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JAYPEE INSTITUTE OF INFORMATION TECHNOLOGY
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JANUARY 28,2026 - JANUARY 30,2026

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IX: International Conference on **Advances in Biosciences and Biotechnology (ICABB 2026)**

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Prof. S.C. Saxena
Pro-Chancellor

January 14, 2026

MESSAGE

It gives me immense pleasure to announce the upcoming **9th International Conference on Advances in Bioscience and Biotechnology (ICABB-2026)**, organized by the Department of Biotechnology, Jaypee Institute of Information Technology, Noida. The conference will be held **from January 28th to January 30th, 2026,** and will revolve around the theme *"Emerging Innovations in Biomedical and Bioengineering Sciences."*

Scientific conferences play a pivotal role in bringing together researchers, scientists, and professionals to exchange ideas, share recent advances, and foster meaningful collaborations. ICABB-2026 is envisioned as a multidisciplinary forum that will promote cross-disciplinary research and open new avenues in areas such as computational biology, drug discovery, and emerging biotechnological applications. Active participation and intellectual contributions from the delegates will be key to the success of this conference, and I am confident that the interactions and collaborations formed here will be highly beneficial.

I extend my sincere appreciation to the organizing team for their dedication and meticulous efforts in planning this event. Their commitment and hard work will undoubtedly ensure that ICABB-2026 is a memorable and successful gathering.

With best wishes,

(Prof. S.C. Saxena)

MESSAGE FROM THE ORGANIZERS

It is with great pleasure and enthusiasm that we extend a warm welcome to all participants of the **9th International Conference on Advances in Bioscience and Biotechnology (ICABB-2026),** being organized by the **Department of Biotechnology, Jaypee Institute of Information Technology, Noida, from January 28th to January 30th, 2026**. The theme of this year's conference is - **"Emerging Innovations in Biomedical and Bioengineering Sciences"** that reflects the convergence of multidisciplinary domains within biotechnology and aims to provide a dynamic platform for the exchange of ideas and scientific knowledge.

The conference will serve as an interactive forum for researchers, academicians, scientists, and students from biological, medical, and computational sciences to share diverse perspectives and experiences. Emerging innovations in biomedical and bioengineering sciences, spanning precision medicine, advanced biomaterials, biomedical devices, systems biology, and translational engineering are rapidly transforming healthcare research. These advancements not only address pressing societal and clinical challenges but also contribute significantly to economic growth and technological self-reliance. The theme of ICABB-2026 resonates strongly with India's scientific aspirations and complements the development of advanced research infrastructure, including high-performance computational facilities such as the Ramanujan Universe at JIIT. Together, these interdisciplinary developments are reshaping the scientific landscape, fostering collaboration, and paving the way toward a more sustainable and healthier future.

We sincerely thank all the distinguished speakers and delegates who have graciously accepted our invitation and shown keen interest in this event. We acknowledge with deep gratitude, the generous sponsorship support from **Department of Biotechnology (DBT)**, and the **Department of Science and Technology (DST), Government of India**, along with our industry and publishing partners. We are equally grateful to the members of our Advisory Committee for their invaluable guidance throughout the planning process. The tireless efforts of our organizing team, including faculty members and students, are deeply appreciated.

We express our heartfelt thanks to Shri Manoj Gaur ji, Hon'ble Chancellor; Prof. S.C. Saxena, Hon'ble Pro-Chancellor; for their constant encouragement and guidance, which have been instrumental in bringing this conference to fruition. On behalf of the organizing committee, we wish all participants a comfortable stay and a rewarding research experience during the conference. We look forward to a highly engaging and productive ICABB-2026.

Prof. Pamini Gauba
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Dr. Manisha Singh
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Dr. Nivedita Mishra
Convenor

SPEAKERS

Dr. Stephen Kerr

Associate Provost for Academic and International Affairs
Professor, Medicinal Chemistry,
Massachusetts College of Pharmacy and Health Sciences (MCPHS),
Boston, United States

Dr. Stephen Kerr is a pharmaceutical scientist and educator specializing in drug design, drug metabolism, and pharmacy education. As Associate Provost for Academic and International Affairs within the School of Pharmacy, he leads academic policy initiatives, curriculum development, and international collaborations.

Dr. Kerr also serves as a Board Member of the ISPE–Boston Chapter (2024–2026), reflecting his active engagement in professional organizations that bridge the gap between industry and academia. His involvement promotes collaboration, knowledge sharing, and the advancement of pharmaceutical sciences at both regional and global levels.

Through the integration of administrative leadership, research expertise, and professional advocacy, Dr. Kerr plays a pivotal role in advancing pharmacy education and developing a globally competent healthcare workforce.

Prof. Dr. Kamal Dua

Professor, Pharmaceutics Research
National Institute of Complementary Medicine (NICM) Health Research Institute,
Western Sydney University (WSU), Australia

Dr. Prof. Kamal Dua is an award-winning pharmaceutics researcher specializing in advanced drug delivery systems, with experience across academia, research, and industry. He holds dual doctoral degrees in Pharmaceutical Sciences and Immunology & Microbiology, reflecting strong interdisciplinary expertise in drug delivery and immune-mediated diseases.

His research centers on nano-carrier-based delivery of therapeutic agents, including phytoconstituents and novel bioactive compounds, for chronic inflammatory airway diseases. At the NICM Health Research Institute, Western Sydney University, he leads collaborative research initiatives, mentors postgraduate researchers, and builds national and international partnerships to advance innovative pharmaceutics and nanomedicine solutions.

Dr. Ivy Chung

Professor, Department of Pharmacology
Faculty of Medicine, University of Malaya, Malaysia

Dr. Ivy Chung is a distinguished cancer researcher specializing in tumor–stroma interactions, metabolic reprogramming, and drug resistance, with a research focus on endometrial, breast, and colorectal cancers. Her work combines molecular oncology and translational research to advance innovative cancer therapies.

At the University of Malaya, she has held key leadership roles, including Director of the Innovation and Enterprise Centre and Deputy Dean across multiple research clusters. Her research spans fibroblast-mediated cancer progression, nanomedicine, lipid metabolism, and translational therapeutics. Dr. Chung is actively involved in national and international research grants, scientific advisory roles, and mentorship, collaborating widely to translate research discoveries into clinical and societal impact.

Dr. Vinod Tiwari

Associate Professor
Department of Pharmaceutical Engineering & Technology
Indian Institute Of Technology
BHU Varanasi, India

Dr. Vinod Tiwari is a distinguished academic and researcher at IIT (BHU) with extensive expertise in pharmacology, neuropathic pain, and toxicology. His research bridges fundamental neuroscience with translational pharmaceutical applications, focusing on the development of novel therapeutic strategies to address neurological disorders, chronic pain, and drug-induced toxicities.

Dr. Tiwari’s work bridges molecular pharmacology, neurobehavioral studies, and advanced drug delivery systems to develop clinically relevant therapeutic interventions. He is an experienced mentor and educator, actively fostering interdisciplinary collaboration and contributing to pharmaceutical science through research and teaching. His expertise is widely recognized through high-impact publications, invited talks, and participation in major national and international scientific meetings.

Dr. Brian G. Oliver

Distinguished Professor and Discipline Leader
School of Life Sciences, University of Technology Sydney (UTS), Australia

Dr. Brian G. Oliver is a distinguished academic and internationally recognized researcher specializing in the molecular and genetic mechanisms of chronic respiratory diseases. He is a Distinguished Professor and Discipline Leader in the School of Life Sciences at the University of Technology Sydney (UTS).

His research focuses on the pathophysiology of respiratory diseases, investigating factors that drive disease development and severity. His work spans environmental health, respiratory virology, and respiratory pharmacology, including cellular responses to air pollution, infections, cigarette smoke, and e-cigarettes. Dr. Oliver is also Head of the Respiratory Cellular and Molecular Biology Group at the Woolcock Institute of Medical Research and Immediate Past President of the Thoracic Society of Australia and New Zealand (NSW Branch).

Dr. Keshav Raj Paudel

Senior Research Fellow, Pharmaceutics Research
National Institute of Complementary Medicine (NICM) Health Research Institute, Western Sydney University (WSU), Australia

Dr. Keshav Raj Paudel is a Senior Research Fellow at Western Sydney University specializing in chronic respiratory diseases, including asthma, COPD, airway remodelling, and lung cancer. His research focuses on disease mechanisms, inflammatory pathways, and pharmacological evaluation of novel therapeutics using in vitro, in vivo, and ex vivo models.

He has led studies on the impact of environmental pollutants such as bushfire smoke, particulate matter, and microplastics on respiratory disease progression.

Dr. Paudel has contributed to lung cancer biomarker discovery through fellowships from the Prevent Cancer Foundation and IASLC. His work also explores phytochemical-based nanoformulations and advanced drug delivery strategies. He actively publishes, reviews, and mentors researchers in translational science.

Dr. Vandana Patravale

Professor and Head, Department of Pharmaceutical Sciences and Technology
Institute of Chemical Technology (ICT), Mumbai, Maharashtra, India

Dr. Vandana Patravale is a distinguished pharmaceutical scientist with extensive expertise in nanotechnology-based drug delivery and advanced pharmaceutical formulation systems. Her research focuses on developing innovative therapeutic platforms for malaria, cancer, and neurodegenerative disorders, with strong translational and clinical relevance.

She is Professor and Head of the Department of Pharmaceutical Sciences and Technology at the Institute of Chemical Technology (ICT), Mumbai, where she provides academic and research leadership in teaching, innovation, and capacity building. Dr. Patravale's work integrates pharmaceutics, nanotechnology, and drug delivery to enhance therapeutic safety, efficacy, and targeting. She has made significant contributions to pharmaceutical research and education, actively mentoring postgraduate and doctoral students and fostering strong academic, clinical, and industry collaborations.

Dr. Dinesh Kumar Chellappan

Associate Professor
Department of Life Sciences, School of Pharmacy,
International Medical University (IMU), Kuala Lumpur, Malaysia

Dr. Dinesh Kumar Chellappan is an Associate Professor at the School of Pharmacy, International Medical University (IMU), with expertise in pharmaceutical sciences. His academic activities encompass teaching, research, and professional service, with a strong focus on advancing pharmacy education and evidence-based pharmaceutical practice.

He is actively involved in professional pharmacy and diabetes-related associations, reflecting his commitment to interdisciplinary collaboration and community-focused healthcare. His research interests align with key areas of pharmaceutical sciences, contributing to the development and optimization of therapeutic strategies. Within the Department of Life Sciences, Dr. Chellappan plays an important role in curriculum development, student mentorship, and research supervision, supporting both undergraduate and postgraduate education at IMU.

Dr. Tewin Tencomnao

Assistant Professor
Department of Clinical Chemistry, Faculty of Allied Health Sciences
Chulalongkorn University, Patumwan, Bangkok, Thailand

Dr. Tewin Tencomnao is an Assistant Professor in the Department of Clinical Chemistry, Faculty of Allied Health Sciences, Chulalongkorn University, Bangkok, Thailand. He is a biomedical scientist specializing in drug discovery, natural products, herbal medicine, and neuroprotection, with a research focus on healthy ageing and neurodegenerative diseases.

His work integrates molecular pharmacology, cellular biology, and model organism studies, including Caenorhabditis elegans, to elucidate mechanisms of neuroprotection and anti-ageing. Dr. Tencomnao is actively involved in the Natural Products for Neuroprotection and Anti-ageing Research Unit, leading research on plant-derived therapeutics. He has published extensively in high-impact journals and mentors students in translational biomedical research.

Dr. Flavia Zacconi

Associate Professor
Institute for Biological and Medical Engineering,
Pontificia Universidad Católica de Chile, Santiago, Chile

Dr. Flavia Zacconi is a chemist and interdisciplinary researcher whose work integrates organic, medicinal, and biological chemistry with engineering and nanotechnology to address challenges in biomedical science. She earned her PhD in Chemistry from the Universidad Nacional del Sur, Argentina, and completed postdoctoral training at the Universidade de Santiago de Compostela and the Institute of Organic Synthesis, Spain.

She has served as an invited professor at Boston College, the University of Sussex, and the University of Notre Dame. Dr. Zacconi is currently an Associate Professor at the Pontificia Universidad Católica de Chile and the Institute of Biological and Medical Engineering, where her research focuses on translating chemical and nanotechnological approaches into biomedical and engineering applications.

Prof. Dr. Jata Shankar

Professor and Head, Department of Biotechnology and Bioinformatics
Jaypee University of Information Technology (JUIT), Solan, Himachal Pradesh, India

Dr. Jata Shankar is a senior academic and research leader in biotechnology and bioinformatics, currently serving as Professor and Head of the Department of Biotechnology and Bioinformatics at Jaypee University of Information Technology (JUIT).

He has been associated with JUIT since 2013, playing a key role in strengthening academic programs and research culture. He earned his PhD from CSIR–Institute of Genomics and Integrative Biology (IGIB), Jamia Millia Islamia, and completed postdoctoral research at Stanford University School of Medicine,

USA. Prof. Shankar is actively engaged in research supervision, curriculum development, and interdisciplinary collaboration, and is committed to mentoring students and advancing excellence in biotechnology and bioinformatics education and research.

Dr. Khalid Raza

Associate Professor, Department of Computer Science
Jamia Millia Islamia, New Delhi, India

Dr. Khalid Raza is an Associate Professor in the Department of Computer Science at Jamia Millia Islamia, New Delhi, with over 14 years of experience in teaching, research, and academic administration, including service as Assistant Controller of Examinations.

He earned his PhD in Soft Computing and Computational Biology and has served internationally as an ICCR Chair Visiting Professor at Ain Shams University, Egypt. Dr. Raza has authored over 150 publications with leading publishers and focuses on AI and computational intelligence applications in bioinformatics, systems biology, and health informatics. He is an Academic Editor for PeerJ Computer Science and recognized among the Top 2% Scientists globally.

Dr. Prashant Kumar Gupta

Assistant Professor & incharge of Ayurinformatics Lab
Dept of Kaumarabhritya, (Ayurveda Pediatrics)
All India Institute of Ayurveda.

Dr. Prashant Kumar Gupta is an Assistant Professor and In-charge of the Ayurinformatics Laboratory in the Department of Kaumarabhritya (Ayurveda Pediatrics) at the All India Institute of Ayurveda, New Delhi. He is engaged in teaching, academic mentoring, and research activities with a focus on strengthening pediatric healthcare through integrative and evidence-based Ayurvedic practices.

His research interests include Ayurinformatics, pediatric health sciences, and the application of computational and data-driven approaches for systematic analysis of traditional Ayurvedic knowledge. Dr. Gupta has contributed to interdisciplinary research initiatives and institutional programs aimed at advancing digital integration, scientific validation, and translational relevance of Ayurveda. His work reflects a commitment to bridging classical Ayurvedic wisdom with contemporary scientific methodologies for innovation in healthcare and biomedical research.

