indicating efficient utilization of pentose sugars. To further enhance the economic feasibility of the process, six lignocellulosic wastes were subjected to physical pre-treatment to produce a sugar-rich hydrolysate, which can be fermented by the bacteria. Among them, coconut husk generated the highest reducing sugar concentration of 7.38 ± 0.04 g/L, significantly higher than the untreated control (5.31 ± 0.04 g/L). Given its superior sugar yield, coconut husk hydrolysate was used as a low-cost carbon feedstock for PHA production. Cultivation of *B. aenigmatica* in coconut husk hydrolysate resulted in a dry cell weight of 1.96 ± 0.01 g/L and a PHA yield of 0.98 ± 0.03 g/L, corresponding to 50% intracellular polymer accumulation. The extracted polymer was characterized using UV-Visible spectroscopy and ^{1}H and ^{13}C nuclear magnetic resonance (NMR), confirming that it is polyhydroxybutyrate (PHB). The process achieved a volumetric PHB productivity of 0.0147 g/L/h. The findings highlight the potential of *B. aenigmatica* for efficient PHB production and demonstrate the feasibility of utilising coconut husk, an abundant lignocellulosic waste, as an economical substrate for sustainable bioplastic production.

Keywords: Polyhydroxybutyrate, Lignocellulosic waste, Sustainable production, Carbon-feedstock.

MESS-OP-21

Fatty acid profiling of indigenous edible mushrooms: an evaluation of their potential nutritional benefits

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Abstract

Edible mushrooms are highly valued as culinary delicacies and nutritionally important foods, recognized for their rich composition of bioactive compounds and essential nutrients. In addition to their proteins, vitamins, and minerals, mushrooms contain lipids that include essential fatty acids beneficial to human health. Although the overall lipid content of mushrooms is relatively low compared with many other food sources, they are considered valuable sources of nutritionally important fatty acids with potential functional and therapeutic properties. The present study aimed to characterize the comprehensive fatty acid composition of various fresh and dried indigenous mushrooms available in the Bengaluru market. Total lipids were extracted using the method of Folch *et al.* (1941) and fatty acid profiles were analyzed using Gas Chromatography–Mass Spectrometry (GC–MS). The total lipid content of the analyzed mushroom samples ranged from 0.14 % to 5.88 %. Fatty acid profiling revealed a diverse composition, with palmitic acid (C16:0, 13.1 – 36.8%), linoleic acid (C18:2 Δ9,12; ω-6, 27.9 – 63.5%), and oleic acid (C18:1 Δ9; ω-9, 1.2 – 22.4%) being the predominant fatty acids detected. Linoleic acid was particularly abundant in *Morchella esculenta* (61.06%), *Cantharellus cibarius* (62.35%), and *Agaricus bisporus* (59.79%), whereas oleic acid dominated in *Tremella fuciformis* (41.39%). The analysis further revealed several bioactive and rarely reported fatty acids, including α-eleostearic acid (C18:3 Δ9c, 11t, 13t), pinolenic acid (C18:3 Δ5c, 9c, 12c), ricinoleic acid (C18:1 Δ9c,12-OH), and 10-ketostearic acid (C18:0, 10-oxo). Notably, gamma-linolenic acid (GLA; C18:3 Δ6,9,12; ω-6) and rumenic conjugated linoleic acid (CLA; C18:2 9c,11t), which are rarely documented in edible mushrooms, were also detected. Furthermore, the presence of the neuroprotective fatty acid nervonic acid (C24:1 Δ15; ω-9) in *Hericium erinaceus* and *Pleurotus eryngii*, along with very-long-chain fatty acids such as behenic acid (C22:0) and lignoceric acid (C24:0), highlights the potential medicinal significance of these species. Overall, the findings demonstrate that edible mushrooms can serve as valuable vegan dietary sources of essential and bioactive fatty acids with potential anti-inflammatory, neuroprotective, and metabolic health benefits. These results further support the growing interest in mushrooms as promising nutraceutical ingredients and functional foods with significant health-promoting potential.

Keywords: Edible mushrooms, Fatty acid profiling, Gamma-Linolenic acid, Nervonic acid, Nutraceuticals

MESS-OP-22

Endophytic fungi of *Santalum album* L. as sustainable sources of bioactive metabolites: isolation, characteristics, and antimicrobial evaluation

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Abstract

Santalum album L. (Indian sandalwood) is a valuable medicinal and economically important plant known for producing bioactive sesquiterpenol compounds. However, traditional extraction methods depend on mature trees, which are under threat due to overexploitation and slow growth. This study focuses on the isolation of endophytic fungi and pathogens from healthy and infected sandalwood samples, followed by extraction and evaluation of their secondary metabolites. The isolates were characterized through morphological and molecular methods, including *Colletotrichum siamense* and *Fusarium solani*. Secondary metabolites were extracted *via* submerged fermentation and analyzed using Thin Layer Chromatography (TLC). The solvent front travelled 6.5 cm, with R_f values of 0.48 (SAC) and 0.95 (SAF), indicating variation in metabolite composition. Antimicrobial activity was evaluated against selected bacterial strains. The test extracts showed zone of inhibition of 15 mm against *Escherichia coli* and 14 mm against *Pseudomonas* species, compared to 35 mm for the control. The percentage inhibition was calculated as 57.14% and 60%, respectively. No activity was observed against *Bacillus* species and *Klebsiella* species. This study demonstrates endophytic fungi as a sustainable alternative source of bioactive metabolites, reducing reliance on mature sandalwood trees.

Keywords: Santalum album, Endophytic fungi, Secondary metabolites, TLC, Antimicrobial activity

MESS-OP-23

Exploring phyllosphere competence traits in plant growth-promoting bacterial strains

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Abstract

The phyllosphere, defined as the above-ground surfaces of plants, hosts diverse microbial communities influenced by environmental and host factors. This study aimed to explore key phyllosphere competence traits of plant growth-promoting bacterial isolates, focusing on biofilm formation, biosurfactant production, siderophore synthesis, motility and volatile production are the critical attributes for successful leaf surface colonization. Biofilm formation assessed *via* Congo Red Agar (CRA), tube, and crystal violet assays revealed that *Bacillus* sp. M9 exhibited the strongest biofilm-forming capacity with an optical density (OD_{570}) of 1.42, while *Bacillus* sp. 36 (OD_{570} = 1.38) also performed strongly. Correspondingly, exopolysaccharide (EPS) production ranged from 10.76 to 21.34 µg/mL, with *Bacillus* sp. M9 yielding the highest value. Biosurfactant activity tested through blue agar and drop collapse assays identified *Bacillus* sp. M9 as positive in both assays, whereas *Bacillus* sp. 27 and *Bacillus* sp. 36 were positive only in the drop collapse test. All isolates produced siderophores, with *Bacillus* sp. 36 showing the largest zone (2.5 cm) and maximum siderophore yield (32.64% units). Motility assays revealed that seven strains were motile, exhibiting optimal swimming at 0.3% agar, with *Bacillus* sp. MM4 and M9 demonstrating maximum swarming motility of 4 cm. *Pseudomonas psychrotolerans* 25 was non-motile. Collectively, these findings highlight *Bacillus* sp. M9 and *Bacillus* sp. 36 as highly competitive phyllosphere colonizers possessing multiple competence traits. Such traits underpin their potential application as plant growth-promoting agents in sustainable agriculture, offering resilience-enhancing benefits under phyllospheric stress conditions.