Dr. Ritu Sethi

MD (Ayurved), Chief of Services
Senior Consultant – Ayurveda
Holy Family Hospital, New Delhi, India

Dr. Ritu Sethi is Chief of Services and Senior Consultant in the Ayurveda department at Holy Family Hospital, New Delhi, overseeing clinical services and the development of personalized, holistic Ayurvedic treatments. She specializes in managing chronic and lifestyle-related conditions through tailored protocols that restore balance and enhance overall well-being.

With deep expertise in integrative healthcare, Dr. Sethi combines classical Ayurvedic principles with contemporary therapeutic approaches. Actively engaged in professional networks and public health initiatives, she promotes Ayurveda's role in healthcare policy. Her leadership, patient-centered approach, and contributions to the field have earned her recognition as a leading authority in Ayurvedic medicine.

Dr Deep Jyoti Bhuyan

Senior Research Fellow - Healthy Ageing: Therapeutic Potential of Natural Products NICM Health Research Institute
Western Sydney University
Sydney, Australia

Dr Deep Jyoti Bhuyan, PhD is a Senior Research Fellow at the NICM Health Research Institute, Western Sydney University, Australia, where he leads research in Healthy Ageing, focusing on the therapeutic potential of natural products and gut microbial metabolites (postbiotics). He holds additional roles as International Engagement Coordinator and Higher Degree Research (HDR) Coordinator at the institute, contributing to academic leadership and research collaboration programs

He established The GutBiotics Lab, which investigates the role of gut microbiota and their metabolites in health and disease, including cancer, antimicrobial and antiviral strategies, and the synergistic interactions of phytochemicals with conventional therapies. His work spans molecular mechanisms, natural product chemistry, and microbiome science, with substantial publications and international research partnerships. Dr Bhuyan earned his PhD from the University of Newcastle and has a strong record of peer-reviewed journal articles and invited presentations.

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Session 1:
Biomedical and Health Innovations
Poster Presentations

ICABB26-BM-P01

Claudins in gastrointestinal tumours: Site-specific expression and oncogenic modulation

Shefali Rawat[1],[2], Rajni Yadav[2] and Ankit Mathur[1*]

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Abstract

Gastrointestinal (GI) tumours originating from diverse regions of the digestive tract often share common molecular mechanisms driving malignant transformation. Despite significant advances, a major gap persists in understanding the biomarker landscape driving GI tumour carcinogenesis. Claudins, essential component of epithelial tight junctions is increasingly recognised to modulate tumorigenesis. This study aims to investigate the expression profile of claudins across GI tumours originating from different anatomical sites to understand association with GI carcinogenic events. In this study we systematically reviewed over 100 peer-reviewed publications to elucidate association between dysregulation of claudins (Cldns), and GI cancer pathology. Our analysis revealed 93 studies reported the overexpression of claudins 1, 2, 3, 4, 6, 7, 11, 14, and 18.2 in gastric cancer, while 7 studies documented lower expression levels of CLDN 2, 6, 11, 17, 18.2, and 23, indicating a dual role of claudins as either tumour suppressors or oncogenes based on their expression profiles. Notably, CLDN18.2 has emerged as a highly specific therapeutic target, with clinical trials of zolbetuximab demonstrating promising outcomes in advanced gastric and gastroesophageal junctions. However, its role in other GI malignancies such as gallbladder cancer remained unclear. To address this gap, we collected 50 tissue and blood samples from patients with gallbladder carcinoma (CaGB) and gallstone disease (GSD), alongside adjacent normal tissues. By employing immunohistochemistry, we are assessing the expression of CLDN 18.2 and its correlation with overall survival rates in gallbladder cancer. Our findings indicate that claudins frequently undergo dysregulation in GI tumours, suggesting their potential as diagnostic or prognostic biomarkers, as well as therapeutic options. This context-dependent functionality emphasizes the role of claudins in the early detection, classification, and prognosis of GI cancers. Our future investigations will further clarify the molecular mechanisms surrounding claudins to enhance personalized treatment strategies for GI cancers.

Keywords: Carcinogenesis, Zolbetuximab, Molecular Mechanisms and Immunohistochemistry

ICABB26-BM-P02

Bridging Damage and Recovery: Regenerative Frontiers in Neuro-Oncology

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Abstract

Brain cancer affects millions of people annually and frequently causes serious neurological consequences, making it a growing worldwide challenge. Conventional therapy, including medication and cognitive rehabilitation, offers limited relief for the cellular and structural damage caused by cancer treatments like chemotherapy and radiation. While these treatments are critical for survival, they can result in long-term neurological issues such as vascular injuries, chronic inflammation, white matter degradation, and reduced neurogenesis, collectively contributing to cognitive decline, emotional difficulties, and diminished overall wellbeing, a phenomenon known as the "post-cancer brain.". Regenerative medicine (RM) presents a viable solution for repairing brain damage caused by cancer treatments by utilizing stem cells, biomaterials, and repair strategies. Recent advancements in

3D scaffolds and animal model studies indicate potential for restoring brain structure and function. This approach is complemented by a treatment plan incorporating healthy lifestyle modifications, neuroplasticity training, and cognitive rehabilitation. However, clinical application is limited by a number of issues. The advantages of treatment must be carefully evaluated against risks of immune side effects, persistent inflammation, and tumour recurrence. Widespread implementation is further complicated by practical and financial hurdles. According to future projections, treatment outcomes may be improved by combining personalized treatments, drug delivery via nanotechnology, and collaboration between oncology, neuroscience, and bioengineering. The review highlights the potential of regenerative medicine in improving cognition and quality of life after brain cancer, stressing the importance of continued investment in translational research, clinical trials, and collaboration for successful application.
Keywords: Regenerative Medicine, Neuro-oncology, Neuroplasticity, 3D Scaffold, Cognitive Rehabilition

ICABB26-BM-P03

In vitro Analysis of Antifungal Activity of the *Ocimum Sanctum* against *Alternaria Solani*, *Fusarium Oxysporum Candida Albicans* and *Candida Tropicalis*

Mukesh Kumar[1*], Haneesh Saini[2 *]

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Abstract

Ethanomedicinal and aromatic plants have been attributed to be the main source of exhibiting antimicrobial activities. The goal of the current investigation is planned to assess the antifungal activity of Ocimum sanctum having strong therapeutic properties that prevent the growth of pathogenic fungi. Crude extracts of stem, leaf and seed were extracted with distilled water using the maceration method. Using food poison method, different plant extracts in various concentrations (6.25, 11.76 and 16.66 mg/ml) individually and in combination were employed due to their in vitro antifungal ability against a variety of pathogenic fungus that affect plants, viz. Alternaria solani, Fusarium oxysproum Candida albicans and Candida tropicalis. The plant extracts were analysed using technique UV-Visible spectroscopy, FTIR, Gas Chromatography and Mass Spectroscopy to determine and characterize the active antifungal components responsible for inhibiting the growth of fungi. The aqueous extract (6.25 mg/ml) of Ocimum sanctum showed significant antifungal activity against A. solani, F. oxysporum fungi, Candida albicans while 16.66 mg/ml of plant extract displayed significant activity against Candida tropicalis.

Keywords: Aqueous extract, Ethanomedicinal, FTIR, *Ocimum sanctum*

ICABB26-BM-P04

CRISPR-Mediated Chromosome Therapy in Down Syndrome: Current Progress and Translational Prospects

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Abstract

Down Syndrome is the most common chromosomal aneuploidy that supports postnatal survival. Arising from trisomy 21, this condition produces a global gene dosage imbalance comprising disturbances of neural, metabolic, and general physiology. Currently, standard therapies are mainly directed at managing symptoms, co-existing disorders and involves symptomatic management. However, these standard procedures do not aim at correcting the underlying cause of the disease, that is the presence of the additional chromosome. This major therapeutic gap has driven growing interest in CRISPR-Cas9–mediated genome editing as a potential approach to treat Down Syndrome by targeting chromosomal aneuploidy at its root cause. Experimental studies have shown the ability of CRISPR-Cas9 mediated systems targeting and eliminating the supernumerary chromosome 21 in human trisomic cells. This evidence reported rescuing of trisomy and partially reversing it at a gene expression level via disruption and silencing of extra chromosome restoring a typical pattern and cellular phenotype. These approaches are derived from natural chromosome inactivation and represent a paradigm shift in the management strategy for chromosomal disorders. However, there are a number of caveats that should be resolved, such as exact target identification, overcoming genomic instability, and ensuring effective delivery of the drug into tissues. Chromosomal changes raise novel bioethical concerns because CRISPR-based correction of trisomy 21 entails permanent genome-level modifications, frequently in situations where informed consent is limited. In addition to raising more general concerns about neurodiversity, disability, and fair access to new chromosomal therapies, these interventions carry the risk of unanticipated long-term or heritable effects. Early evidence shows CRISPR's potential influence on Down Syndrome management based on the key difference between repairing the genome and treating symptoms of a disorder. This shall also act as evidence regarding the potency of future therapies directed at chromosomal disorders with a similar approach and intention as targeted therapies. The development of these targeted therapies seeks to harness the natural process of chromosome inactivation while treating the trisomy 21(Down Syndrome).

Keywords: Down Syndrome, Trisomy 21, Genome editing, CRISPR-Cas9, Precision medicine

ICABB26-BM-P05

Beating Models: Cardiac Organoids for the Future Medicine

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Abstract

Cardiovascular diseases account for increasing mortality rates in modern times. Despite its early development during embryogenesis, early heart development is poorly understood due its limited regenerative capacity. In-vitro 2D models were developed to investigate cardiac development and its working, but they failed to replicate the native structural, cellular and functional complexity of the human heart. Recent discoveries in stem cell research led to the formation of 3D models. These self-organizing “beating hearts in a dish” have emerged as transformative systems in cardiovascular

research, linking basic developmental biology and translational medicine. They are generated from hiPCS through precise temporal modulation of WNT signaling, using small molecules (CHIR99021, IWP2). Cardiac organoids possess the ability to differentiate and assemble into rhythmically contracting structures that closely resemble early human heart tissue. Recently, distinct cardiac layers, chamber-like morphology, and synchronized beating patterns, replicating fetal-stage heart development have been designed in-vitro. Integrating endothelial and epicardial cells with microfluidic perfusion platforms improves vascularization, nutrient exchange, and electrophysiological stability, allowing longer-term culture and enhanced functionality. These advanced models provide a platform for studying congenital heart defects, ischemic injury, and drug-induced cardiotoxicity, while enabling patient-specific disease modeling and personalized therapeutic testing. Despite their promise, challenges such as incomplete cardiomyocyte maturation, limited vascular integration, and absence of standardized protocols still exist. Future strategies using mechanical and electrical stimulation, perfusable vascular networks, and scalable bioreactor systems are expected to overcome these limitations and accelerate clinical translation. Cardiac organoids represent a revolutionary step in cardiovascular research and regenerative medicine. By accurately replicating key aspects of native cardiac structure and function, they hold the potential to reduce reliance on animal models, enhance precision in disease modeling, and pave the way towards the bioengineering of transplantable heart tissue. This study highlights the necessity for development of cardiac organoids, methodology employed and their applications.

Keywords: Cardiac organoids; Human pluripotent stem cells; WNT signaling; self-organization; Electrophysiology; Regenerative cardiology

ICABB26-BM-P06

Functional Graphene Analogues: Bridging Nanoscience and Biomedicine

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Abstract

Owing to the outstanding mechanical strength, large surface area, electrical conductivity, and tunable chemical functionality, Graphene and its derivatives are highly appealing nanomaterials for biomedical applications. The blending of graphene derivatives in the form of hydrogels and aerogels has resulted in the creation of innovative hybrid materials that possess novel physicochemical and biological characteristics. Particularly, Reduced Graphene oxide (rGO) hydrogels exhibit good biocompatibility, tunable porosity, and improved mechanical stability and hence are relevant to drug delivery, tissue engineering, wound healing, and biosensing. In the same manner, graphene aerogels, with lightweight, highly porous three-dimensional structures, have a very good application in cell scaffolding, antibacterial systems, and neural tissue regeneration where conductivity and mechanical pliability are essential. Surface modification and composite building routes further improve dispersion, biocompatibility, and responsiveness to physiological stimuli for these materials. This review outlines recent advances in the design, synthesis, and biomedical deployment of graphene-derived hydrogels and aerogels, with main emphasis on the multifunctional applications in next-generation regenerative and therapeutic technologies. Also, this study presents the current trend and limitations on large-scale production of graphene-based aerogel for technological applications, especially in biomedical devices. A broad literature survey will be conducted on the published literature in the past ten years directing on synthesis of different graphene-based aerogels & hydrogels and their utilization from laboratory to

industrial level. A comprehensive review that sums up the designing of graphene scaffolds at bulk level with future technological advancement for next-generation biomedicines and societal upliftment is required in this field. Despite substantial advances, issues persist regarding long-term biocompatibility, biodegradability, and controlled synthesis for clinical translation. This review highlights the possible research in this area.

Keywords: Graphene based aerogels, Hydrogels, Gel technology, Next generation.

ICABB26-BM-P07

Investigating the Tumor Microenvironment (TME) Differences in Rare Histologic Subtypes of Ovarian Cancer

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Abstract

Ovarian cancer is a diverse disease made up of several histologic subtypes that differ in their biology, clinical behaviour, and treatment outcomes. While high-grade serous carcinoma has been studied extensively, the rarer forms, such as clear cell, mucinous, and endometrioid carcinomas, remain less understood, especially in terms of their tumor microenvironment (TME). The TME includes immune cells, stromal fibroblasts, and signaling molecules that influence tumor growth and response to treatment. This review brings together findings from existing studies to compare how the TME differs across these rare subtypes. It summarises evidence on immune cell infiltration, stromal activity, cytokine expression, and immune checkpoint markers, and how these factors may contribute to differences in aggressiveness and treatment resistance. Research suggests that clear cell and mucinous ovarian cancers, for example, often show lower immune cell infiltration and stronger stromal activation than serous types, which may partly explain their poor response to chemotherapy and immunotherapy. However, published data remain limited and sometimes inconsistent due to small sample sizes and varied study methods. By analysing the current literature, this review aims to highlight patterns that are emerging as well as the major research gaps that need further investigation. A clearer understanding of the tumor microenvironment in these rare subtypes could eventually support more tailored and effective therapeutic approaches for ovarian cancer.

Keywords: Clear cell carcinoma, Immune infiltration, Mucinous carcinoma, Ovarian cancer, Tumor microenvironment

ICABB26-BM-P08

Bacterial Type VI Secretion System Augments Resistance Against Biotic and Abiotic Stress

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Abstract

In their natural environment, bacteria constantly face competition and must employ various mechanisms to survive and protect themselves from neighbouring microorganisms. Among these defence strategies, one of the most noteworthy features found in a minority of bacteria, specifically less than 25% of Gram-negative species, is the Type VI Secretion System (T6SS). T6SS gene clusters are exclusive to Gram-negative bacteria, with the number of clusters varying significantly from one to six per organism, indicating its varied importance and potential roles across different species. Bacteria utilize the T6SS

as a potent competitive weapon, primarily to deliver toxic effectors responsible for eliminating their microbial competitors. This is achieved through a lancet-like apparatus that rapidly transports materials outside the cells, effectively acting as a molecular harpoon. This aggressive system is crucial for ensuring survival in a stressful, resource-limited environment. Beyond inter-bacterial warfare, the T6SS also plays a role in interactions with host organisms, often serving to subvert host cells during infection or colonization processes. Since its initial discovery in 2006, research on the T6SS has expanded rapidly, encompassing rigorous biochemical, structural, and molecular studies. These investigations have been instrumental in leading to the detailed identification and characterization of the T6SS's full cycle, including its assembly, loading of effectors, rapid firing, and subsequent disassembly processes. Ongoing research, frequently coupled with powerful bioinformatics approaches, is continually expanding our knowledge of new T6SS effectors and their diverse functionality. This continuous effort is shedding light on previously unexplored aspects of both prokaryotic and eukaryotic organism biology, highlighting the system's broad biological significance. The present review focuses on synthesizing recent and significant discoveries related to T6SS effectors, their diverse mechanisms of action, and their intricate regulation, ultimately enhancing our understanding of this sophisticated and combative bacterial system.

Keywords: Effectors, Regulation, Secretion, Signals, T6SS

ICABB26-BM-P09

Diagnostic Potential of Menstrual -Derived Exosomal Proteins in Early Ovarian Cancer

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Abstract

Ovarian cancer remains the most lethal gynaecologic malignancy, largely due to asymptomatic early stages and the absence of reliable screening biomarkers. Conventional serum indicators such as CA-125 and HE4 lack sensitivity in early-stage disease and show poor specificity in benign conditions. Menstrual effluent has emerged as a biologically rich, underexplored and clinically promising diagnostic substrate for early detection containing exfoliated endometrial and tubal epithelium, immune-derived factors, extracellular vesicles, and cell-free molecular cargo reflective of the reproductive tract microenvironment. Exosomes isolated from menstrual fluid, characterized by canonical tetraspanins CD9, CD63, and CD81, encapsulate proteins, lipids, and regulatory non-coding RNAs associated with tissue remodelling, immune tolerance, and mucosal repair. The review dwells on the growing evidences indicating that ovarian tumour derived extracellular vesicles exhibit distinct proteomic signatures enriched in heat-shock proteins (HSP70/90), Annexin-A2, EpCAM, MUC16, integrins (α6β1), matrix-remodelling enzymes (MMP-2/9), and angiogenic mediators such as VEGF-A and TGF-β. Additionally, oncogenic miRNA clusters, including the miR-200 family and miR-21, are recognized contributors to epithelial–mesenchymal transition, invasion, and chemoresistance in ovarian malignancy. Notably, menstrual exosomes harbour proteins and nucleic acids intricately involved in pathways relevant to carcinogenesis, including PI3K-AKT signaling, Wnt signaling, oxidative-stress response, complement activation, and cytokine-driven immune modulation. The biological overlap between menstrual-derived exosomal components and known ovarian cancer vesicle cargo suggests that menstrual effluent may capture early neoplastic molecular shifts occurring at the tubo-ovarian interface prior to systemic dissemination.

Keywords: Early diagnosis, Exosomal proteomics, EVs, Menstrual effluent, Ovarian cancer

ICABB26-BM-P10

Precision mRNA Immunotherapy for Solid Tumors and the Role of Cancer-Specific Neoantigen Design Immune Activation Clinical Advances and Approaches for Relapse Prevention: A Review

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Abstract

Cancer remains one of the leading causes of death worldwide, with many advanced-stage tumors still considered terminal despite progress in surgery, chemotherapy, and radiation. Conventional chemotherapeutic regimens often fail due to drug resistance, systemic toxicity, and the inability to eliminate highly heterogeneous tumor cell populations. This leaves patients with metastatic cancers especially melanoma, pancreatic, and lung cancers with limited survival benefits and high relapse rates. In this urgent landscape of unmet clinical need, mRNA-based cancer immunotherapy is emerging as a transformative strategy capable of achieving what conventional treatments cannot. By encoding tumor-specific or patient-specific neoantigens, mRNA vaccines can precisely engage the immune system, strengthen antigen presentation, and activate robust cytotoxic T-cell responses that directly target resistant tumor clones. Recent trials have shown promising tumor shrinkage, improved recurrence-free survival, and strong immunogenicity, particularly when mRNA vaccines are paired with checkpoint inhibitors or adoptive cell therapy. Although challenges such as immune evasion, delivery optimization, and tumor microenvironment suppression remain, rapid advancements in mRNA engineering and nanoparticle delivery position this platform as a true game changer poised to redefine the future of oncology. To further strengthen its clinical potential, ongoing research is exploring multi-epitope mRNA constructs, self-amplifying mRNA platforms, and targeted delivery systems that improve stability and tissue-specific uptake. These innovations may allow mRNA vaccines to adapt in real time to a tumor's evolving mutational profile, offering a dynamic, personalized, and minimally toxic therapeutic option. As evidence accumulates, mRNA immunotherapy is rapidly transitioning from an experimental concept to a next-generation pillar of cancer treatment.

Keywords: Cancer immunotherapy, mRNA-encoded cancer vaccines, personalized neoantigen targeting, tumor-specific antigen discovery, immunogenic epitope prediction, next-generation vaccine adjuvants.

ICABB26-BM-P11

Cell fate conversion: turning star cells into nerve cells a new path for Regenerative Medicine

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Abstract

Glial cells are the most abundant cells in our central nervous system, and they work as supporting cells of neurons. Astrocytes are a type of glial cell that ensure the continuous function of their signalling mechanism in damaged conditions, such as in injuries, strokes, trauma, and neurodegenerative diseases like Alzheimer's or Parkinson's. These cells are an essential component of the brain and participate in many physiological processes, including blood-brain barrier formation, axon growth regulation, neuronal support, and higher cognitive functions such as memory. Although the conventional treatment of neurodegenerative diseases like transplantation of donor cells or stem cell therapy has proved to be promising, it has been hit with a big challenge. Their effectiveness is usually constrained by problems such as immune rejection, cancer risk, and extreme complexity. To enhance medical treatment the direct

reprogramming of astrocytes-to-neurons provides a new strategy for regenerative medicine. It can generate neurons that can replace the ones lost due to disease or any injury. Researchers can also coax these supportive cells into functional neurons using viruses or nanoparticles to deliver certain microRNAs and transcription factors such as NeuroD1, Ascl1, or Dlx2, effectively replacing those that were damaged or diseased. Predictions in the future must prove the ability of the functionally integrated reprogrammed neurons to interact with the already existing neurons in the circuits. The bioengineered scaffolds, with the possibility of improved cure, improve the microenvironment necessary to reprogram neurons, and molecular knowledge of the fundamental mechanisms is necessary in ensuring safe treatment in the translation of this promising science into clinical treatments.

Keywords: Regenerative Medicine, Astrocytes, Bioengineered scaffold, Nanoparticles, Transcription factors

ICABB26-BM-P12

Gene Therapy for Hemoglobinopathy

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Abstract

Hemoglobinopathies are among the most common inherited diseases around the world. They have become much more common. Hemoglobinopathy is defined as a group of inherited blood disorders involving the hemoglobin (major protein of red blood cells). Sickel cell disease is one of the most common hemoglobinopathy. Gene therapy for hemoglobinopathy has been a talk of the town for around two years now in the US, UK and EU but still very unpopular and a concerning topic in India. Gene therapy for hemoglobinopathies—especially sickle cell disease (SCD) and transfusion-dependent beta thalassemia (TDT)—has made dramatic advances, with CRISPR-based and lentiviral therapies now FDA approved and showing curative outcomes in 2025. The main approaches are gene addition, which uses viral vectors like lentiviruses to add a working copy of the gene, and gene editing, which uses techniques like CRISPR-Cas9 to either correct the mutation or activate the production of fetal hemoglobin (HbF). The research directions for hemoglobinopathy include base & prime editing; correction of single point mutations in HBB gene to further reduce off-target effects and safety risks, in-vivo editing; direct editing in the body to potentially eliminate the need for stem harvesting and conditioning, and targeting non-coding regions; Strategies include editing regulatory elements (BCL11A enhancer, HBG promoters) to boost HbF and minimize disease symptoms. Gene editing has recently emerged as a potential alternative to vector-mediated gene addition for gene therapy of β-hemoglobinopathies. Gene therapy has fundamentally changed the outlook for hemoglobinopathy patients, with curative therapies now real-world options. This technique definitely seems a little unachievable in India at the moment, but recent studies and future practices can make it available for people around the globe.

Keywords: Hemoglobinopathy, CRISPR, lentiviral therapy, gene editing, sickle-cell disease

ICABB26-BM-P13

Impact of Physical Activity and Lifestyle Modifications in Preventing Hypertension

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Abstract

The "silent killer," hypertension, is one of the most prevalent cardiovascular risk factors worldwide and a significant cause of morbidity and mortality. Exercise and lifestyle modifications are now essential non-pharmacological strategies for the prevention and treatment of hypertension. Regular aerobic exercise, resistance training, and mind-body exercises like yoga and tai chi can effectively lower blood pressure by improving endothelial function, lowering systemic inflammation, increasing vascular compliance, and decreasing sympathetic overactivity, according to an increasing body of research. To further reduce the risk of hypertension, dietary therapy such as the DASH and Mediterranean diets, regulating weight, cutting back on sodium intake, and moderate alcohol use are all crucial. These protective actions are further enhanced by stress reduction and quitting smoking. Crucially, changing one's lifestyle not only lowers the risk of developing hypertension but also improves the effectiveness of medication for those who already have the diagnosis. Despite the overwhelming evidence in favor of these interventions, behavioral, cultural, and economical hurdles continue to provide a significant obstacle to adherence. To enhance long-term compliance and results, future studies should concentrate on community-based interventions, digital health technologies, and customized lifestyle recommendations. The importance of physical exercise and lifestyle changes as affordable, long-lasting, and internationally applicable strategies for avoiding hypertension and lessening its toll on public health systems is emphasized in this review.

Keywords: Hypertension, Physical activity, Lifestyle modifications, non-pharmacological interventions, Exercise, Prevention, Cardiovascular health

ICABB26-BM-P15

Advancing Therapeutic Strategies for Celiac Disease: From Gluten-Free Diets to Novel Biopharmaceutical Approaches

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Abstract

Gluten, a protein complex found in wheat, barley, and rye, is essential for providing elasticity, structure, and texture to baked products. It is primarily composed of two protein fractions gliadins and glutenins—which enable dough formation and trapping of gas during fermentation. Although gluten is harmless to most individuals, it poses significant health risks to people with celiac disease or gluten intolerance. In such individuals, gluten consumption triggers an abnormal immune response that damages the small intestinal mucosa, leading to inflammation, impaired digestion, and a range of long-term complications. In celiac disease, the immune system mistakenly identifies gluten peptides as harmful, resulting in the destruction of intestinal villi—microscopic structures responsible for nutrient absorption. This leads to gastrointestinal symptoms such as bloating, diarrhea, abdominal pain, nausea, and fatigue, as well as systemic conditions including malnutrition, osteoporosis, and neurological disorders. Additionally, gluten exposure is associated with increased intestinal permeability, or "leaky gut," allowing harmful antigens to enter the bloodstream and further escalate immune activation. Currently, strict and lifelong adherence to a gluten-free diet is the only effective treatment, enabling intestinal recovery and symptom management. However, complete avoidance remains challenging due to hidden gluten sources in processed foods. Emerging therapeutic strategies, including gluten-degrading enzymes and probiotic-based interventions, are under investigation and may offer improved management options in the future.

Keywords: glutenins, osteoporosis, neurological disorders

ICABB26-BM-P16

Emerging Alternatives to Gluten-Free Diet Therapy in Celiac Disease: Enzyme, Probiotic, and Pharmacological Interventions

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Abstract

Celiac disease is a chronic autoimmune disorder triggered by an abnormal immune response to gluten, a protein present in wheat, barley, and rye. Upon gluten ingestion, affected individuals experience inflammation and villous atrophy in the small intestine, leading to impaired nutrient absorption. Common symptoms include diarrhea, abdominal pain, bloating, fatigue, and micronutrient deficiencies. If untreated, the condition can progress to serious complications such as malnutrition, osteoporosis, neurological impairments, infertility, and increased cancer risk. Although the presence of HLA-DQ2 or HLA-DQ8 haplotypes is necessary for susceptibility, these genetic factors alone are insufficient for disease development. Environmental triggers, epigenetic influences, and immune dysregulation also play critical roles in disease onset and severity. Currently, a strict lifelong gluten-free diet (GFD) remains the only established treatment, effectively controlling symptoms and preventing further intestinal damage. However, adherence to a GFD is challenging due to the widespread presence of gluten in processed foods and the risk of accidental exposure. To address these limitations, several alternative therapeutic approaches are under investigation. Promising pharmaceutical interventions include larazotide acetate, which strengthens the intestinal barrier, and transglutaminase inhibitors that

prevent gluten peptide modification. Enzyme-based therapies such as AN-PEP and EP-B2 aim to degrade gluten before it activates immune responses. Additionally, probiotics such as *Lactobacillus casei* and *Bifidobacterium longum* show potential in modulating immunity and reducing gut inflammation. This study reviews current and emerging therapeutic strategies for celiac disease. While the gluten-free diet remains central to disease management, ongoing research into pharmacological agents, enzyme therapies, and probiotic interventions offers promising avenues for complementary or alternative treatments to enhance patient outcomes and quality of life.

Keywords: Gluten-Free Diet, Celiac Disease, Probiotic

ICABB26-BM-P17

COVID-19 and Autoimmunity: Pathogenic Mechanisms and Clinical Implications

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Abstract

The ongoing pandemic caused by the coronavirus disease 2019 (COVID-19) has strangely sped up our understanding of changes in the human immune system. It has also revealed a range of different autoimmune issues that arise from infection with the SARS-CoV-2 virus. Current data on the epidemiology shows that patients who had a COVID-19 infection may be at a higher risk for developing new autoimmune diseases. Conditions like rheumatoid arthritis, systemic lupus erythematosus, and Multisystem Inflammatory Syndrome in Children (MIS-C) are more common in these patients compared to those who did not have the infection.