Keywords: Phyllosphere, Biosurfactant, Siderophore, Exopolysaccharide

MESS-OP-24

Micropropagation potential of Indian sandalwood through axillary bud induction using BAP and coconut water

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Abstract

Indian sandalwood (*Santalum album* L.) saplings are in high demand, particularly to produce disease-free planting material required for sustainable cultivation. Furthermore, elite trees with high oil content can be effectively propagated *via* tissue culture, underscoring the need for reliable *in vitro* regeneration protocols. In this context, the present study was undertaken to evaluate the influence of different plant growth regulators on the *in vitro* response of *S. album*. Leaf and stem nodal explants collected from a mature *S. album* tree were cultured on Murashige and Skoog (MS) medium supplemented with varying concentrations of Thidiazuron (TDZ), 2,4-dichlorophenoxyacetic acid (2,4-D), and 6-benzylaminopurine (BAP). Among the treatments, a positive morphogenic response was observed, with axillary bud induction from stem internodes in MS medium supplemented with BAP (2 mg/L) and 15% coconut water (CW). In contrast, all other treatments, including TDZ alone (0 – 3.3 mg/L) and its combination with 2,4-D and 15% CW, did not exhibit any significant morphogenic response. These results indicate that BAP plays a crucial role in inducing axillary bud formation in *S. album* under the present experimental conditions, suggesting its potential for direct organogenesis. However, further optimization of explant type and hormonal combinations is required to establish an efficient and reproducible micropropagation protocol for large-scale production of elite, disease-free sandalwood plants.

Keywords: *Santalum album*, Micropropagation, Axillary bud, 6-benzylaminopurine, Direct organogenesis

MESS-OP-25

S4 Choco pearls: a novel functional chocolate for cognitive health enriched with Brahmi and postbiotics

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Abstract

In recent years, lifestyle changes, high stress have contributed to declining cognitive functions including memory, learning, and concentration across the world, leading to a greater interest in natural compounds that can support brain health. Traditional medicinal herb, *Bacopa monnieri* (Brahmi), has been widely recognized for its ability to enhance cognitive well-being through its bioactive compounds like bacosides. However, another major challenge affecting the effectiveness of such supplements is reduced nutrient absorption. Modern food habits often lead to inflammation and disruption of epithelial tight junctions, resulting in increased intestinal permeability, commonly referred to as leaky gut. This condition limits the efficient absorption of bioactive compounds, therefore reducing the effectiveness of consumed supplements. This dual challenge highlights the need for innovative functional foods that can support both cognitive function and enhance absorption of the bioactive compound. S4 Choco Pearls is a functional food which addresses this dual challenge. The formulation includes dark chocolate, ragi as a natural source of dietary fiber, and Brahmi, which contains bioactive compounds known as bacosides that are associated with improved cognitive performance. The product also incorporates postbiotics, which are beneficial metabolic by-products of microorganisms that help support intestinal absorption. The objective of this product is to reduce inflammation and enhance functioning of intestinal tight junctions (gut barrier) through postbiotic; improve neurotransmitter activity and promote memory and learning processes through bacosides and utilize nanoparticle which provide increased surface area and smaller particle size, facilitating improved interaction and transport across the intestinal barrier while also adding stability to Bacosides. This concept includes the integration of traditional nutritional ingredients with modern biology. By combining postbiotics, brain supporting bacosides, and nanoparticle - based delivery systems, S4 Choco Pearls represents a novel functional food concept that help address challenges related to nutrient absorption and cognitive health.

Key words: Cognitive, Bacosides, Leaky gut, Postbiotics, Nanoparticles

MESS-OP-26

Screening and detoxification of peroxides and aldehydes in reused cooking oils by microbial biodegradation and biodiesel preparation

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Abstract

The repeated use of cooking oils during deep frying is a widespread practice driven by economic constraints, particularly in small-scale food establishments. However, prolonged, and repeated heating of oils at high temperatures (160 – 190 °C) induces significant physicochemical changes, including oxidation, hydrolysis, and polymerization, leading to the formation of toxic compounds such as free fatty acids, peroxides, aldehydes, and ketones. These degradation products are associated with adverse health effects, including oxidative stress, inflammation, and increased risk of chronic diseases such as diabetes, hypertension, and various cancers. This study aims to evaluate the quality and toxicity of reused cooking oils collected from selected food vendors in Bengaluru and to explore eco-friendly bioremediation strategies. A systematic approach was adopted involving survey-based data collection, physicochemical analysis of oil samples, and screening for key toxic components using standard qualitative and quantitative assays. Lipolytic microorganisms were isolated from environmental samples and assessed for their ability to degrade harmful compounds present in used cooking oils. Overall, this work integrates analytical, microbiological, and applied approaches to address both health and environmental concerns associated with reused cooking oils, promoting sustainable waste management and safer food practices.

Keywords: Cooking oils, Waste management, Toxic peroxides, Lipolytic microbes, Detoxification

MESS-OP-27

Production of vegan leather: extracting leather from Kombucha tea

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Abstract

The fashion industry, on a global scale, is one of the most significant contributors to environmental degradation, primarily due to the trend of fast fashion, which leads to an increase in waste deposits, especially in the case of leather production. The conventional leather produced at present is, at most, an animal-based product. With the booming market of leather and its phenomenal contribution to the economic high, one tends to disregard the fact that the animals pay the ultimate price. This puts the leather industry under constant environmental and ethical scrutiny. The process of tanning used to preserve animal skin involves powerful chemicals that are both toxic to people and the environment. Thereby, encouraging multipurpose living cells to produce biomaterials provides an eco-friendly alternative to the increasing demand for sustainable fashion. The goal of this study is to explore the production of "vegan leather" or "faux leather" without causing any harm to animals and by using symbiotic culture of bacteria and yeast (SCOBY), grown in a probiotic medium, Kombucha tea. The SCOBY is a consortium of microbes that produces the nanofibers of pure cellulose by biochemical processes. The methodology involved is a month-long fermentation of sweetened Kmbucha inoculated with liquid and solid SCOBY culture. The culture is incubated in the dark to promote the synthesis of a dense cellulose layer. The flexibility of the naturally fragile material is improved by using plant-based emollients and vegetable-derived oils, which maintain a cruelty-free status. In addition to the "vegan" factor, anti-microbial capacity is induced by using turmeric, which serves to increase the durability of the leather and acts as a source of dye. Hence, a biomaterial is produced that is biodegradable, does not involve the skinning of animals, and is a safer alternative to the leather used currently.

Keywords: Kombucha, SCOBY, Vegan leather, Cellulose, Antibacterial activity

MESS-OP-28

Optimization and cultivation strategies of *Cordyceps militaris* for enhanced cordycepin production and its quantitative analysis

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Abstract

Cordyceps militaris (*C. militaris*) is a medicinally significant entomopathogenic fungus renowned for producing diverse bioactive compounds, among which cordycepin (3′-deoxyadenosine) is considered one of the most pharmacologically important. With increasing demand for nutraceuticals in current scenario, controlled cultivation and biochemical evaluation of this fungus have become essential. This study was undertaken to optimize physicochemical parameters for precision culture, enhance cordycepin yield, and evaluate associated bioactive properties under laboratory conditions. Pure cultures of *C. militaris* were maintained using standard microbiological techniques. Growth optimization was achieved by varying temperature (22 – 25 °C), pH (6.5 – 7), and nutrient composition. Submerged fermentation at 150 rpm ensured oxygen saturation for mycelial biomass, while fruiting body induction was carried out on brown rice substrates using light intensity of 800 lux with blue LED photo stimulation under 16:8 light/dark cycle. Humidity was maintained at 80 – 90% to prevent desiccation. Biomass was harvested and subjected to extraction and cordycepin was quantified using High Performance Liquid Chromatography (HPLC). Preliminary antioxidant assays were also conducted to assess additional bioactive constituents. Results revealed consistent growth under optimized conditions with nutrient availability influencing biomass yield. Successful detection and quantification of cordycepin from laboratory grown *C. militaris* confirms its nutraceutical potential. This study establishes a reproducible framework for cultivating *C. militaris* under controlled conditions to achieve hyper-production of cordycepin and other secondary metabolites. The preliminary antioxidants study reveals the presence of alkaloids, and phenols in the laboratory grown *C. militaris*. The findings provide a scientific basis for future research aimed at improving yield, molecular characterization, and scaling cultivation strategies for pharmaceutical and nutraceutical applications.

Keywords: *Cordyceps militaris*, Cordycepin, Mycelial biomass, Fermentation, Antioxidant

MESS-PP-01

Enzymatic activities of endophytic fungi and their role in biodegradation and biotechnological applications

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Abstract

Endophytic fungi are microorganisms that inhabit internal tissues of plants without causing visible disease symptoms and play an important role in plant–microbe interactions. These fungi are widely recognized for their ability to produce diverse extracellular enzymes that contribute to the degradation of complex plant biomolecules. Various studies have reported the isolation of endophytic fungi from several medicinal and agricultural plants such as *Santalum album*, *Citrofortunella microcarpa*, *Albizia lebbeck*, *Azadirachta indica*, *Aloe secundiflora*, *Litsea glutinosa*, *Cymbopogon citratus*, *Ziziphus spina*, and *Taxus cuspidata*. These fungal endophytes exhibit significant enzymatic activities and produce enzymes such as cellulase, amylase, protease, lipase, laccase, pectinase, and chitinase, which facilitate the degradation of plant polymers including cellulose, lignin, starch, and other lignocellulosic compounds. Genera such as *Fusarium* sp., *Colletotrichum* sp., *Penicillium* sp., *Aspergillus* sp., and *Trichoderma* sp. have been frequently identified as efficient producers of hydrolytic and lignocellulolytic enzymes. These enzymes play a crucial role in nutrient cycling, plant growth promotion, and ecological balance within plant tissues. Furthermore, the enzymatic potential of endophytic fungi has gained attention for various industrial and environmental applications, including biomass degradation, agricultural waste management, biofuel production, and pharmaceutical processes. This review highlights the diversity of enzyme-producing endophytic fungi and emphasizes their potential as sustainable sources of industrially important enzymes.

Keywords: Endophytic fungi, Extracellular enzyme, Biodegradation, Medicinal plants

MESS-PP-02

Development of a sustainable herbal microbiome-modulating formulation from *Senna alexandrina* for targeted suppression of *Helicobacter pylori*

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Abstract

Gastrointestinal infections caused by *Helicobacter pylori* remain a major global health concern and are commonly treated with broad-spectrum antibiotic regimens. While effective, these treatments can severely disrupt the gut microbiome and contribute to the rising challenge of antimicrobial resistance. Sustainable and microbiome-preserving alternatives are therefore increasingly important. In this study, we explore the therapeutic potential of *Senna alexandrina*, a medicinal plant traditionally recognized for its bioactive phytochemicals, as the basis for a novel herbal microbiome-modulating formulation. The primary objective is the selective suppression of *H. pylori* while preserving the beneficial microbial balance within the gastrointestinal tract. Preliminary investigations focused on evaluating the gene expression and therapeutic potential of *S. alexandrina* extracts against pathogenic *H. pylori* and assessing their potential role in targeted gut microbial modulation. This conceptual framework emphasizes a sustainable and "microbiome-friendly" strategy for managing gastrointestinal infections. This work represents an early stage in the development of a plant derived therapeutic product; further studies are currently ongoing to characterize clinical efficacy, safety profiles, and complex microbiome interactions. The study highlights the potential of herbal bioactives as innovative tools for sustainable microbial control and developing a herbal product that inhibits pathogenic microbial effect in the gut.

Keywords: *Helicobacter pylori,* Microbiome modulation, *Senna alexandrina*

MESS-PP-03

Phosphate-solubilizing actinomycetes: molecular mechanisms and translational potential for sustainable biofertilizer development

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Abstract

Although a significant amount of soil phosphorus is found in insoluble forms that are not easily accessible to plants, phosphorus is a crucial macronutrient for plant growth. Soil degradation, ineffective nutrient use, and environmental issues have resulted from an over-reliance on artificial phosphate fertilizers. Microbial biofertilizers have become a viable substitute for increasing the availability of phosphorus in agricultural systems. Actinomycetes are becoming increasingly well-known among these because of their diverse metabolism and capacity to generate a variety of bioactive substances that aid in the mobilization of nutrients. This paper examines the molecular processes that actinomycetes use to solubilize phosphate and assesses how these processes might be applied to the creation of sustainable biofertilizer technologies. By secreting organic acids including gluconic, citric, and oxalic acids, which reduce soil pH and chelate mineral-bound phosphate, actinomycetes solubilize insoluble phosphate. Additionally, the mineralization and mobilization of phosphorus in soil ecosystems are facilitated by the synthesis of siderophores and phosphatase enzymes. These processes promote soil health and plant growth in addition to increasing phosphorus bioavailability. Beyond their biological function, phosphate-solubilizing actinomycetes provide intriguing prospects for the microbial-based biofertilizer and agricultural biotechnology sectors. The poster outlines the main obstacles to scaling microbial biofertilizers for field applications as well as current research trends and commercialization paths. Comprehending the functional potential of these microorganisms can aid in the creation of economically feasible and ecologically sustainable solutions for contemporary agriculture.

Keywords: Phosphate-solubilizing actinomycete, Biofertilizers, Sustainable agriculture, Microbial biotechnology

MESS-PP-04

Development and evaluation of a cosmeceutical product from agricultural waste

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Abstract

The global shift toward sustainable and environmentally responsible products has created new opportunities for innovation and entrepreneurship in the cosmeceutical industry. Agricultural residues often considered low-value byproducts are increasingly recognized as valuable sources of bioactive compounds with significant potential in skincare and cosmetic formulations. The utilization of these natural resources not only contributes to the development of sustainable cosmeceutical products but also promotes the sustainable use of agricultural byproducts, fostering innovation and entrepreneurial opportunities. This study focuses on the development of a cosmeceutical product derived from agricultural waste highlighting its relevance to sustainability and entrepreneurial innovation. The present study investigates the utilization of rice bran and rice husk (*Oryza sativa. L*) obtained from local agricultural sources as low-cost substrates to produce bioactive compounds. Microorganisms are isolated from natural sources using standard microbiological techniques and identified based on their morphological and biochemical characteristics. Microbial strains demonstrating potential for metabolite production are selected and further employed in solid-state fermentation using rice bran and rice husk as substrates. This fermentation process enhances the production and release of valuable bioactive metabolites such as antioxidants, enzymes, and other compounds beneficial for skin health. Following fermentation, the bioactive components mainly γ-oryzanol, squalene, silica, flavonoids and phenolics extracted from fermented and non-fermented raw materials are analyzed and compared to determine their functional potential for cosmeceutical applications. These extracts are subsequently incorporated with suitable cosmetic base ingredients to formulate a natural cosmeceutical product. The prepared formulation is evaluated using basic physicochemical and stability parameters to ensure its quality, safety, and effectiveness. Overall, this study demonstrates a sustainable approach for transforming agricultural waste into value-added cosmeceutical products through microbial biotechnology, thereby promoting sustainable product development, and creating opportunities for innovation and entrepreneurship in green and translational microbiology.

Keywords: Cosmeceutical formulation, Agricultural waste, Bioactive metabolites

MESS-PP-05

Isolation, identification, and characterization of enzyme producing endophytic fungi for sustainable biotechnological applications

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Abstract

Endophytic fungi are microorganisms that inhabit internal plant tissues without causing visible disease symptoms and play an important role in plant–microbe interactions. These fungi are widely recognized as potential sources of industrially important enzymes with significant applications in biotechnology and sustainable microbial processes. The study of endophytic fungi involves several methodological approaches for their isolation, identification, and characterization. Isolation is commonly performed by collecting healthy plant tissues followed by surface sterilization to remove epiphytic microorganisms. Sterilized tissue segments are cultured on suitable media such as potato dextrose agar to promote fungal growth. Identification of fungal isolates can be achieved through morphological and molecular approaches. Morphological identification includes examination of colony characteristics, hyphal structures, and spore morphology under microscopic observation, while molecular identification commonly involves amplification and sequencing of the internal transcribed spacer (ITS) region of fungal DNA. Several endophytic genera, including *Colletotrichum* spp. and *Fusarium* spp., are known to produce extracellular enzymes such as cellulase, amylase, protease, and lipase. This review highlights that, these enzymes play a crucial role in biodegradation, biomass conversion, and other sustainable biotechnological applications.