There are multiple immunopathological mechanisms that can lead to autoimmunity during COVID-19 infection. These include molecular mimicry, where homology exists between proteins in viruses and autotargets; cross-reactive immunity, or bystander activation of autoreactive lymphocytes during massive inflammation; and antigen-driven epitope spreading secondary to tissue injury and antigen release. Furthermore, the COVID-19 cytokine storm, characterized by hypersecretion of interleukins and interferons, results in immune regulatory disturbance and ensuing tolerance emergence against autotargets. More specifically, COVID-19 infection is associated with hyperactivation of extrafollicular B-cell responses in lymphoid secondary sites, including hypersecretion of autobodies against cytokines, nuclear, and tissue-specific proteins.

It is imperative to understand these mechanisms of autoimmunity that occur as a result of COVID-19 infection for an accurate diagnosis, treatment, and management of these patients to receive. The aim of this review article is to try to outline these mechanisms of autoimmunity that result from COVID-19 infection, manifestations associated with these infections, as well as the importance of these autoantibodies as a predictor of patient outcomes. It is with this premise that new treatment approaches can be developed to avoid autoimmunity complications associated with COVID-19 infection.

Keywords: COVID-19, SARS-CoV-2, Autoimmunity, Molecular mimicry, Autoantibodies, Cytokine storm, Long COVID, MIS-C

ICABB26-BM-P18

UNCOVERING THE QUIET CLUES: EMERGING BIOMARKERS FOR BREAST CANCER DETECTION

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ABSTRACT

Breast cancer has become the most common cancer globally, even surpassing lung cancer, especially in women. On average,1 in 20 women worldwide is diagnosed with breast cancer in their lifetime. Breast cancer is also the fifth leading cause of cancer-related deaths. Hence, need for its early detection and effective cure arises. Traditionally, biomarkers like Estrogen Receptor (ER), Progesterone Receptor (PR), Human Epidermal Growth Factor Receptor2 (HER2), Breast Cancer gene1/2 (BRCA1/2) have been used but due to their low sensitivity for detection in early stages and low specificity causing false-positive results, they are often used along with other detection methods to establish a diagnosis. Therefore, better non-invasive biomarkers like liquid biopsy which includes analysing body fluids such as blood, urine, tears, sweat, nipple aspirate fluid, exhaled breath; circulating biomarkers like circulating tumour cells (CTCs), cell-free DNA (cfDNA), MicroRNAs (miRNAs), long non-coding RNAs (lnc RNAs); multi-omics driven biomarkers are arising which show potential for early detection and in guiding personalized treatments. This study aims at uncovering such innovative biomarkers offering an alternative to traditional biomarkers. Such biomarkers would prove to be less invasive, help in early detection of cancer, provide more accurate diagnosis by identifying specific characteristics of tumour and how it may respond to specific treatments, thus allowing targeted therapies and better risk assessment, finally saving millions of lives.

Keywords: Biomarkers, Breast cancer, Early detection, Accurate diagnosis, Personalized treatment, Targeted therapies, Risk assessment, Mortality rate

ICABB26-BM-P19

Epigenetic Dysregulation in Glioblastoma: A Pathway to Precision Therapy

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Abstract

Glioblastoma (GBM), previously known as glioblastoma multiforme, is an extremely aggressive brain cancer. Its highly vascularized and resistant to most of the treatments and therapies because of epigenetic changes. Chances of recurrence are very high due to significant genetic and epigenetic diversity. The epigenetic processes include DNA methylation, histone modifications, RNA-related regulation and chromatin changes, which are vital in the development, enhancement and treatment resistance of GBM. DNA repair is inhibited by the hypermethylation of the O6-Methylguanine-DNA-methyltransferase, therefore increasing sensitivity to Temozolomide (TMZ). A hypermethylated CpG phenotype is created by Isocitrate Dehydrogenase (IDH), which results in extensive transcriptional alterations. Dysregulated activity of histone-modifying enzymes such as EZH2 and HDACs supports the persistence of glioma stem cell populations, promoting tumor invasion and relapse. Additionally, non-coding RNAs and RNA methylation (m6A) contribute to oncogenic signalling and the maintenance of the tumor.

Reversing these epigenetic changes offers a hopeful treatment approach. Advancing studies on agents like DNMT inhibitors, HDAC inhibitors and MGMT modifying drugs are being conducted to re-

establish typical gene expression and combat chemoresistance. Even so, major challenges persist due to tumor heterogeneity and the emergence of adaptive resistance mechanisms. A deeper and more cohesive understanding of the GBM epigenetic landscape is expected to facilitate precise, multi-targeted therapeutic strategies that elevate patient response, extend survival, and reduce recurrence.

Keywords: DNA Methylation, Epigenetics, Glioblastoma, Histone Modification, Temozolomide Resistance.

ICABB26-BM-P20

Antioxidant Potential of Mushroom Polysaccharides in Attenuating Oxidative Stress, β-Cell Dysfunction, and Insulin Resistance

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Abstract

Diabetes mellitus is a systemic endocrine disorder indicated by hyperglycemia, hyperlipidemia and oxidative stress. Commercial medicines available for the treatment of diabetes can only manage the symptoms and they have adverse side effects with limited efficacy in preventing diabetic complications in the long terms. Hyperglycemia leads to arise in ROS and RNS species causing oxidative stress in the body. This results in cellular damage, insulin resistance, β-cell dysfunction, and the development of micro- and macrovascular complications in diabetes mellitus. Therefore, scientists are exploring natural sources for the treatment of diabetes. As a safe alternative, polysaccharides from the mushroom have been explored as they have multifunctional pharmacological properties with minimal side effects. β-D-glucans is known for antidiabetic and antioxidant effects by scavenging free radicals, protecting β cells, modulating insulin signaling pathways. Other important compounds from mushrooms are Lentinan, Schizophyllan, Grifolan, polysaccharopeptide, polysaccharide-K (Krestin). These bioactives of mushrooms activate insulin signaling pathways like GLUT-4, PI3K/Akt reduce inflammation, β cells damage and insulin resistance in the body. They also reduce hyperglycemia-induced ROS and normalize PPAR-γ, NF-κB, PKC, MAPK/JNK, polyol and AGE pathways. Major mushroom species known for such properties are: *Ganoderma spp., Pleurotus spp., Phellinus linteus, Grifola frondosa and Auricularia auricular,* having secondary metabolites resulting in neutralizing these pathways. The polysaccharides of mushroom activate autophagy which reduces β- cell stress and fat deposition, which increases insulin sensitivity promoting GLUT-4 translocation, inhibiting inflammatory cytokine production, and activating autophagy, thereby reducing fat deposition and protecting pancreatic β-cells. Mushroom polysaccharides exhibit strong antioxidant potential by reducing oxidative stress, protecting pancreatic β-cells, and improving insulin sensitivity through modulation of key signaling pathways, highlighting their promise as natural adjuncts for diabetes prevention and management. Present study is a systematic review exploring the antidiabetic potential of various mushrooms.

Keywords- Antioxidant activity, Insulin signaling pathway, Reactive oxygen species, Autophagy, β-D-glucans

ICABB26-BM-P21

Applications of Protein Structure Prediction in Biotechnology

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ABSTRACT

Understanding the three-dimensional structure of a protein is essential for understanding how it functions inside a cell and how it interacts with other biomolecules. Earlier, techniques like X-ray, crystallography and NMR spectroscopy were used to determine protein structures, but these methods are slow, expensive and not always successful for every protein. So, with the growth of computational biology, protein structure prediction has become an important and efficient alternative. Modern tools, especially deep-learning-based platforms such as AlphaFold, can predict protein structures with remarkable accuracy using only amino acid sequences. This advancement has transformed several areas of biotechnology. Protein structure prediction plays a major role in drug discovery, where understanding the shape of disease related proteins helps scientists design molecules that can bind to them effectively. It also supports enzyme engineering, allowing researchers to modify enzymes for improved stability, activity, or industrial use. In medical research predicted structures help identify how genetic mutations affect protein function, contributing to the study of genetic disorders. These tools are also used in vaccine development, where structural information assists in identifying suitable antigen targets. Additionally, protein structure prediction is valuable in synthetic biology, enabling the design of new proteins with novel functions. Overall, computational structure prediction reduces experimental workload, lowers research costs, and speeds up scientific progress. This review highlights how predictive tools are becoming an essential part of biotechnology and are reshaping the way researchers study proteins and develop new therapeutic and industrial applications.

Keywords: Protein structure prediction, AlphaFold, Computational biology, Biotechnology

ICABB26-BM-P22

Recombinant Therapeutic Proteins: Advances, Challenges, and Future Prospects in Biopharmaceutical Innovation

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ABSTRACT

Recombinant therapeutic proteins have revolutionized modern medicine by enabling the large-scale production of biologically active molecules through recombinant DNA technology, where the gene encoding the desired protein is inserted into an appropriate expression system such as Escherichia coli, yeast, mammalian, or insect cells. This technology has facilitated the development of life-saving therapeutics including insulin, growth hormones, monoclonal antibodies, and interferons with buffer-free formulations, which aim to reduce immunogenicity, improve tolerability, and simplify production. Recent advancements in host cell engineering, vector optimization, and purification technologies have significantly improved yield, stability, and post-translational modifications critical for therapeutic efficacy. Technologies such as Fc-fusion, PASylation, and XTENylation enhance stability without conventional buffers. Despite these achievements, challenges persist in terms of production cost, protein folding, and regulatory compliance. Emerging trends, such as the use of CRISPR-based genome editing, cell-free synthesis systems, and artificial intelligence-driven protein design, promise to enhance the

precision and efficiency of recombinant protein production. This presentation aims to provide an overview of the key methodologies, applications, and future directions of recombinant therapeutic proteins, highlighting their transformative impact on global healthcare and personalized medicine.

Keywords: Recombinant DNA technology, Therapeutic proteins, Biopharmaceuticals, Monoclonal antibodies, Buffer free formulations

ICABB26-BM-P24

Psychobiotics: Harnessing Gut Microbes to Support Mental Health Through Biotechnology

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Abstract

Mental health disorders such as anxiety, depression, and ADHD are increasing worldwide due to growing academic, social, and lifestyle pressures. This has created a strong demand for safe, natural, and effective therapeutic solutions. Recent studies have revealed a close link between the gut and the brain, suggesting that probiotics and prebiotics can influence emotional, cognitive, and neural functions. Psychobiotics—specific strains of beneficial gut microbes—offer a natural strategy to enhance emotional stability and mental resilience by reducing stress and regulating mood. These microbes act through gut–brain signalling mechanisms such as metabolite production, modulation of neurotransmitters, and immune regulation. Gut microbiota imbalance (dysbiosis) has also been linked to various neurological and neuropsychiatric conditions such as Alzheimer's disease, Parkinson's disease, ADHD, and depression. Certain species of *Lactobacillus, Bifidobacterium, Streptococcus, Escherichia,* and *Enterococcus* are known for their ability to modulate gut–brain signalling and contribute to improved mental health. Growing public interest in gut health has expanded opportunities for developing psychobiotic-based products including fortified yogurts, functional beverages, capsules, and synbiotic formulations. This study highlights the scientific basis and commercial potential of psychobiotics as innovative nutraceutical solutions for mental wellness, while also discussing challenges in product development, regulatory compliance, and market acceptance.

Keywords: Microbiota–Gut–Brain Axis, Psychobiotics, Probiotics, Neuroactive Compounds, Cognitive Wellness, Nutraceuticals

ICABB26-BM-P25

Decellularized scaffolds as ECM in Regenerative Medicine

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ABSTRACT

The increasing need for organ transplantation and the unavailability of organ samples from donors resulted in major breakthroughs in the field of tissue engineering and regenerative medicine. Decellularized scaffolds are seen as a notable breakthrough in the text of tissue engineering. It will aid in the development of functional tissues and organs in-vitro, in a 3D environment. It resembles the natural ECM of the tissue, offering mechanical support, as well as biochemical stimulation, necessary for cell adhesion, growth, differentiation, nutrition, and biochemical signaling. This paper covers a full review of classifications in scaffolds, materials in scaffolds, requirements in design, and their use in the transplantation of bioengineered organs based on their biocompatibility, mechanical strength,

degradation rate, and clinical use. Static and dynamic methods in scaffold culture, involving bioreactors, are also described. The advent of new technologies involving bioprinting in three dimensions, nanofibers, and the fabrication of personalized scaffolds is also covered. Although there is substantial progress, there is still a need in the areas of vascularization, integration, and translation on a massive scale. Innovation in both biomaterials, designs, and cellular technology will aid in the rapid translation of organ transplantation using scaffolds from experimental to clinical systems. A recent study of bone tissue regeneration using plant-based scaffolds is also discussed.

Keywords: Tissue engineering; Biomaterial scaffolds; Organ transplantation; Regenerative medicine; 3D bioprinting

ICABB26-BM-P27

SARS-CoV-2 to Long COVID: Mechanistic Insights and Emerging Therapeutic Strategies

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Abstract

Severe Acute Respiratory Syndrome Coronavirus 2, the causative agent of COVID-19, has triggered a global health burden that extends well beyond acute infection. Recent research although showed reduction in COVID 19 mortality, however serious long-term effects of the disease such as fatigue, muscles or joints pain, breathlessness, headaches, brain-fog etc affect COVID-19 affected person's ability to work and perform his daily activities. These long persisting symptoms are collectively termed Long COVID conditions. It is now clear that even after viral clearance, antigen persistence in some patients can contribute to ongoing clinical symptoms. Global data suggest that roughly 6 out of every 100 individuals infected with COVID-19 develop this condition. Several overlapping mechanisms have been implicated in the physiology of Long COVID, including but not limited to persistent viral reservoirs, immune dysregulation, autoantibody production, endothelial dysfunction with microthrombosis, mitochondrial impairment, neuroinflammation. These pathways contribute to a wide clinical spectrum, including fatigue, dyspnea, cardiometabolic disturbances, neurocognitive impairments, and autonomic dysfunction. Thus, creating a considerable global healthcare and socioeconomic burden. Therapeutically, antivirals, and immunomodulators have improved acute outcomes, but effective and targeted treatments for Long COVID are limited because of the complex nature of the disease involving host factors. Therefore, it is believed that better mechanistic understanding and biomarker-guided interventions will be critical to reducing the long-term global burden and improving quality of life among COVID-19 survivors. This review summarizes the current state of knowledge on the mechanisms driving progression from acute SARS-CoV-2 infection to Long COVID, as well as ongoing treatments, toward development of optimal clinical care in affected patients.

Keywords: Antigen persistence; Biomarkers; COVID-19; Long COVID; SARS-CoV-2; Therapeutic strategies

ICABB26-BM-P28

Redefining Implants and Healing Through Biopolymer-Driven 3D Bioprinting

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Abstract

3D bioprinting is transforming healthcare by providing the on-demand fabrication, healthcare devices, and scaffolds that traditional materials currently used can't provide. Standard metals and plastics used in implants and wound dressings often lack precise structural fit, show short-term biocompatibility, and contribute to continuous medical waste, creating the need for biodegradable, customized solutions. Natural and synthetic biopolymers such as alginate, chitosan, gelatin, collagen, PLA, PCL, PHA, and hydrogel systems fill this gap by combining biocompatibility with customizable mechanical and degradation properties while supporting cell adhesion, proliferation, and extracellular matrix formation. When formulated as printable bioinks or filaments and processed through extrusion-based 3D printing and bioprinting, these materials can be shaped into highly porous, architecturally controlled constructs that match patient-specific geometry and functional requirements.

Compared with traditional materials, these platforms allow greater personalization, better tissue integration, and may also lower environmental impact. The cost and printability of advanced bioinks, achieving sterilization without damaging bioactivity, and navigating regulatory approval remain major challenges, but ongoing progress in multifunctional, cell-laden bioinks and smart, responsive constructs makes 3D-printed biopolymers a central technology for shaping the future of regenerative and personalized medicine.

Keywords: 3D bioprinting, biopolymers, Chitosan, Hydrogels, Alginate.

ICABB26-BM-P29

Differential Diagnosis of Differential Sexual Disorder using Genetics Tools.

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ABSTRACT

Ambiguity in genitalia is a rare phenotypic presentation of the genitourinary system that requires immediate attention to evaluate life-threatening disorders like DSD (Differential Sexual Disorder) and determine sex assignment. Therefore, promptly identifying the underlying cause when ambiguity is observed is highly important. This study aimed to investigate the origins and characteristics of ambiguous genitalia in newborns. Biochemical, cytogenetic, and molecular assessments were performed in this study. A total of 100 cases were evaluated for DSD through biochemical analysis. GTG karyotyping was used for cytogenetic analysis. The patients were further tested for Y chromosomal loci (SRY) using Polymerase Chain Reaction (PCR). Additionally, PCR and sequencing-based assays were conducted on one case with DSD to analyze CYP21A2 gene mutations. All 100 cases were successfully screened. Biochemical testing for 17-OH progesterone identified 4 patients positive for DSD. Cytogenetic analysis showed that, out of the 100 cases, 4 (4%) exhibited mosaicism, while the remaining 96 (96%) had a 46, XX or 46, XY karyotype. Six cases (6%) carried a Y chromosome (46, XY) but were phenotypically female, and five cases (5%) had a female karyotype (46, XX) but were phenotypically male. Among the 11 sex-reversed cases, 7 tested positives for the SRY gene. In cases of children suspected of having chromosomal anomalies, molecular cytogenetic assessments can provide valuable insights into the genetic basis of sexual ambiguity. This information can help resolve the issue swiftly and facilitate effective genetic counseling.

Keywords: Ambiguous genitalia, SRY gene, karyotype, DSD

ICABB26-BM-P30

Biogeographical Blueprints Matter in Designing Precision Microbiome Therapies

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Abstract:

Human gut microbiome composition varies widely across populations due to geography, diet, ethnicity, urbanization and environmental exposures. High-fiber traditional diets promote diverse microbiota enriched in Prevotella, whereas industrialized, low-fiber diets reduce diversity with dominance of Bacteroides and Firmicutes. These environmental factors often outweigh host genetics, challenging the notion of a universal “healthy” microbiome and highlighting the need for region-specific baselines and interventions. This study examines how geographic, ethnic, and lifestyle factors shape microbiome variation and their implications for developing effective microbiome-based therapeutics. The aim is to design probiotics, fecal microbiota transplantation (FMT) strategies and live biotherapeutic products (LBPs) aligned with population-specific microbial profiles to improve clinical efficacy and reproducibility. A comparative review of literature on global microbiome variation, IBD cohorts and microbiota targeted trials was conducted. Analysis emphasized regional microbial composition, donor–recipient engraftment, probiotic strain variability and ethnicity-linked dysbiosis patterns relevant for product formulation. In Inflammatory bowel disease (IBD) patients, gut microbial diversity was found

to influence drug absorption and therapeutic responses. Regional microbiome differences and donor–recipient compatibility are reported to impact outcomes of probiotics, FMT and LBPs. Though IBD shows global patterns—loss of butyrate producers and enrichment of pathobionts—regional distinctions persist among different ehtenic groups having diverse food culture. Most microbiome-based products originate from Western datasets; they may not translate effectively across diverse global populations. Tailoring formulations to regional microbiome characteristics and incorporating native donor profiles can enhance the global success of probiotics, FMT and LBPs. This work positions microbiome variation as a central parameter for designing precision, population-specific microbiome therapeutics. Incorporating geographic and ethnically diverse microbiome data into product pipelines will enable next-generation, population-tailored microbiome therapeutics with improved efficacy and regulatory robustness.

Keywords: Next-Generation Biotheraputics, Gut Microbiome, Microbiome Diversity, Gut Dysbiosis

ICABB26-BM-P31

Advances in Skin Anti-Aging: Mechanisms and Multilevel Intervention Strategies

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Abstract

Skin, the body's largest organ stretching roughly 1.5 to 2 m2 acts as our frontline defense against the outside world. Its ability to renew cells, maintain a strong barrier, and regulate immune activity is essential for keeping it healthy. Over time, however, these functions gradually decline. Cells age, the epidermis turns over more slowly, the dermal matrix weakens, and both blood flow and immune responsiveness deteriorate. These internal changes eventually show up on the surface as dryness, uneven texture, reduced elasticity, pigmentation issues, and wrinkles. Beneath those visible signs lie deeper shifts, including slower barrier repair, increased inflammation, and greater vulnerability to environmental damage. Recent research has moved past traditional anti-aging methods to explore more holistic strategies that target both cellular aging and the skin's microbiome. Studies show that as skin ages, its microbial balance changes, beneficial metabolites decrease, and low-grade, chronic inflammation becomes more common. These shifts can further disrupt the barrier, elevate oxidative stress, and interfere with collagen maintenance. Within this evolving field, postbiotics, the non-living microbial components and their bioactive substances have emerged as a promising next-generation approach. These preparations contain metabolites such as organic acids, peptides, polysaccharides, and cell-wall fragments that offer antioxidant, barrier-supporting, anti-inflammatory, and reparative benefits. They help boost hydration, support lipid production, balance pH, modulate immune responses, and slow the breakdown of structural proteins. Because they contain no live organisms, postbiotics are more stable, safer, and easier to formulate than probiotics.

Keywords: Skin Anti-Aging, anti-inflammatory, probiotics

ICABB26-BM-P32

Harnessing Probiotics and Postbiotics for Skin Microbiome Restoration: A Modern Biocosmetic Strategy

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Abstract

Maintaining immunological balance, barrier integrity, and general skin health depend on the complex and dynamic ecology known as the skin microbiome. Dysbiosis within this microbial community has been linked to inflammation, acne, eczema, and early aging, which has sparked interest in microbiome-focused biocosmetic treatments. Probiotic and postbiotic-based skincare have emerged as a promising strategy to restore microbial homeostasis through anti-inflammatory activity, competitive inhibition of pathogens, and enhancement of the skin barrier. This review highlights recent advancements in the use of probiotics—live beneficial microorganisms—and postbiotics—non-viable microbial components and metabolites—in dermatological and cosmetic formulations. Research demonstrates that applying strains like Lactobacillus and Cutibacterium topically can alter the skin microbiota, lessen inflammation, and enhance therapeutic results. Research interest in probiotic skincare is also rapidly increasing, according to global bibliometric trends. Additional advantages of postbiotics include increased formulation stability, enhanced safety, and multifunctional properties like antibacterial, antioxidant, and barrier-repair effects. Bacterial consortia, parabiotics, and metabolite-rich extracts are examples of emerging therapeutic approaches that show promise in treating inflammatory diseases and skin infections. Technological innovations including encapsulation and controlled-release systems further enhance the delivery and efficacy of microbial components. Overall, probiotic and postbiotic skincare represents a sustainable and scientifically grounded approach for restoring microbial balance and maintaining healthy skin. However, the successful integration of microbiome-based cosmetics into consumer skincare will rely on addressing regulatory challenges and establishing standardized clinical validation. The present review, targeted probiotic and postbiotic treatments can positively alter the skin microbiota; however further mechanistic research is essential to optimize targeted probiotic and postbiotic treatments for routine dermatological and cosmetic use.

Keywords: Biocosmetics; Probiotics; Postbiotics; Skin microbiome; Skin barrier function

ICABB26-BM-P33

Synaptic Neurokinase Signalling Transduction Linked Dysregulation of Tau in Neurodegenerative Disorders (NDDs)

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ABSTRACT

Neurodegenerative disorders (NDDs), particularly Alzheimer's disease, are increasingly recognised as conditions driven by dysregulated synaptic Neurokinase signalling rather than solely by protein aggregation. Emerging evidence indicates that chronic activation of stress-responsive pathways slowly impairs neuronal communication and circuit integrity. The main trigger is the p38 mitogen-activated protein kinase (p38 MAPK) axis. Typically, p38 signalling supports synaptic plasticity and cellular

stress responses; however, sustained activation—especially of the p38α isoform—causes pathological Tau hyperphosphorylation, neuroinflammation, excitotoxicity, and ultimately neuronal loss. Conversely, another subtype, p38γ, seems to provide neuroprotection, particularly against amyloid-β toxicity, and decreased activity of this isoform has been linked to cognitive decline, underscoring the complex, isoform-specific nature of p38 signalling. This dysregulation is further compounded by pathological crosstalk with other kinase pathways. JNK activation under oxidative and inflammatory stress promotes apoptosis and Tau phosphorylation, while MARK diminishes Tau's interactions with microtubules, increasing its tendency to aggregate. Altered ERK signalling contributes to abnormal phosphorylation patterns and neuronal hyperexcitability early in disease progression. Collectively, these kinase pathways form a convergent feed-forward network that sustains Tau dysregulation and accelerates synaptic degeneration. Recent discoveries also implicate abnormal Tau glycosylation in controlling kinase access and fostering inflammation, possibly facilitating the prion-like spread of Tau across neural networks.

Despite extensive therapeutic exploration of these pathways, clinical translation has been limited by poor selectivity, insufficient brain penetration, and intervention at late disease stages. Consequently, current research is shifting towards precision modulation strategies, such as isoform-specific targeting, disrupting pathological kinase–Tau interactions, refining glycan-regulated signalling, and employing biomarker-guided delivery systems. Selectively inhibiting pathogenic kinase pathways while enhancing protective signalling may provide a promising approach to preserving synaptic resilience and slowing neurodegeneration.

Keywords: Tau hyperphosphorylation; Alzheimer's disease; Glycan-mediated regulation; Synaptic dysfunction; Neuroinflammation; Amyloid-β toxicity; Kinase modulation.

ICABB26-BM-P34

RNA Therapeutics in Skin Cancer: Emerging Strategies, Challenges, and Future Perspectives

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ABSTRACT

Skin cancer is one of the most frequently diagnosed malignant diseases worldwide and represents a significant public health challenge. A comprehensive understanding of its natural history is essential for the development of effective preventive and therapeutic strategies. The skin, being the largest and most accessible organ of the human body, offers unique advantages for localized and targeted drug delivery, making it an attractive platform for innovative therapeutic interventions.

Current therapeutic strategies for skin cancer include surgery, radiotherapy, topical treatments, cryotherapy, chemotherapy, and systemic options such as immunotherapy and targeted therapy for advanced disease. However, these modalities are often limited by tumour recurrence, development of drug resistance, immune-related adverse effects, and challenges associated with effective drug delivery to deeper skin layers. These limitations highlight the urgent need for less invasive, more precise, and durable treatment strategies.

Although ribonucleic acid (RNA)–based therapeutics have been investigated for several decades, recent advances in molecular biology, chemical modification, and delivery technologies have enabled their emergence as clinically viable treatment modalities. RNA therapeutics offer several advantages, including high target specificity, the ability to modulate previously undruggable molecular pathways, reduced systemic toxicity, and the potential for multiplexed targeting within a single therapeutic platform. These features make RNA-based approaches particularly promising for dermatological applications, including skin cancer.

This review systematically examines emerging RNA-based therapeutic approaches for skin cancer, including RNA interference, antisense oligonucleotides, and messenger RNA–based therapies. Additionally, it discusses key biological, technological, and translational challenges and explores strategies to overcome barriers to clinical implementation. Overall, RNA therapeutics represent a promising and transformative platform for advancing skin cancer treatment and improving dermatological care.

KEYWORDS: Skin cancer; RNA therapeutics; RNA interference; Antisense oligonucleotides; Messenger RNA; Dermatological drug delivery; Targeted therapy; Molecular dermatology

ICABB26-BM-P35

Role Of Medicinal Plants Against Non-Alcoholic Fatty Liver Disease in Teenagers

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Abstract

Prevalence rates of non-alcoholic fatty liver disease (NAFLD), the most prevalent chronic liver disease in children and adolescents, are rising in tandem with the global obesity epidemic. NAFLD is a liver disease that also serves as a measure of greater cardio metabolic risk in teenagers since it is closely linked to insulin resistance, dyslipidaemia, and elements of the metabolic syndrome. According to epidemiological research, prevalence estimates vary significantly by location, ranging from 7–10 % in the general paediatric population to over 30% among teenagers who are obese. Notably, disease susceptibility is influenced by sex, ethnicity, and genetic predisposition (e.g., PNPLA3 polymorphisms), with Asian and Hispanic teenagers exhibiting greater rates than their African American and Caucasian counter parts. Early identification of epidemiological patterns is essential because of its stealthy progression and propensity to develop into cirrhosis, non-alcoholic steatohepatitis (NASH), and even hepatocellular cancer in later life. To stop the increased prevalence of NAFLD among teenagers worldwide, it is imperative to strengthen monitoring systems, standardize diagnostic procedures, and put preventive measures centered on lifestyle change into action. Herbal interventions such as *Astragalus membranaceus* (Astragalus) – supports liver repair and helps liver to adapt to stress, *Vitis vinifera Linn* (Draksha) – detoxifying effects on liver and improves liver function, *Embelia ribes* (Vidanga) – lowering down lipid levels and antioxidant properties , *Silybum marianum* (milk thistle) – reduces hepatic inflammatory and reduces steatosis and insulin resistance , *Camellia sinensis* (green tea extract) – insulin resistance, reduces AST and ALT levels , antioxidant and anti-inflammatory , and *Curcuma longa* (turmeric) – powerful antioxidant , anti-inflammatory and helps in insulin resistance , show promising hepato protective effects through antioxidant, anti-inflammatory, lipid-lowering, and detoxifying actions. These herbs may complement lifestyle-based prevention by improving liver function, reducing steatosis, and supporting metabolic balance in adolescents at risk of NAFLD.