Keywords: Endophytic fungi, ITS sequencing, *Colletotrichum* spp., *Fusarium* spp., Enzymes

MESS-PP-06

Comparative evaluation of conventional and *Bacillus*-seeded bio-sand filters for rapid water purification

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Abstract

Access to safe drinking water remains a major public health challenge, especially in rural and low-resource settings where affordable household water treatment methods are needed. Bio-sand filters (BSF) are widely used due to their low cost, simple design, and ability to remove suspended particles and microorganisms. However, conventional bio-sand filters require a ripening period for the formation of a biologically active layer. The present study aims to improve early-stage purification by seeding the filter with spores of non-pathogenic *Bacillus* species to accelerate biofilm formation and enhance filtration efficiency. The study was designed as an experimental, comparative laboratory investigation using two identical bio-sand filter units constructed with PVC columns containing layers of drainage gravel, support gravel, and fine sand. One filter served as the conventional bio-sand filter (C-BSF), while the second filter was inoculated with NCIM-certified *Bacillus* spores in the top sand layer to form a *Bacillus*-enhanced bio-sand filter (BESF). Both filters were operated under identical gravity-driven conditions using contaminated rural surface water as an influent to simulate household filtration. Performance was evaluated by analyzing influent and effluent samples for total coliforms, *Escherichia coli,* and turbidity at regular intervals. The main parameter assessed was time-to-efficacy, defined as the number of days required for the filter to achieve consistent microbial reduction during the ripening phase. The *Bacillus* spore-seeded filter is expected to show faster biofilm development, improved microbial removal, and reduced turbidity compared to the conventional filter, providing a simple and cost-effective method to improve drinking water safety in rural communities.

Keywords: Bio-sand filter, *Bacillus* spore, Drinking water purification, Microbial removal

MESS-PP-07

Characterization and selection of probiotic lactic acid bacteria from different dietary sources for development of functional foods

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Abstract

Probiotic microorganisms play an important role in improving gut health and in the development of functional foods. However, some individuals exhibit dairy intolerance, which limits their ability to consume milk and milk products such as curd and yogurt. Therefore, the present study aimed to isolate and characterize potential probiotic bacteria and evaluate their tolerance to conditions like the human gastrointestinal environment. The isolates were identified as Gram-positive rods through morphological and biochemical characterization and showed non-pathogenic behaviour, with some strains exhibiting proteolytic activity. The isolates demonstrated good tolerance to acidic pH, salt, and bile salts, indicating their ability to survive under simulated gastrointestinal conditions. These findings suggest that the strains possess promising probiotic potential for use in functional foods that can be consumed even by individuals with dairy intolerance.

Keywords: Probiotic, Gut health, Milk products, Functional foods

MESS-PP-08

Exploring plant growth promoting traits of earthworm gut microbiota in natural farming ecosystems

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Abstract

The gut of earthworms provides a favorable niche for diverse microorganisms, enhancing microbial activity through the secretion of gut mucus and maintaining suitable physico-chemical conditions. Although earthworm-associated microorganisms play a significant role in soil fertility, nutrient cycling and organic matter decomposition, the diversity and functional potential of these microbial communities require further investigation. In the present study, the composition and diversity of gut-associated bacteria in earthworms inhabiting a natural farming system were examined. Earthworm samples were collected from natural farming fields at different depths of the soil profile (up to 1 m) and transported to the laboratory for further analysis. Based on morphological characteristics, the earthworms were identified as *Eudrilus eugeniae*. Gut contents were aseptically extracted through dissection and subjected to bacterial isolation using standard plating techniques. A total of forty-four bacterial isolates were obtained from the earthworm gut and characterized based on morphological features. Qualitative screening for plant growth–promoting traits, including siderophore production, phosphate and potassium solubilization, resulted in the selection of nine superior isolates for further evaluation. These isolates were assessed for their ability to produce ammonia, fix atmospheric nitrogen, and synthesize phytohormones such as indole-3-acetic acid (IAA) and gibberellic acid (GA). All selected isolates exhibited nitrogen-fixing ability and phytohormone production. The nitrogen fixation potential ranged from 1.42 to 4.13 mg L^{-1} among the isolates. Maximum IAA production was recorded in isolates EGNF-12 (35.23 µg ml^{-1}) and EGNF-8 (32.14 µg ml^{-1}), while the highest GA production was observed in EGNF-12 (6.14 µg ml^{-1}) and EGNF-20 (6.16 µg ml^{-1}). These results indicate that earthworm gut-associated bacteria possess significant plant growth–promoting attributes and may serve as potential microbial resources for enhancing soil fertility and supporting sustainable agriculture in natural farming systems.

Keywords: Earthworm, Gut bacteria, Natural farming, Phytohormone

MESS-PP-09

L-Glutaminase from *Irpex alboflavescens* TRE3: Submerged fermentation, characterization, and application in deamidation of soy protein extract

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Abstract

L-glutaminase converts L-glutamine into glutamic acid releasing of ammonia and holds significant potential across food, pharmaceutical, and industrial sectors. This study presents the isolation, optimization, purification, characterization, and application of L-glutaminase produced by Basidiomycetes. Primary screening of 13 Basidiomycetes isolates (from wood) on modified Czapek Dox Agar supplemented with L-glutamine (1% w/v) and phenol red (0.009% w/v) demonstrated the highest zone index value (5.581 ± 0.045) for isolate TRE3. TRE3 was identified as *Irpex alboflavescens* (GenBank Acc. No: PZ093008) using ITS method of gene sequencing. Physical optimization under submerged fermentation (SmF) established pH 7, 25 ± 2 °C, 120 h at 100 rpm using 2 agar plugs per 50 mL broth for highest L-glutaminase production. Nutritional optimization *via* one-factor-at-a-time (OFAT) approach identified starch (0.5% w/v) and ammonium chloride (0.5% w/v) as the best carbon and nitrogen source, respectively. The optimized mineral salt composition (% w/v) was as follows – KH_2PO_4, 0.2; KCl, 0.1; $MgSO_4$, 0.02; $FeSO_4$, 0.005; $CuSO_4$, 0.005; and $ZnSO_4$, 0.002. OFAT media optimization yielded a 4.87-fold increase in enzyme synthesis. The enzyme activity reached 1269 U/mL under SmF. A three-step purification process—comprising ammonium sulfate precipitation, dialysis, and ion-exchange chromatography—yielded a 20.37-fold purified enzyme. The enzyme exhibited an apparent molecular mass of 65 kDa as determined by SDS-PAGE. The enzyme showed optimal activity at pH 7 and 40 °C, retaining 82.8% residual activity after 1 h. Cu^{2+} enhanced activity, while sodium azide, SDS, and 2-mercaptoethanol acted as inhibitors. Kinetic analysis revealed a K_m of 0.002 mM and V_{max} of 27.39 U/mL, indicating high substrate affinity. Application of TRE3-derived glutaminase to soy protein extract significantly enhanced its solubility, foaming, emulsion activity, and stability. The use of valorized agro-waste residues in OFAT mediated fermentation condition optimization coupled with appreciable protein solubilizing characteristics underscores the strong potential of *I. alboflavescens* TRE3 L-glutaminase for food industry applications.

Keywords: *Irpex alboflavescens* TRE3, L-Glutaminase, Submerged fermentation, OFAT

MESS-PP-10

Sustainable bio-detergent production using saponins and immobilized enzyme technology

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Abstract

Synthetic detergents are effective cleaning agents but can cause environmental pollution and potential toxicity. This study focuses on developing a sustainable bio detergent using saponins extracted from licorice as a natural biosurfactant, combined with immobilized enzymes to enhance cleaning efficiency. Saponins were extracted using Soxhlet extraction with methanol. Lipase, protease, and amylase were produced from bacterial sources, purified, and immobilized using sodium alginate. Optimal pH and temperature conditions for enzyme activity were determined. The bio detergent was evaluated for its organoleptic and qualitative properties. Cleaning efficiency was tested through fabric washing and heavy oil removal, and results were compared with conventional detergents. The reusability of immobilized enzymes and potential toxicity were also assessed. The study demonstrates that the formulated bio detergent is an effective and environmentally friendly alternative to synthetic detergents.