Keywords: Non-alcoholic fatty liver disease, Teenagers, Epidemiology, Obesity, Metabolic syndrome

ICABB26-BM-P36

A Natural Anti-Virulence Approach Against MRSA Using *Dregea volubilis*

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Abstract

Antimicrobial resistance is one of the major global health concerns, including Methicillin-Resistant *Staphylococcus aureus* (MRSA) representing a major threat due to its multi drug resistance and high virulence. Two-Component Systems, particularly HssRS and SaeRS, play crucial roles in regulating MRSA virulence and adapting to hostile environment, making them as promising targets for ant virulence therapy. To explore plant

based alternatives, we virtually screened ~17,000 phytocompounds from the IMPPAT 2.0 database against HssR and SaeS using molecular docking and molecular dynamics simulations. Several phytocompounds showed stable binding and strong interaction profiles with both target proteins. To experimentally validate the *in-silico* predictions, methanolic extract of *Dregea volubilis* was tested against the MRSA *COL* strain and saeS mutant (ΔsaeS). The extract exhibited reduced inhibitory activity in ΔsaeS compared to the wild type in both Well diffusion assay and Broth Microdilution assays, indicating the possible involvement of SaeS related pathways. However, no significant effect was observed on pre-formed biofilms. These findings suggest that phytocompounds from *D. volubilis* may interfere with MRSA virulence regulation rather than directly exhibiting bactericidal effects. Further studies with *hssR* mutant are required to precisely validate in-vivo molecular target. Overall, this study emphasizes the potential of traditional medicinal plants as valuable sources for developing novel, plant derived anti-virulence approaches to combat AMR.

Keywords: Antimicrobial Resistance, *S. aureus,* Two-Component System (TCS), Phytocompounds, *Dregea volubilis*

ICABB26-BM-P37

Advances in Hemophilia a Therapy: The Development and Impact of Efanesoctocog Alfa

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Abstract:

Hemophilia A is an X-linked recessive hemorrhagic disorder caused by the dysfunction or deficiency of coagulation factor VIII (FVIII), a key protein that forms the tenase complex which is required for conversion of factor X to Xa during blood clot formation. Recombinant FVIII was developed to address these limitations of plasma derived FVIII, which eliminates risks of viral transmission, batch variability and inconsistent supply. But conventional recombinant FVIII products produced in Chinese Hamster Ovary (CHO) cells have clinical utility limited by a short half-life due to dependence on von Willebrand factor (VWF) and also the development of neutralizing antibodies reduces therapeutic effectiveness. Recent advances have led to the development of ultra-extended half-life recombinant FVIII, most notably efanesoctocog alfa, which represents a major breakthrough. A novel CHO-derived FVIII is engineered incorporating Fc-portion, XTEN polypeptides chains and the VWFD 'D3 domain. These modifications eliminate the dependency of binding of VWF which led to the prolonged circulation time. This new design, efanesoctocog alfa, supports once weekly dosing while FVIII level remains maintained, which offers better blood loss prevention and reduced treatment burden.

Keywords: Hemophilia A; recombinant factor VIII; extended half-life; efanesoctocog alfa; VWF-independent design

ICABB26-BM-P38

Mycobacterium Tuberculosis Interface with Host Macrophages- An Update on Interaction and Molecular Perturbations

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Abstract

Tuberculosis (TB) caused by the bacterial pathogen *Mycobacterium tuberculosis* (Mtb) is one of the worst infectious illnesses, with over a billion deaths in the last 200 years. The barriers that make tuberculosis difficult to treat and eliminate are inextricably tied to Mtb's intracellular habitat. However, researchers do not fully understand how Mtb survives within the human host or how certain cells can remove this devastating disease. The lungs are affected by this airborne infection, which interacts with macrophages. It is a crucial stage in Mtb infection because macrophages present in the lungs are the first cells of the immune system that Mtb interacts with in the host. Thus, it is relevant to understand the insights related to the interactions between Mtb effectors and macrophages. In the present review, we highlighted the interactions between Mtb effectors and macrophages. We additionally explored and discussed how Mtb manipulates the defense mechanisms of macrophages to survive and the ability of macrophages to govern and destroy Mtb. The processes mentioned in the review explain the control and elimination of Mtb through a variety of mechanisms, including autophagy, apoptosis, inflammasome stimulation, ncRNA activity, phagosomal pH imbalances, and the production of antimicrobial chemicals. However, these difficult conditions reveal Mtb's limitations in its capacity to manage and make use of them for survival. The discrepancy in Mtb-macrophage crosstalks, where macrophages fail to successfully manage Mtb infection, supported by the expanding discovery of Mtb egress mechanisms, should be the key problem in TB control. These insights offer important clues related to the pathways and events providing information essential for TB diagnosis, treatment and prevention.

Keywords: Tuberculosis, *Mycobacterium tuberculosis*, macrophages, Mtb effectors, Mtb-macrophages interaction

ICABB26-BM-P39

Significance of Physiological & Metabolic Characterisation of Medicinally Important Mushrooms

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Abstract

Medicinally important mushrooms constitute a significant source of biologically active metabolites with well-established therapeutic and nutraceutical importance. A critical evaluation of the available scientific literature indicates that the medicinal value of these mushrooms is closely associated with their physiological characteristics and metabolic efficiency. Physiological characterization involves the assessment of mycelial growth kinetics, biomass productivity, substrate utilization efficiency, and physiological responses to environmental parameters such as temperature, pH, moisture, aeration, and nutrient availability, all of which play a decisive role in regulating fungal metabolism. Numerous studies

have demonstrated that optimization of these physiological factors markedly enhances the biosynthesis and accumulation of primary and secondary metabolites, including polysaccharides, proteins, free amino acids, phenolic compounds, and antioxidant molecules, which are responsible for immunomodulatory, anticancer, antimicrobial, and anti-inflammatory activities. Literature further suggests that variations in culture media composition, particularly carbon and nitrogen sources, induce significant physiological and metabolic changes, leading to qualitative and quantitative differences in bioactive compound profiles. Physiological characterization has therefore been widely recognized as a fundamental approach for the standardization of cultivation practices and for ensuring reproducibility and consistency in medicinal quality. Despite extensive research on the pharmacological properties of individual mushroom species, comprehensive and comparative physiological studies under controlled experimental conditions remain relatively limited. Based on the reviewed literature, systematic physiological characterization is essential to establish a clear correlation between growth behaviour, metabolic regulation, and therapeutic potential. Such an understanding is crucial for optimizing large-scale cultivation strategies, enhancing bioactive compound yield, and promoting the sustainable utilization of medicinal mushrooms in pharmaceutical and nutraceutical industries.

Keywords: Medicinal mushrooms, Physiological characterization, Mycelial growth, Bioactive metabolites, Polysaccharides, Therapeutic potential

ICABB26-BM-P40

The Role of Tumor Microenvironment in Cancer Therapeutics: Analysis of Clinical Status, Challenges, and Synergistic Combination Strategies

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ABSTRACT

The technology of advanced cancer therapeutics has rapidly evolved with the emergence of immunotherapy, anti-angiogenic agents, cellular therapy, and oncolytic virotherapy, yet treatment outcomes remain heavily constrained by the complex and immunosuppressive tumor microenvironment (TME). This study highlights the integrated analysis of the translational potential and mechanistic challenge of major therapeutic classes, emphasizing the TME as the central determinant of therapeutic resistance. The review examines immune checkpoint inhibitors, anti-angiogenic and vascular normalization therapies, CAR-T and other cellular therapies with a specific focus on resistance mechanisms such as hypoxia, stromal barriers and metabolic suppression. A comprehensive evaluation of next-generation innovations, including bispecific antibodies and allogeneic CAR-T are emerging strategies capable of overcoming TME-driven therapy failure. The work further outlines rational, mechanism-driven synergistic combinations such as ICI+AAT, OV+ICI, and CAR-T+TME modulators, which collectively target priming, conditioning, and cytotoxic phases of the cancer-immunity cycle. Targeting universal immunosuppressive pathways, including the adenosinergic axis, TGF-β signalling, and myeloid-mediated suppression, is identified as essential for future therapeutic success. This review underscores the need for multimodal combination therapies, TME-informed therapeutic design to achieve durable and broadly effective outcomes in advanced solid and haematological malignancies.

Keywords: TME; Checkpoint Inhibitors; Anti-Angiogenic Therapy; Normalization Therapy; CAR-T Therapy, Combinational Therapies; Adenosynergic Axis.

ICABB26-BM-P41

Strictinin–ROR1 Kringle Binding Dynamics: An *In-Silico* Study for Cancer Therapy

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ABSTRACT

Receptor tyrosine kinase-like orphan receptor 1 (ROR1) is an oncofetal surface protein aberrantly re expressed in multiple malignancies, including breast, lung, ovarian, hematologic, and gastrointestinal cancers. Its negligible expression in normal adult tissues and its essential roles in tumor cell survival, epithelial–mesenchymal transition, metastasis, and therapy resistance make ROR1 a highly selective target for cancer therapy. Within its extracellular architecture, the Kringle domain contributes to receptor stability, ligand recognition, and initiation of downstream signalling. Strictinin, an ellagitannin, has been reported to suppress ROR1-mediated PI3K/AKT/GSK3β signalling in vitro, but its structural mode of binding to ROR1 has not been elucidated.

This study investigates the binding dynamics of Strictinin to the ROR1 Kringle domain using structure based in-silico approaches. Using molecular docking followed by molecular dynamics simulations, this work defines the interaction profile and stability of the Strictinin–ROR1 Kringle complex. The dynamic behaviour of the complex supports the feasibility of extracellular inhibition of ROR1. Overall, the findings provide mechanistic insight into Strictinin's anticancer potential and position ellagitannins as promising natural scaffolds for ROR1-directed cancer therapeutics.

Keywords: Cancer, Oncofetal Antigen, ROR1, Kringle Domain, Strictinin

ICABB26-BM-P42

Pesticide Exposure & Its Adverse Effects on Female Reproductive Health

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Abstract

Pesticides are pervasive environmental contaminants that pose significant risks to female reproductive health. Exposure to diverse pesticide classes, including organochlorines, organophosphates, pyrethroids, and emerging insecticides, has been increasingly associated with adverse reproductive outcomes. Biomonitoring studies frequently detect multiple pesticide residues in human biofluids, underscoring the complexity and cumulative nature of real-world exposures. These compounds act as endocrine-disrupting chemicals, interfering with hormone synthesis, signalling, and receptor function, thereby disrupting the hypothalamic–pituitary–ovarian axis. Mechanistically, pesticide exposure induces oxidative stress, inflammation, and genotoxic effects in ovarian and endometrial tissues. Epidemiological and experimental evidence links pesticide exposure to menstrual irregularities, prolonged time to conception, reduced fecundability, spontaneous abortion, intrauterine growth restriction, gestational hypertension, premature ovarian insufficiency, early menopause, polycystic ovary syndrome, and diminished ovarian reserve. Collectively, these disruptions impair folliculogenesis, oocyte quality, and embryo implantation, ultimately compromising fertility and pregnancy outcomes. This review highlights the substantial impact of pesticide exposure on the female reproductive lifespan and emphasizes the urgent need for stricter regulatory policies and further mechanistic and longitudinal research to better understand and mitigate these risks.

Keywords: Pesticides; Female reproductive health; Endocrine-disrupting chemicals; Ovarian function; Oxidative stress; Environmental exposure

ICABB26-BM-P43

Pro-oxidant Phytocompounds and Mitochondrial Vulnerabilities: A Novel Paradigm in Cancer Therapy

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ABSTRACT

Cancer continues to be a major global health burden, with conventional treatments such as surgery, chemotherapy, and radiation therapy often limited by systemic toxicity, drug resistance, and invasive procedures. These challenges necessitate the exploration of innovative therapeutic approaches that selectively target cancer cells while minimizing harm to normal tissues.

Natural phytocompounds with intrinsic pro-oxidant properties have gained increasing attention as promising anticancer agents. Cancer cells, characterized by high metabolic activity and mitochondrial dysfunction, exist in a state of persistent oxidative stress. This altered redox homeostasis makes them particularly susceptible to further elevations in reactive oxygen species (ROS). By driving ROS levels beyond the cellular threshold, pro-oxidant phytocompounds can selectively induce mitochondrial damage, disrupt energy metabolism, and activate apoptotic pathways, leading to cancer cell death while sparing healthy cells.

Emerging evidence highlights a diverse range of plant-derived compounds—including polyphenols, terpenes, and alkaloids—that exert pro-oxidant activity through mechanisms such as mitochondrial membrane depolarization, inhibition of antioxidant defense systems, and modulation of redox-sensitive signalling pathways. However, challenges remain in optimizing their specificity, bioavailability, and delivery mechanisms.

This review discusses the therapeutic potential of natural pro-oxidant phytocompounds in targeting mitochondrial vulnerabilities of cancer cells, their underlying mechanisms of action, and the hurdles that must be addressed for successful clinical translation. Harnessing these agents may pave the way for safer and more effective cancer treatments that exploit the intrinsic weaknesses of tumor bioenergetics.

Keywords: *Proxidants, Oxidative stress, Reactive Oxygen Species, Mitochondrial membrane depolarisation*

ICABB26-BM-P44

Tumor microenvironment in anti-cancer therapy: a new weapon or a blind spot

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Abstract

The tumor microenvironment (TME) has become a vital focus in cancer biology, impacting tumor initiation, progression, metastasis, and response to therapy. The TME is not simply passive scaffolding; it consists of a heterogeneous array of stromal cells, immune infiltrate, vasculature, extracellular matrix, and metabolic cues, and it stores, exchanges, and modulates signals and responses to malignant cells. This complexity provides an interesting duality: TME induced immunosuppression, drug resistance,

and metabolic reprogramming can be barriers to therapy; however, the TME may contain new therapeutic entry points. The TME has many targets for therapeutic TMEs that have evolved in the last few years (immunotherapy, nanomedicine, stromal reprogramming, vascular normalization, and metabolic targeting) to change the TME from a "blind spot" to a "weapon" in the fight against cancer. However, clinical implementation is complicated by cellular heterogeneity, context-dependent effects, and treatment-related toxicities. New technologies and experimental methodologies, such as spatial transcriptomics, single-cell profiling, and TME-based biomarkers, are driving the emergence of precision strategies. This review describes the promise and pitfalls associated with therapeutic targeting of the TME and traditional approaches to targeting tumors. We advocate for dynamic, integrative strategies to establish when the TME is a valuable ally and should remain a part of the anti-cancer therapy, and when it remains an obstacle.

Keywords: Tumour microenvironment (TME); cancer therapy; immunotherapy resistance; cancer-associated fibroblasts (CAFs); extracellular matrix (ECM); vascular normalization; tumour metabolism; nanomedicine; spatial biology; biomarkers; therapeutic targeting; tumour immunology.

ICABB26-BM-P45

Flexible Wearable Patch for Real-Time Sweat Creatinine and Uric Acid Analysis

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Abstract

A major breakthrough in the life sciences is represented by wearable biosensor devices that may provide quantitative assessment and real-time monitoring of human health indicators. Impaired filtration of metabolic waste products including uric acid and creatinine is a hallmark of chronic kidney disease (CKD), a degenerative and progressive condition. The majority of conventional diagnostic techniques rely on intrusive, sporadic blood sampling, which restricts ongoing evaluation of renal function and postpones early detection. However, early detection is essential to avoiding permanent CKD consequences. The promise for real-time, non-invasive monitoring of clinically significant indicators utilising easily accessible biofluids like sweat is highlighted bby recent advancements in wearable biosensing devices. In order to screen for kidney illness early on, this study investigates the suitability of flexible, skin-adherent wearable biosensor patches for the simultaneous detection of uric acid and creatinine in human sweat. In terms of user comfort, mechanical stability, and skin compatibility important design factors are covered, such as the incorporation of enzyme-based and non-enzymatic electrochemical sensing elements on soft, flexible substrates. Additionally, investigated is the function of microfluidic sweat-handling channels in regulated sample collection, decreased contamination, and enhanced analytical dependability. The main drawbacks of current wearable platforms are addressed by electrochemical detection techniques, which are highlighted for their high sensitivity, selectivity, quick response, and applicability for small sample volumes. Additionally, the integration of wireless communication and low-power electronics into an Internet-of-Medical-Things (IoMT) framework is emphasised as a way to facilitate real-time data transmission to cloud-based systems or smartphones. All things considered, wearable sweat-based biosensing devices present a viable route towards decentralised, individualised, and preventive kidney health monitoring by continuously monitoring uric acid and creatinine levels.

Keywords: Wearable biosensor, Sweat analysis, Creatinine, Uric acid, kidney disease monitoring.

ICABB26-BM-P46

Therapeutic Role of Probiotics in Autism Spectrum Disorder

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Abstract

Autism Spectrum Disorder (ASD) is a neurodevelopmental disorder characterized by repetitive behavior, impaired social responsiveness and varying degrees of intellectual disability. In addition to neurological features, many patients experience gastrointestinal complications, often referred to as autistic enterocolitis. This condition is marked by constipation, flatulence, bloating, and other gastrointestinal abnormalities. These manifestations have been associated with alterations in the composition and diversity of the gut microbiome, commonly described as dysbiosis. This dysbiosis further affects the neuroendocrine system, neuroimmune system, central nervous system and hypothalamic pituitary axis via the bidirectional gut brain network thereby amplifying the symptoms of autism. Along with several mainstream treatments of autism such as occupational therapy and applied behaviour analysis, various adjunct therapies have emerged in the last few decades. One such therapy is the supplementation of probiotics for management of autism which confer health benefits by reforming the gut microbiome and modulating the gut-brain axis. Several placebo-controlled studies suggest that probiotic administration over a duration of period with strains such as Lactobacillus, Bifidobacterium, Streptococcus, and others, result in improvement in social responsiveness of the patients, reduced irritability, lethargy, hyperactivity and gastrointestinal symptoms such as diarrhea, constipation and abdominal pain. By restoring the microbial balance and improving gut health, probiotics can favourably influence the gut-brain axis, thereby bringing about marked improvements not only in gastrointestinal but also in behavioural symptoms. These findings support the potential use of microbiome-based interventions as part of holistic management in ASD, although large-scale, placebo-controlled trials are needed to validate these findings and unravel the underlying mechanisms.

Keywords- dysbiosis, gut brain axis, probiotics, autism.

ICABB26-BM-P47

Closed-Loop Bio-Neural Control (CLBNC) for Adaptive Neurorehabilitation: A Novel Paradigm for Neurological Disorders with Impaired Neural Structure

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ABSTRACT

Closed-loop bio-neural control (CLBNC) is a neurorehabilitation control strategy in which biological signals such as neural activity, muscle responses, and movement-related feedback are continuously monitored and integrated to dynamically modulate stimulation or assistive control in real time. Conventional paralysis treatment technologies, including physiotherapy-based rehabilitation, passive orthotic support, functional electrical stimulation (FES), robotic-assisted therapy, spinal or peripheral nerve stimulation, and brain–computer interface (BCI)-based systems, largely rely on open-loop or pre-programmed control strategies. As a result, these techniques fail to accurately mimic the feedback-driven function of the human nervous system, which leads to limited motor coordination, limited flexibility, limited customization, and an early start of muscle fatigue.

These limitations are addressed by CLBNC through the integration of real-time biological feedback into adaptive control loops that continuously adjust stimulation parameters according to the patient's neural and muscular state. This individualized, task-specific modulation of stimulation and assistive forces leads to improved movement accuracy, enhanced neuromuscular efficiency, and a reduction in non-physiological motor patterns that are frequently associated with static stimulation systems. CLBNC-based therapies are particularly useful for neurological conditions like hemiplegia, paraplegia, stroke-induced paralysis, and incomplete spinal cord damage where neuronal pathways are impaired but not completely disrupted. Collectively, CLBNC represents a shift from inflexible, technology-focused rehabilitation methods to flexible, patient-specific neuro-control systems that can enhance long-term rehabilitation results and facilitate functional recovery.

Keywords: Closed-Loop Bio-Neural Control (CLBNC), spinal cord injury, stroke-induced paralysis, neuro-control systems, neurorehabilitation

ICABB26-BM-P48

Modeling Alzheimer's Disease Using Cerebral Organoids

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ABSTRACT

Alzheimer's disease (AD), the leading cause of dementia globally, continues to be a significant neurodegenerative condition with few treatment alternatives. Traditional two-dimensional (2D) cultures and animal models, while useful for examining disease mechanisms, do not accurately reflect the structural and functional intricacies of the human brain, especially in sporadic AD, which represents most of the cases. Progress in stem-cell research has facilitated the creation of three-dimensional (3D) brain organoids, or "mini-brains," originating from human embryonic or induced pluripotent stem cells (iPSCs). These self-organizing systems replicate essential features of neurodevelopment and disease, such as amyloid-β aggregation, hyperphosphorylation, neuroinflammation, and synaptic loss, in a physiologically pertinent setting. Recent advancements have incorporated vascular and immune elements into organoid models, enabling the exploration of neuroimmune interactions and treatment responses. Organoids treated with Alzheimer's brain extracts show characteristic pathologies and react favourably to Lecanemab, highlighting their translational potential. Additionally, integrating organoid models with bioengineering techniques-like microfluidics, omics analyses, and computational modelling-boosts their ability for personalized drug evaluation and mechanistic investigations. Despite ongoing issues with reproducibility and development, cerebral organoids serve as a ground-breaking platform connecting traditional models and human clinical studies in Alzheimer's disease. This study highlights cerebral organoids as a powerful and human-relevant model for understanding Alzheimer's disease and improving therapeutic development.

Keywords: Alzheimer's disease; cerebral organoids; induced pluripotent stem cells (iPSCs); neurodegeneration; amyloid-β; disease modelling

ICABB26-BM-P49

Therapeutic Potential of Postbiotics as Immunomodulators in IBD

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Abstract
Inflammatory Bowel Disease (IBD), a chronic inflammatory condition of the gastrointestinal tract, is a lifelong chronic condition with relapses (periods of active symptoms) and remissions (periods of little to no symptoms) with no permanent cure. Rapid urbanization, changing diet patterns comprising of high sugars and fat with low fibre content along with increased environmental stress resulted into the rising incidence and early onset of IBD among the Indian population. Existing treatments manage symptoms of IBD through using broad immunosuppression and are often followed by adverse effects and relapse upon discontinuation. Probiotics are considered as a viable addition for modulating gut inflammation; however their therapeutic outcomes are inconsistent due to their strain-specific activity, instability during storage and possible risk of infection in immunocompromised individuals suffering from IBD. These challenges have highlighted the need for shifting research attention towards alternative and relatively newer solution like postbiotics. Postbiotics are bioactive microbial derivatives such as short-chain fatty acids (SCFAs), microbial cell fragments, metabolites and other substances like vitamins and polysaccharides that confer health benefits to the host. The postbiotic compounds have emerged as promising alternatives in the management of IBD and provide advantages such as enhanced stability, precise dosing, predictable nature of effects and absence of infection risk. This review compiles findings from diverse experimental and clinical studies which demonstrates the ability of various postbiotic compounds to modulate inflammation and promote mucosal healing and explores the immunomodulatory mechanisms that are exerted by postbiotics in IBD, including modulation of pro inflammatory cytokines, intestinal barrier reinforcement, regulation of T-cell responses and bacterial homeostasis restoration. While further clinical studies are required to standardize formulations and verify long-term effects, current evidence strongly support the therapeutic potential of postbiotics in IBD.
Keywords: Inflammatory Bowel Disease (IBD); Postbiotics; Immunomodulation; Gut microbiota; Intestinal barrier; Mucosal healing; Cytokine regulation

ICABB26-BM-P50

A Comprehensive Review and Literature Screening to Identify Potential Biomarkers in Acute Myeloid Leukemia

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Abstract
Acute Myeloid Leukemia (AML) is an aggressive hematological malignancy characterized by uncontrolled proliferation of immature myeloid cells resulting from a differentiation block and sustained by therapy-resistant Leukemic Stem Cells (LSCs), which contribute to poor prognosis and high relapse rates. A comprehensive literature review was conducted using approximately 50 peer reviewed publications to evaluate the expression patterns, molecular mechanisms, and prognostic relevance of potential biomarkers in both normal hematopoiesis and AML pathology. It focuses on non-coding RNAs (ncRNAs), including microRNAs (miRNAs), long non-coding RNAs (lncRNAs), and circular RNAs (circRNAs). The analysis revealed consistent upregulation of oncogenic miRNAs such as miR-155, miR-125b, and miR-126, which promote leukemic stemness, proliferation, differentiation arrest, and chemo resistance through targeting key regulators including BAK1, GATA1, Lin28A, and PU.1, while tumor-suppressive miRNAs such as miR-29a and miR-223 were frequently downregulated and associated with poor overall survival and impaired myeloid differentiation. Additionally, lncRNAs such as HOTAIR and CCDC26 and circRNAs like circ-PVT1 were found to enhance LSC maintenance

and drug resistance via miRNA-sponging mechanisms, highlighting a complex regulatory network driving AML progression. These findings emphasize the clinical relevance of ncRNA-based biomarkers for improved diagnosis, prognosis, and risk stratification, and support their potential as therapeutic targets to eradicate therapy-resistant LSCs when combined with conventional chemotherapy.

Keywords: Acute Myeloid Leukemia (AML), Leukemic Stem Cells (LSCs), Biomarkers, Non-coding RNAs, microRNAs, Chemo resistance, Targeted Therapy

ICABB26-BM-P51

Role of Salvia officinalis Phytochemicals in the Management of Oral Squamous Cell Carcinoma

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ABSTRACT

Oral cancer represents a major public health challenge in India accounting for 2% of new cancer cases diagnosed and contributes to high (~1.8%) mortality rate among cancer patients globally. It is among the most common cancers in the south-eastern asian region, due to prevalent risk behaviour involving smokeless and smoking tobacco use and betel quid chewing. Oral squamous cell carcinoma (OSCC) is the most common malignant tumor of the oral cavity, accounting for nearly 90% of all oral cancers. *Salvia officinalis L.* (common sage) is a widely used Mediterranean medicinal herb of the Lamiaceae family and has long been valued in traditional healing systems. Over recent decades, scientific research has increasingly focused on its pharmacological potential. T The bioactivity of *Salvia officinalis* is due to a diverse profile of phytochemicals, such as rosmarinic acid, carnosic acid, and carnosol; terpenoids such as 1,8-cineole, α-pinene, camphor, and thujone; triterpenoids such as ursolic and oleanolic acids; and flavonoids such as luteolin, apigenin, and quercetin.Preliminary findings suggest that Sage extracts act through inhibition of pro-inflammatory NF-κB signaling pathways and regulation of MAPK/ERK signalling cascades involved in tumor progression. These are also involved in scavenging of reactive oxygen species (ROS) to protect cells from oxidative cellular damage and lead to programmed cell death (apoptosis) by modulating mitochondrial associated pathways. Emerging research also indicates possible epigenetic influences having regulatory effects on gene expression. Sage extracts report significantly reduced viability of human carcinoma cells, altering the expression of genes regulating cell cycle control, DNA repair, and p53 signalling, suggesting activation of tumor-suppressive pathways. One of the major bioactive compounds in sage, rosmarinic acid, has been shown to suppress proliferation of oral cancer cells, by inducing G_2/M cell-cycle arrest, trigger endoplasmic reticulum stress, and promote apoptosis, while also reducing their migratory capacity. Clinical investigations further indicate that sage preparations offer therapeutic benefits in managing inflammatory and metabolic disorders and are generally safe for human use. Overall, these findings highlight Salvia officinalis as a scientifically relevant medicinal resource rich in bioactive phytochemicals for management of OSCC. Further research, particularly mechanistic investigations and in-vivo validation, is required to establish its clinical efficacy and safety.

Keywords: Oral squamous cell carcinoma; Salvia officinalis; phytochemicals; antioxidant; anti-inflammatory; Sage; anticancer phytochemicals

ICABB26-BM-P52

Eliminating Supernumerary Chromosome at Neonatal Stage Using Crispr-Cas9 Gene Editing from Trisomy Cells

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Abstract

Down Syndrome (DS), a genetic disorder caused by trisomy 21, results in a variety of cognitive, developmental, and physiological impairments. Advances in CRISPR-Cas9 genome-editing technology have created new therapeutic opportunities to address the underlying cause of DS by targeting chromosome 21. This study explores the scientific feasibility, challenges, and ethical implications of using CRISPR-Cas9 to either silence or remove the extra copy of chromosome 21 or modify the expression of key overexpressed genes such as DYRK1A, APP, and SOD1. In a 2025 study, researchers used an allele-specific method to specifically cut and remove the extra copy of chromosome 21 induced pluripotent stem cells and fibroblasts, in laboratory-derived human cells, leading to a more typical gene expression and improved cell behaviour. Initial studies showed that edited cells began to exhibit more typical behaviour and gene expression patterns after the extra chromosome was removed. These studies have shown that editing DS cells can reverse some cellular deficits, like improved proliferation and neural rosette formation, highlighting the potential for future therapies. Conclusion: The article concludes with a reflection on whether societal perceptions of genetic diversity should evolve alongside scientific innovation, highlighting that the greatest breakthrough may come not from altering genomes, but from fostering inclusion and understanding.