Keywords: Bio-detergent, Saponins, Immobilization, Eco-friendly, Biosurfactants

MESS-PP-11

Evaluation of xylanase production potential in *Trichoderma* species using agro-residues as raw material

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Abstract

Microbial enzymes are emerging as eco-friendly alternatives to chemical processes in industry. Xylanase, produced by *Trichoderma* species, breaks down hemicellulose, a major component of plant biomass, making it valuable for applications such as biofuel production, paper processing, and agricultural waste management. In this study, we developed a sustainable submerged fermentation process using *Trichoderma* spp. with beechwood xylan as the substrate. Key conditions like pH, temperature, and substrate concentration were optimized to enhance enzyme yield. Qualitative assays confirmed the enzyme's effectiveness in hemicellulose degradation. Our findings highlight the potential for scaling this process as a cost-effective and environmentally sustainable solution for industrial enzyme production. This work demonstrates how microbial biotechnology can contribute to sustainable industry practices and commercial applications.

Keywords: *Trichoderma*, Xylanase, Sustainable bioprocess, Enzyme production

MESS-PP-12

Isolation, characterization, and molecular identification of soil bacteria showing antibacterial activity against human pathogenic bacteria

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Abstract

The present study focused on screening soil bacteria with antibacterial activity from diverse locations in Bengaluru, India. Antibiotics, produced as secondary metabolites, serve as self-defense mechanisms for bacteria against competing microorganisms. With the rise of antibiotic resistance among pathogenic bacteria, the search for novel antibacterial agents has become critical. Standard isolation and characterization techniques were employed to identify soil bacteria exhibiting antibacterial activity. The isolates were tested against human pathogens including *Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas aeruginosa*, and *Klebsiella pneumoniae* through primary and secondary screening. Among 263 isolates, only three—PR1, PR2, and PR3—demonstrated consistent antibacterial activity against all four pathogens. Further evaluation of culture filtrates under different treatments revealed that filter sterilization preserved antibacterial activity most effectively, compared to autoclaving or proteinase K treatment. The reduction in activity following proteinase K treatment indicated that the active antibacterial factor was proteinaceous in nature. Nutritional studies showed that each isolate had distinct preferences for carbon and nitrogen sources to enhance antibacterial activity. Comparative assays revealed that filter-sterilized culture filtrates produced inhibition zones of 18.5 mm, surpassing the 15.5 mm zone produced by streptomycin, a standard antibiotic. Molecular identification through 16S rRNA sequencing classified the isolates as *Bacillus aryabhattai* strain PR-D07, *Arthrobacter humicola* strain PR-F07, and *Neomicrococcus lactis* strain PR-F11, all Gram-positive bacteria. This is the first report of antibacterial activity from these three strains against the tested pathogens. The findings highlight their potential as promising candidates for the development of new antibacterial agents, offering encouraging prospects for applied research in combating antibiotic resistance.

Keywords: Soil bacterial communities, 16S rRNA sequencing, Antagonistic activity

MESS-PP-13

Exploring the antimicrobial properties of wood apple (*Limonia acidissima*) shell for sustainable applications

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Abstract

The increasing prevalence of antibiotic-resistant bacteria has prompted the search for sustainable and natural antimicrobial agents. This study evaluates the antibacterial potential of shell powder derived from Wood apple (*Limonia acidissima*), an underutilized native Indian fruit, transforming agricultural biowaste into valuable bioresource. Traditionally valued for its pulp, leaves, seeds, bark, and roots have been used in Ayurvedic medicine. They are rich in bioactive phytochemicals with significant biochemical potential, which have been evaluated against selected bacterial strains. The dried shells were powdered and extracted using aqueous, dimethyl sulfoxide (DMSO), ethanol, and methanol, to obtain wide range of bioactive compounds into the solvent. The antibacterial activity was assessed using the well diffusion method at varying concentrations of solvent extracts, and efficacy was evaluated by measuring the zones of inhibition. Among the tested extracts, ethanol and DMSO exhibited pronounced antibacterial activity, while methanol showed moderate effects and aqueous extracts demonstrated comparatively lower inhibition. This enhanced activity of organic extracts highlights the role of solvent polarity in extracting potent bioactive constituents such as phenolics, coumarins, and quinones. These findings position wood apple shell powder as a promising, cost-effective, eco-friendly, and sustainable alternative to conventional antibiotics, with its potential applications in future pharmaceutical, healthcare, food preservation, and biopolymer innovations.

Keywords: *Limonia acidissima,* Wood apple, Antibacterial activity, Sustainable alternatives, Phytochemicals

MESS-PP-14

Isolation and evaluation of antagonistic endophytic fungi from *Leucas aspera* against its pathogen *Colletotrichum* species

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Abstract

Medicinal plants are known to harbor diverse endophytic microorganisms that contribute to their biological and therapeutic properties. *Leucas aspera*, a widely used medicinal plant in traditional systems, was selected for the isolation and evaluation of endophytic fungi from its leaves. Both healthy and infected leaf samples were collected and subjected to surface sterilization using ethanol, sodium hypochlorite, and sterile distilled water to eliminate epiphytic contaminants. The sterilized leaf segments were inoculated onto Potato Dextrose Agar (PDA) plates and incubated for fungal growth. Distinct fungal colonies obtained were sub cultured, and their morphological characteristics were studied using lactophenol cotton blue staining. The antifungal potential of the isolates was evaluated using the dual culture method. Initial assays between endophytes and the pathogen did not show significant inhibition. However, a *Penicillium* species isolated during the study exhibited strong antagonistic activity against *Colletotrichum* species producing a clear zone of inhibition. The percentage inhibition of pathogen growth was calculated, with isolate *Penicillium* sp. L1 showing the highest inhibition of 88.88%. The presence of such antagonistic endophytic fungi highlights their potential role in suppressing pathogenic fungi and underscores the significance of *L. aspera* as a source of bioactive endophytes for applications in biological control and development of natural antifungal agents.

Keywords: *Leucas aspera*, Endophytic fungi, *Penicillium* sp., *Colletotrichum* sp., Antifungal activity, Biocontrol

MESS-PP-15

Exploring the antimicrobial potential of endophytic bacteria from *Aegle marmelos* and *Cynodon dactylon*

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Abstract

In the current study, leaves of sacred plants commonly used in Hindu rituals, *Aegle marmelos* and *Cynodon dactylon* commonly called as Bilva and Durva grass respectively, were selected for the isolation of bacterial endophytes. The leaves were surface sterilized to eliminate epiphytic microorganisms, followed by inoculation on sterile nutrient agar plates. After incubation, bacterial growth was observed and isolated. A total of nine endophytes were isolated from Bilva leaves and six from Durva grass. These isolates were characterized using Gram staining. Among the Bilva endophytes, 66.66% were Gram-positive rods, 22.22% were Gram-positive cocci, and 11.11% were Gram-negative rods. In contrast, the Durva grass endophytes comprised 50% Gram-positive rods, 33% Gram-positive cocci, and 16% Gram-negative rods. The antibacterial activity of the isolated endophytes was evaluated using a dual culture assay against common human pathogens, including *Escherichia coli*, *Bacillus* sp., and *Klebsiella* sp. The results revealed that Bilva endophytes BC1 and BC2 from dilutions 10^{-1} and 10^{-2} respectively exhibited significant inhibition against *Bacillus* sp. with a maximum inhibition of 92.22%. Similarly, Durva endophytes GC1 and GC2 from the dilutions 10^{-5} and 10^{-4} showed strong inhibitory activity against *Klebsiella* sp. (93.33%), while GC3 from dilution 10^{-2} demonstrated 92.22% inhibition against *E. coli*. These findings suggest that Bilva endophytes are highly effective against *Bacillus* sp., whereas Durva grass endophytes exhibit strong antibacterial activity against *Klebsiella* sp. and *E. coli*. The study highlights the potential of endophytes from sacred medicinal plants as promising sources of antibacterial agents, supporting their traditional ayurvedic use and offering scope for the development of novel biocontrol agents and therapeutic compounds.

Keywords: Bacterial endophytes, Medicinal plants, Pathogenic bacteria, Antimicrobial property

MESS-PP-16

LPS-TNF-α axis in chronic otitis media: translating inflammation into therapeutic strategy

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Abstract

Chronic otitis media (COM) is a persistent infection of the middle ear associated with prolonged inflammation and fluid accumulation behind the eardrum. It can result in complications such as hearing loss, facial nerve paralysis, and intracranial infections. In children, hearing impairment may also affect speech development and learning, emphasizing the importance of understanding its underlying biology to improve treatment strategies. Toll-like receptor 4 (TLR4) is a key mediator of innate immune responses, recognizing lipopolysaccharide (LPS) from gram-negative bacteria and initiating inflammatory signaling. Although TLR4 has been linked to COM, its precise role in disease progression is not fully understood. We hypothesized that the TLR4 pathway is overactive in CSOM patients, leading to an exaggerated inflammatory response. To investigate this, 63 blood samples from CSOM patients were collected and matched. Healthy controls were stimulated with LPS. The levels of TNF-α and IL-10 were measured as indicators of pro- and anti-inflammatory responses. TNF-α levels were significantly increased in COM patients (~4-fold; $p = 0.002$), while IL-10 levels showed no significant difference ($p = 0.06$). Additionally, the TNF-α/IL-10 ratio was significantly higher (2.5-fold; $p= 0.006$), suggesting a shift toward a pro-inflammatory state. Overall, these results indicate that the TLR4 pathway is dysregulated in CSOM, contributing to heightened inflammation. This pathway may serve as a might be potential target for microbial-based therapies and as a biomarker for disease monitoring by controlling or Inhibiting pathway.

Keywords: CSOM, TLR4, LPS, TNF-α, Cytokine imbalance

MESS-PP-17

Expression profiling of miRNA-21 in chronic otitis media and its role in inflammatory pathways

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Abstract

Chronic Otitis Media (COM) is a long-standing inflammatory disorder of the middle ear associated with recurrent infections, tympanic membrane perforation, and progressive hearing loss. Despite its clinical importance, the molecular mechanisms driving its persistence are not fully understood. Emerging evidence suggests that microRNAs (miRNAs), particularly miRNA-21, play a critical role in regulating inflammation and tissue remodeling. This study aims to evaluate the expression of miRNA-21 in COM patients and explore its potential as a biomarker and therapeutic target. A case–control study will be conducted involving 63 COM patients and 63 age and gender matched healthy controls. Peripheral blood mononuclear cells (PBMCs) will be isolated and cultured under lipopolysaccharide (LPS)-stimulated conditions, with and without curcumin treatment. Total RNA will be extracted, and miRNA will be converted to complementary DNA (cDNA). Quantitative real-time PCR (qRT-PCR) will be performed to assess miRNA-21 expression, using U6 RNA as an internal control. Relative expression levels will be calculated using the $2^{-}\Delta\Delta Ct$ method. It is hypothesized that miRNA-21 expression will be significantly upregulated in COM patients. Increased levels are expected to correlate with elevated pro-inflammatory cytokines such as IL-6 and TNF-α *via* activation of NF-κB signaling pathways. Furthermore, miRNA-21 may contribute to epithelial remodeling and chronic inflammation by targeting regulatory genes such as PTEN and PDCD4. This study aims to provide insights into the molecular mechanisms of COM and highlights miRNA-21 as a promising biomarker and potential therapeutic target.

Keywords: miRNA-21, Chronic otitis media (COM), Peripheral blood mononuclear cells (PBMCs)

MESS-PP-18

Impact of ozone treatment on seed germination, plant growth, pesticide degradation, and postharvest quality of tomato, *Lycopersicon esculentum* L.

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Abstract

Ozone treatment emerges as a versatile, eco-friendly technology for enhancing tomato safety, quality, and productivity across production stages, from seeds to post-harvest fruits. In seed applications, gaseous ozone at low concentration effectively breaks dormancy in tomato seeds, accelerating germination with benefits sustained during early storage; however, prolonged, or high doses induce oxidative damage, reduce membrane integrity and viability, and effects decline over extended storage. At the same time, elevated atmospheric ozone acts as an abiotic stressor, triggering reactive oxygen species (ROS) production-including oxygen radicals, superoxide, H_2O_2 and hydroxyl radicals-that disrupts plant redox homeostasis, induces oxidative stress and influences growth, yield, and agricultural sustainability. Plants counter this *via* enzymatic (e.g., superoxide dismutase, peroxidases) and non-enzymatic antioxidant defences, with ROS serving as dual signalling molecules in programmed cell death, pathogen defence, abiotic stress responses, and systematic signalling. In seedlings, ozone water irrigation or spraying enhances antioxidant enzyme activity (SOD, POD, CAT), reduces harmful ROS levels, increases chlorophyll content, and promotes nutrient uptake, thereby improving stress tolerance and photosynthetic efficiency. Post-harvest, optimized gaseous ozone reduces surface microbes significantly without comprising physiochemical properties such as firmness, colour and texture, thereby extending shelf life and maintaining market quality. Ozonated water remove a substantial proportion of pesticides like Malathion and DDT through oxidative degradation, making it more effective than conventional washing methods. Bubbling ozone achieves effective fungicide reduction in tomatoes while maintaining fruit integrity and minimizing residue levels. Overall ozone balances decontamination and nutrient preservation at optimized parameters, but its application requires careful regulation of dosage and exposure time to maximize benefits while minimizing adverse.

Keywords: *Lycopersicon esculentum*, Ozone treatment, Malathion, ROS, Post harvest quality

MESS-PP-19

Isolation and characterization of biofilm forming soil microbiota in the rhizosphere of agricultural important crops

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Abstract

The rhizosphere is a soil zone rich in nutrients that directly affected by plant root secretions. This area plays a key role in microbial activity and is crucial for plant health and agricultural productivity. Among the various microbial communities in this zone, biofilm-forming bacteria are especially important because they help with nutrient exchange, support microbial survival, and boost plant resilience to environmental stresses. This study aims to isolate and understand biofilm-forming soil microbes from the rhizosphere of five economically significant crops, including cereals (Sorghum, Corn), oilseeds (Groundnut), and vegetables (Tomato, Dolichos). Soil samples from rhizosphere soil of healthy and disease-free plants were collected after obtaining necessary permissions from agronomists in the GKVK research field. Standardized methods for soil sample collection and invitro cultivation of microbes using R2A culture media in 24 wells of a microplate will be used for this purpose. Cytological characterization of microbes will be done by dual staining and digital microscopic observation of colonies formed on cover glasses for the identification of biofilm-forming strains. Statistical analysis will be done using IBM-SPSS and MATLAB for data interpretation of microbial diversity and distribution. The outcomes of this research will be the identification of microbial diversity in various crop genotypes and beneficial biofilm-forming microbes, and standardized *in vitro* growth of microbes. Ultimately, this research will help in the identification of biofilm-forming microbes of agricultural importance and lay a foundation for future microbiome engineering for promoting sustainable crop growth and development.

Keywords: Rhizosphere, Microbial diversity, Plant-microbe interactions, Sustainable agriculture

MESS-PP-20

Harnessing indigenous *Lysinibacillus sphaericus* for soil health improvement and sustainable crop protection

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Abstract

Lysinibacillus sphaericus has emerged as a multifunctional soil bacterium with significant contributions to soil health, microbiome stability, and agroecological sustainability. Although classically known for its insecticidal action against dipteran larvae, the present study highlights its broader ecological roles in plant growth promotion and pathogen suppression. Here, five indigenous *L. sphaericus* strains were isolated from diverse agricultural soils and insect cadavers across India and characterized through morphology, microscopy, and 16S rRNA sequencing, confirming strong similarity to reference strains. Comprehensive biochemical assays revealed substantial hydrolytic enzyme activity across the collection: 4 strains produced protease (1.06 – 1.53) and lipase (1.09 – 1.65), 3 exhibited lecithinase (1.13 – 1.49), and 2 produced chitinase (0.44 – 1.55), indicating strong mycolytic potential. These enzymatic activities, along with catalase and oxidase production, support soil nutrient turnover, and microbe–microbe interactions. Plant growth promoting (PGP) screening further demonstrated that all strains synthesized indole-3-acetic acid and ammonia (10 – 100 µg/mL), while 4 produced siderophores, reflecting their capacity to enhance plant nutrient acquisition and resilience. Antagonistic assay identified strain NBAIR LS52 as particularly potent, inhibiting *Alternaria sp.* by 67% in dual culture. Overall, the study underscores the agroecological importance of *L. sphaericus*, identified as a promising dual-function bacterium combining strong PGP capabilities with robust antifungal activity in soil microbiome and biocontrol applications.

Keywords: *Lysinibacillus sphaericus*, 16S rRNA sequencing, Plant growth promoting, Crop protection

MESS-PP-21

Bioprospecting *Terminalia chebula*-derived cyclopentane compounds as DNA gyrase inhibitors against MRSA in diabetic foot ulcers

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Abstract

The global escalation of multidrug-resistant pathogens, particularly Methicillin-resistant *Staphylococcus aureus* (MRSA) in diabetic foot ulcers, necessitates the development of innovative and sustainable therapeutic strategies. This study explores the bioprospecting potential of *Terminalia chebula* (Haritaki), a deciduous tree species rich in bioactive secondary metabolites, to identify novel antimicrobial candidates. Preliminary antibacterial screening demonstrated significant inhibitory activity of the plant extract against MRSA isolates, indicating the presence of potent bioactive compounds. Integrating computational and experimental approaches, this study investigated the mechanism of action of a cyclopentane-based compound through *in silico* molecular docking targeting bacterial DNA gyrase, a key enzyme in DNA replication. The compound exhibited a favourable binding affinity with a docking score of -5.3 kcal/mol. This was further supported by DNA gyrase functionality assays and gel electrophoresis, which revealed DNA fragmentation in treated MRSA samples. The findings suggest that the *T. chebula*-derived compound possesses promising anti-MRSA activity, potentially through DNA gyrase inhibition, and highlights its potential as a sustainable therapeutic candidate for diabetic foot ulcer-associated infections.

Keywords: Bioprospecting, Methicillin resistant *Staphylococcus aureus* (MRSA), *Terminalia chebula,*

MESS-PP-22

Metabolic repurposing of Sodium Dichloroacetate (Na-DCA) as a broad-spectrum anti-carcinogenic linker against *Aspergillus flavus* and *Fusarium* spp. secondary metabolites

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Abstract

The prevalence of drug-resistant fungal pathogens and carcinogenic mycotoxins necessitates novel therapeutic strategies. Sodium Dichloroacetate (Na-DCA), a metabolic modulator inhibiting Pyruvate Dehydrogenase Kinase (PDK), offers a unique opportunity to disrupt the Acetyl-CoA pool essential for fungal survival and toxin production. This study proposes a sustainable and green circular economy workflow by valorizing DCA from industrial Monochloroacetic Acid (MCA) mother liquor to create high-value pharmaceutical scaffolds. Na-DCA was synthesized *via* a simulated recovery and neutralization protocol, then characterized using melting point, flame photometry, and colorimetric assays. Antifungal efficacy was assessed using agar well diffusion against *Aspergillus flavus* and *Fusarium* spp., revealing zones of inhibition at 1000 µg/mL and suppression of secondary metabolite pigmentation, indicative of toxin downregulation. To explore its viability as a semi-synthetic bioactive linker, an *in silico* study was performed. Hybrid analogs of Fluconazole-DCA and Ciprofloxacin-DCA were modeled and subjected to ADMET profiling (SwissADME) and molecular docking (AutoDock Vina) against fungal CYP51 and bacterial DNA Gyrase targets. Bioinformatics analysis revealed that DCA-hybridized drugs adhered to Lipinski's Rule of 5 and exhibited enhanced lipophilicity (LogP), suggesting improved membrane permeability. This study establishes Na-DCA as a broad-spectrum antifungal agent that limits growth and carcinogenic mycotoxin biosynthesis. Furthermore, *in silico* validation supports the repurposing of industrial waste-derived DCA as a synergistic linker in hybrid drug design. These findings highlight metabolic interference and green chemistry as promising, underexplored avenues for developing next-generation antimicrobial therapies.

Keywords: Anti-carcinogenic, Pyruvate dehydrogenase kinase, Bioactive linker, Antifungal agent

MESS-PP-23

Cordycepin (3′-deoxyadenosine): sources, synthetic strategies, and translational pharmacological relevance

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Abstract

Cordycepin (3'-deoxyadenosine) is a naturally occurring nucleoside analogue that is mainly derived after *Cordyceps* species, and is known to exhibit various pharmacological activities. This is because the ribose moiety of this molecule lacks a 3'-hydroxyl group, which contributes to its distinct biological functionality, specifically, its regulation of the RNA synthesis process and the intracellular signaling cascade. Cordycepin is a promising therapeutic agent despite recent promising preclinical evidence due to low natural abundance and rapid metabolic degradation. This has led to the massive investment in chemical, semi-synthetic and biotechnological production strategies. This review analyses critically natural biosynthesis, well-known and developing synthetic pathways and advances in microbial production of cordycepin. In addition, pharmacological activity, and translational restrictions of cordycepin are also addressed, and the comparison of naturally produced and synthetic substance is presented. The review points out that variations in biological performance should mostly be attributed to differences in purity, stability, and pharmacokinetics and not molecular origin.

Keywords: Cordycepin, 3′-Deoxyadenosine, Nucleoside analogue, Biosynthesis, Microbial production

MESS-PP-24

Biotechnological applications of endophytic fungi from medicinal trees

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Abstract

Endophytic fungi, ubiquitous symbionts residing asymptomatically within plant tissues, represent a vast reservoir of bioactive compounds and enzymes with profound biotechnological significance. These fungi inhabit the internal tissues of medicinal trees such as *Terminalia chebula*, *Emblica officinalis*, *Aegle marmelos*, *Tinospora cordifolia*, *Andrographis paniculata*, and *Ocimum sanctum* without causing apparent disease, fostering symbiotic relationships that generate valuable biotechnological resources. They produce diverse extracellular enzymes like amylase, cellulase, protease, lipase, laccase, pectinase, and xylanase, primarily from genera *Aspergillus* sp., *Cladosporium* sp., *Fusarium* sp., *Penicillium* sp., and *Trichoderma* sp., facilitating lignocellulosic breakdown for biofuel generation, agricultural waste valorization, and nutrient recycling. Concurrently, they synthesize secondary metabolites including alkaloids, terpenoids, flavonoids, and quinones *via* activated biosynthetic pathways, yielding potent antimicrobial and anticancer compounds effective against bacterial pathogens and tumor cell lines like HepG2. As industrial enzyme sources, endophytes from these trees provide thermostable biocatalysts for pharmaceutical synthesis, food processing, and biorefineries, with genetic and cultivation optimizations boosting commercial viability. This review consolidates their enzyme profiles, metabolite repertoires, bioactivity spectra, and scalable applications, highlighting sustainable biotechnological prospects from medicinal tree endophytes.

Keywords: Endophytic fungi, Medicinal trees, Enzyme production, Secondary metabolites, Anticancer agents

MESS-PP-25

Optimization of Spirulina (*Arthrospira platensis*) growth in modified culture media under controlled artificial illumination

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Abstract

Spirulina (*Arthrospira platensis*) is a high-value microalga widely used as a nutritional supplement due to its rich protein, vitamin, and mineral content. However, large-scale cultivation is often limited by the cost of synthetic media. This study focuses on optimizing Spirulina growth using low-cost organic supplements such as sugarcane juice, groundnut cake, and coffee powder. The effects of these additives on biomass yield, growth rate, and nutritional composition were evaluated. Growth was monitored through optical density, biomass weight, and pigment analysis. The results indicated that specific organic supplements significantly enhanced Spirulina growth and nutrient profile compared to control conditions. This study provides a cost-effective strategy for improving Spirulina production with potential applications in the nutraceutical and aquaculture industries.

Keywords: Spirulina, Artificial illumination, Additives, Increased biomass, Sugarcane juice, Coffee

MESS-PP-26

Frequency analysis of single nucleotide polymorphisms in the *BCL11A* gene among Beta-thalassemia patients

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Abstract

To identify the frequency of *rs11886868, rs7557939, rs766432 and rs4671393* single nucleotide polymorphisms (SNPs) in the *BCL11A* gene among beta-thalassemia patients. To assess the correlation between specific single nucleotide polymorphisms and fetal hemoglobin (HbF) levels in beta-thalassemia. Peripheral blood samples were collected from patients in EDTA-coated vacutainer. Genomic DNA was extracted using a standard salting out method. Specific regions of interest were amplified using polymerase chain reaction (PCR) with gene-specific primers. The PCR products were purified and subjected to Sanger sequencing and the analysis was done using Chromas software. In this study, the frequency of the *BCL11A* gene among beta thalassemia patients was analyzed. HbF levels ranged from 68.2 to 93.1 gm/dL across the haplotype groups, whereas BCL11A expression ranged from 0.67 to 0.78 ($2^{\wedge-\Delta\Delta CT}$ values). A moderate positive correlation was observed (Spearman r = 0.5549), although not statistically significant (p = 0.1008), due to limited sample size (n = 10). Our study showed the expression patterns across haplotype groups suggesting an interaction between HbF and BCL11A gene. Further studies with larger cohort are required to validate the observed findings.

Keywords: Beta-thalassemia, *BCL11A* gene, Fetal hemoglobin, Single nucleotide polymorphism, Sequencing

MESS-PP-27

In vitro evaluation of synergistic antimicrobial effect of selected essential oils against human pathogens

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Abstract

The rising threat of multidrug-resistant (MDR) bacteria and other human pathogens has intensified the search for new antimicrobial strategies beyond conventional antibiotics. Herbal extracts, rich in diverse bioactive phytochemicals, offer a promising alternative due to their broad-spectrum activity, lower toxicity, and multiple mechanisms of action. Combining herbal extracts or herbs with antibiotics can produce synergistic effects, enhance antimicrobial potency while reduce required doses and minimizing the risk of resistance development. Herbal extracts often contain flavonoids, alkaloids, terpenoids, tannins, and phenolic acids, each targeting different bacterial pathways like cell membrane disruption, protein synthesis inhibition, efflux pump inhibition, and biofilm disruption. When combined, these compounds can act cooperatively: one extract may increase membrane permeability, allowing another extract or antibiotic to enter more easily, thereby lowering minimum inhibitory concentration (MIC) values significantly. Studies show that combinations of plant extracts such as *Cinnamon verum, Zingiber officinale, Illicium verum,* and *Trachyspermum ammi* exhibit strong synergistic or additive effects against pathogens like *Escherichia coli, Staphylococcus aureus, Pseudomonas aeruginosa,* and *Klebsiella pneumoniae,* with substantially reduced MICs compared to individual extracts. Despite their promise, synergistic herbal therapies face challenges including standardization of extracts, variability in phytochemical composition, and in methods such as checkerboard assays, and time-kill curves to reliably quantify synergy *vs* antagonism. More in depth pharmacokinetic, toxicological, and clinical studies are needed to validate the safety and efficacy of specific synergistic combinations in humans. Future research should focus on identifying key synergistic phytoconstituents, optimizing formulation and conducting controlled trials to move these natural alternatives into mainstream antimicrobial therapy.

Keywords: Multi-drug-resistant bacteria, Essential oils, Synergism, Minimum inhibitory concentration (MIC)

MESS-PP-28

Sustainable management of idol waste through integrated chemical-microbiological approaches

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Abstract

The large-scale immersion of festive idols introduces significant environmental pollution due to plaster of paris (POP), synthetic dyes, and toxic heavy metals such as lead, cadmium, and mercury. These contaminants increase turbidity, alter pH, reduce dissolved oxygen, and disrupt aquatic ecosystems. This study proposes an integrated chemical and biological treatment system for sustainable management of idol immersion water, focusing on pollutant removal and resource recovery. The process begins with coagulation and precipitation using alum and lime, converting POP into stable gypsum, and forming flocs that capture suspended particles and metal ions. Subsequent pH neutralization ensures optimal conditions for biological treatment. A microbial consortium comprising *Pseudomonas putida, Bacillus subtilis, Desulfovibrio desulfuricans,* and *Aspergillus niger* facilitates biotransformation, biosorption, and sulfide-mediated precipitation of heavy metals. Secondary treatment using micro-algae such as *Chlorella* and *Scenedesmus* enhances nutrient uptake and oxygenation, further improving water quality. The treated water shows significant reductions in turbidity and heavy metal concentrations, with stabilized pH suitable for agricultural reuse. Additionally, the gypsum-rich sludge generated is repurposed for eco-friendly bricks and soil amendment, supporting a circular waste management approach. This system offers a cost-effective, scalable, and eco-friendly solution to mitigate pollution from idol immersion practices while promoting resource recovery and sustainable water reuse.

Keywords: Idol immersion, Plaster of paris, Bioremediation, Heavy metals, Wastewater treatment

MESS-PP-29

Isolation and antibiotic susceptibility pattern of bacterial pathogens from clinical samples

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Abstract

Bacterial infections remain a major global health challenge, causing significant morbidity and mortality worldwide. The increasing emergence of antimicrobial resistance has reduced the effectiveness of commonly used antibiotics. This situation makes treatment more difficult, costly, and time-consuming, highlighting the urgent need for continuous monitoring of bacterial pathogens and antibiotic susceptibility patterns. In the present study, clinical samples including burn wound, blood sore, and pus were collected from Sarji Super Speciality Hospital, Shivamogga, Karnataka, India. The collected samples were transported to the microbiology laboratory in sterile containers or appropriate transport media for immediate processing. Serial dilution of the samples was performed, followed by inoculation onto selective and differential culture media such as Nutrient Agar, Blood Agar, and MacConkey Agar. The inoculated plates were incubated at 37 °C for 18 – 24 hours to allow bacterial growth. Distinct colonies were selected and sub-cultured to obtain pure bacterial isolates. Gram staining was carried out to differentiate the bacteria into Gram-positive and Gram-negative groups. Further identification was performed using standard biochemical tests including Catalase, Indole, Methyl Red, Voges–Proskauer, and Citrate utilization tests. Selected bacterial isolates were subjected to molecular identification through 16S rRNA gene sequencing. Antibiotic susceptibility testing was conducted using the Kirby Bauer disc diffusion method on Mueller Hinton agar. The findings of this study contribute to local antimicrobial resistance surveillance, assist clinicians in selecting appropriate antibiotics, promote rational antibiotic use, and strengthen infection control strategies to improve patient management and protect public health.

Keywords: Bacterial infections, Antibiotic susceptibility testing, Clinical isolates, 16S rRNA sequencing

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Established in 1999, the Department of Microbiology at M. S. Ramaiah College of Arts, Science, and Commerce offers B. Sc., M. Sc., and Ph. D. programs that provide comprehensive education and research opportunities. The department is led by highly qualified faculty with expertise across diverse fields of microbiology, actively engaged in cutting-edge research, publications, and conferences.

Equipped with state-of-the-art laboratories, modern research facilities, and strong industry collaborations, the department creates an ideal environment for learning, experimentation, and innovation. Students gain hands-on training, professional development through workshops, and valuable industry exposure *via* internships. With a strong emphasis on research and holistic growth, the department prepares students for successful careers in academia, research, and industry.

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