Keywords: CRISPR-Cas9, trisomy 21, DYRK1A, APP, and SOD1

ICABB26-BM-P53

Association Between Lung Cancer and Bacterial Infections: Clinical Evidence and Implications

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Abstract

Lung cancer is a major global health burden and is primarily associated with established risk factors such as tobacco smoking, air pollution, and occupational exposures. Lung cancer patients frequently exhibit ccompromised pulmonarydefense mechanisms, altered immune responses, and structural damage to lung tissue, which together create a favourable environment for opportunistic bacterial colonization and infection. While bacterial infections are not considered causative agents of lung cancer, increasing clinical evidence indicates that individuals with lung cancer are highly susceptible to bacterial infections due to disease-associated immune suppression and cancer-related therapeutic interventions. Numerous clinical and epidemiological studies report a higher incidence of bacterial respiratory infections among lung cancer patients, particularly in advanced disease stages and following chemotherapy or radiotherapy. Opportunistic pathogens such as *Pseudomonas aeruginosa*, Streptococcus *pneumoniae*, and *Haemophilus influenzae* are commonly isolated from respiratory samples of lung cancer patients and are associated with increased morbidity, prolonged hospitalisation, and poorer clinical outcomes. Recurrent or chronic bacterial infections in these patients can exacerbate inflammation, impair lung function, and complicate disease management, thereby influencing overall

prognosis rather than initiating tumor development. This review summarizes existing clinical reports and epidemiological evidence highlighting the increased vulnerability of lung cancer patients to bacterial infections and discusses the underlying immunological and physiological factors contributing to this susceptibility. Understanding the relationship between lung cancer and secondary bacterial infections is essential for improving infection surveillance, optimizing therapeutic strategies, and enhancing patient care. Early detection and effective management of bacterial infections in lung cancer patients may significantly reduce complications and improve quality of life and treatment outcomes.

Keywords: Bacterial infection; clinical incidence; immunocompromised patients; lung Cancer; opportunistic pathogens

ICABB26-BM-P54

Sadabahar: A Multifunctional Medicinal Plant for Microbial Infection Control

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Abstract

Sadabahar (*Catharanthus roseus*) is a multifunctional medicinal plant known for its rich phytochemical diversity, which confers a wide range of pharmacological activities, including antimicrobial, anticancer, antidiabetic, anti-inflammatory, and immunomodulatory effects. Owing to these properties, Sadabahar has gained considerable attention as a potential natural resource for microbial infection control. The increasing global burden of microbial infections, coupled with rising antimicrobial resistance and the limited efficacy of existing antibiotics, has intensified the search for alternative and complementary therapeutic agents derived from medicinal plants. Phytochemical investigations of Sadabahar have revealed the presence of biologically active constituents such as alkaloids, flavonoids, tannins, and phenolic compounds, many of which exhibit significant antibacterial and antifungal activities. These bioactive compounds act through multiple mechanisms, including disruption of microbial cell membranes, inhibition of essential metabolic enzymes, interference with nucleic acid synthesis, and suppression of biofilm formation. Such multi-targeted mechanisms enhance the potential of Sadabahar in combating both Gram-positive and Gram-negative bacteria, as well as opportunistic fungal pathogens.

This review consolidates and critically discusses existing literature on the antimicrobial potential of Sadabahar, highlighting its relevance as a multifunctional medicinal plant for microbial infection management. Overall, *Catharanthus roseus* represents a promising, plant-based candidate for the development of affordable, accessible, and effective antimicrobial strategies in the era of escalating antimicrobial resistance.

Keywords: Microbial infections; Antimicrobial activity; *Catharanthus roseus*; Medicinal plants; Infection control

ICABB26-BM-P55

Microbial Fermentation and Gut Health Potential of Traditional Foods from Meghalaya, India

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ABSTRACT:

Indigenous fermented foods rich in probiotics are an intrinsic component of traditional diet of the people of Meghalaya. Fermented foods develop diverse aromas, flavors, textures, and improved digestibility. Traditional fermented foods of Meghalaya, such as tungrymbai (fermented soybean), tungtap (fermented fish paste), and soibum (fermented bamboo shoot), harbor diverse beneficial microorganisms however, scientific studies on the nutritional, medicinal, and probiotic potential of these traditional foods remain limited. Lactic acid bacteria (LAB) isolated from tungrymbai and soibum, including *Lactobacillus*, *Lactococcus*, *Pediococcus*, and *Weissella*, play key functional roles by producing antimicrobial substances and exhibiting probiotic traits. Isolated Bacillus species, particularly *Bacillus subtilis* and *B. pumilus*, have also been reported for acidification and proteolytic activity. Fermentation reduces antinutritional compounds such as phytic acid in legumes and cyanogenic glycosides in bamboo shoots, while enhancing isoflavones, flavonoids, minerals, vitamins, and bioactive peptides associated with health-promoting effects. Microbes isolated from tungtap, including *Lactobacillus pobuzihii*, *L. pentosus*, and *Enterococcus faecalis*, are found to produce high levels of essential minerals (Ca, Fe, Mg, Mn, Zn, etc.) and vitamins such as carotene and retinol. Isolated *Enterococcus faecalis* has also been shown to exhibit gelatin hydrolysis and protease activity. Microbial fermentation in these foods can be broadly categorized into Bacillus-dominated proteolytic fermentation of soybean products, which enhances free amino acids and develops umami properties in fermented food, and LAB-driven lactic acid fermentation of fish and plant substrates, which produces organic acids, bacteriocins, and characteristic sour flavors. These fermented foods deliver live transient microbes, increase the bioavailability of peptides and vitamins, and provide fermentable substrates for the production of short-chain fatty acids by gut commensals.

Integrated approaches involving microbiology, microbiome profiling, metabolomics, and controlled human studies are required to validate their health benefits. With growing awareness of probiotics and functional foods, Meghalayan fermented foods represent a valuable source of novel probiotic strains and sustainable bioactive food resources for future research and applications.

Keywords: Microbial fermentation, Probiotic, LAB, bioactive compounds, Meghalaya, Northeast India, Proteolytic fermentation, Soybean, Bamboo shoot, Fish, Tungtap, Soibum, Tungrymbai

ICABB26-BM-P56

Nature-Inspired Medicine from the Ocean: Marine Biomimicry and the Future of **Biomedical Engineering**

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ABSTRACT

Surgical wound closure is a critical aspect of medical procedures, yet conventional techniques such as sutures, staples, and currently available synthetic tissue adhesives present several limitations when applied to soft and wet biological tissues and cause toxicity or weak tissue bonding in moist

environment. To address these challenges, inspiration is increasingly drawn from adhesive strategies employed by marine organisms. Among them mussels demonstrate exceptional wet-adhesion capabilities, enabling strong and durable attachment to surfaces under water. The adhesive proteins of mussels are heavily decorated with DOPA, a catecholic functionality , allowing effective bonding in physiological conditions while maintaining biocompatibility and mechanical flexibility. These bioinspired adhesives offer promising alternatives for tissue sealing, wound closure, and minimally invasive surgical applications. In addition to mussel-based systems, marine biomimicry has led to other emerging biomedical innovations, including sharkskin inspired antibacterial surfaces that reduce microbial attachment and jellyfish-inspired soft robotic systems with potential applications in targeted drug delivery and minimally invasive diagnostics. This poster presents a conceptual and literature-based overview of marine biomimicry in biomedical engineering , with a primary focus on mussel-inspired surgical adhesives. With increasing demand for minimally invasive
procedures and infection-resistant surgical materials, bioinspired adhesive technologies offer timely and clinically relevant solutions and long-lasting results. Most importantly, biomimicry emphasises REPLICATION of biological principles so no extraction is done , ensuring environmental sustainability and ethical innovation

Keywords-Marine biomaterials, Mussel-adhesion , DOPA-catechol chemistry, Biomimetic replication , Tissue engineering

ICABB26-BM-P57

Cyanobacterial Antimicrobial Peptides: Sources, Biosynthesis, and Biomedical Potential

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Abstract

Cyanobacteria, a group of microorganisms, are known for their ability to synthesize a variety of bioactive compounds that can be of great economic importance. One of the most prominent groups in the lot is antimicrobial peptides (AMPs) that can inhibit the multiplication of both bacteria and fungi. The discovery and study of these peptides have become more prevalent due to the fact that the microbes responsible for many diseases are becoming resistant to the antibiotics that are most commonly used. Cyanobacterial AMPs have a broad spectrum of activity against various microorganisms and consist of several types, including cyclic peptides, lipopeptides, and glycolipopeptides. Among the most prominent ones are hassallidins, laxaphycins, balticidins, and lyngbyabellins, which have all demonstrated potent antibacterial and antifungal effects.

Most of the time, the synthesis of cyanobacterial antimicrobial peptides does not go through ribosomes like that of the conventional proteins. They are instead synthesized via non-ribosomal peptide synthetases (NRPS) or hybrid NRPS- polyketide synthase pathways. The use of these systems enables tunneling of cyanobacteria to produce peptides of various structures due to incorporation of rare amino acids and alteration of the chemical structure which in turn enhance their antimicrobial activity. The analyzing of genomes has shown that a good number of cyanobacterial strains harbor the genes responsible for these peptides, which is an indication that a lot of antimicrobial agents are out there in nature waiting to be discovered. Cyanobacterial peptides not only exhibit antimicrobial properties but also show antiviral and selective cytotoxic activities, particularly against cancerous or infected cells, thereby expanding their potential therapeutic applications.

Keywords: Cyanobacteria, Antimicrobial peptides (AMPs), Non-ribosomal peptide synthetases (NRPS), Lipopeptides, Cyclic peptides, Glycolipopeptides, Antibiotic resistance.

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Therapeutic Repositioning of Cancer Drugs for Leishmaniasis Management

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Abstract

Leishmaniasis is a tropical disease caused by protozoan parasites of the genus *Leishmania* and remains a major public health concern in endemic regions worldwide, which has been neglected over the years. Current treatment options are limited and have significant drawbacks, including toxicity, high cost, lengthy treatment regimens, and the emergence of drug resistance, thereby underscoring the urgent need for novel and effective therapeutic strategies. In this context, drug repurposing has emerged as one of the most pragmatic and efficient approaches for accelerating the identification of new antileishmanial agents. Drug repositioning offers substantial advantages, including reduced development time and cost, improved translational feasibility, and a higher probability of clinical success owing to existing data on safety, pharmacokinetics, and dosing. Furthermore, repurposed drugs can bypass early-stage drug discovery bottlenecks and facilitate rapid deployment, which is particularly beneficial for neglected tropical diseases with limited commercial investment. Due to shared cellular features between cancer cells and protozoan parasites, such as rapid proliferation, altered survival mechanisms, and susceptibility to growth-inhibitory compounds, anticancer drugs have arisen as promising class of candidates for drug repurposing against leishmaniasis, in the near recent years. Several anticancer compounds, including chemotherapeutic agents and targeted therapies, have demonstrated significant antileishmanial activity at sub-toxic concentrations, either alone or in combination with existing antileishmanial drugs. In this work we critically examine anticancer agents that have demonstrated antileishmanial activity evident through *in silico, in vitro, ex vivo, in vivo* and preclinical studies. The advantages of repurposing anticancer drugs, such as well-characterized pharmacokinetics and prior clinical evaluation, are discussed alongside key challenges including host toxicity, therapeutic selectivity, and dose optimization. Overall, this review underscores the potential of anticancer drug repurposing as a promising and efficient strategy to broaden therapeutic options for leishmaniasis and to bridge existing gaps in current therapeutic interventions.

Keywords: *Leishmania*, Leishmaniasis, Drug Repurposing, Anticancer, Therapeutic Switching

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Allosteric Targeting of SARS-CoV-2 PLpro with Indian Ayurveda

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Abstract

Coronavirus Disease 2019 (COVID-19), caused by SARS-CoV-2, continues to pose a serious global health challenge despite the availability of vaccines, which show variable efficacy against emerging variants. Consequently, the identification of effective antiviral therapeutics targeting essential viral proteins remains a priority in this context, plant-derived bioactive compounds particularly those originating from traditional Indian Ayurvedic medicinal plants have gained considerable attention as promising sources of antiviral agents, owing to their rich structural diversity, long-standing therapeutic use, and well-documented pharmacological properties.

In the present study, a comprehensive in-silico framework was employed to investigate the antiviral potential of phytochemicals derived from the Indian Ayurvedic medicinal plant Mulethi (Glycyrrhiza glabra) against the SARS-CoV-2 papain-like protease (PLpro), a crucial viral enzyme responsible for polyprotein processing and modulation of host immune responses. Molecular docking analyses were performed to evaluate the binding affinity and interaction patterns of selected phytochemicals at the allosteric binding regions of PLpro. To further validate the docking results, molecular dynamics simulations were carried out to assess the conformational stability and dynamic behavior of the top-ranked protein–ligand complexes. Additionally, the ADMET properties, of the shortlisted phytochemicals were systematically evaluated using established computational tools, such as SwissADME and ProTox-II.

The present investigation identified a promising Mulethi-derived phytochemical showing strong binding affinity and stable interactions with SARS-CoV-2 PLpro at its allosteric regulatory sites, suggesting a potential role in modulating PLpro-mediated immune evasion mechanisms. The favorable binding behavior, supported by molecular dynamics stability and acceptable ADMET profiles, underscores the suitability of this compound as a potential antiviral lead. Collectively, these findings provide a mechanistic and computational rationale for the antiviral potential of Glycyrrhiza glabra phytochemicals against SARS-CoV-2. This study highlights the relevance of traditional Indian Ayurvedic medicinal plants as valuable sources of bioactive compounds and supports further experimental validation to advance the development of plant-based antiviral therapeutics for COVID-19 management.

Keywords: COVID-19; SARS-CoV-2; PLpro, Indian Ayurveda; Molecular docking; Molecular dynamics simulation, ADMET.

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Therapeutic Potential of Neuropeptides and Proteins in Alzheimer's Disease.

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Abstract

Alzheimer's disease is a complex age-related neurodegenerative disorder characterized by memory impairment, cognitive deficits, neuronal loss, disorientation and behavioral issues. It is caused mainly by an increased accumulation of neurofibrillary tangles formed by Tau proteins inside the cells and amyloid-beta plaques extracellularly which are obtained by an abnormal processing of the amyloid-beta precursor proteins (APP). These trigger chronic inflammation, vascular damage, endoplasmic reticulum stress, synaptic dysfunction and ultimately neuronal apoptosis. Numerous studies have indicated that neuropeptides may function as a therapeutic intervention to prevent and cure Alzheimer's disease. Neuropeptides are peptides produced by neurons that help them communicate within themselves and with other cells by regulating brain and body functions. Recent studies revealed that neuropeptides including ghrelin, neuropeptide Y, orexin, pituitary adenylate cyclase-activating polypeptide (PACAP) exert neuroprotective roles such as modulating amyloid-beta accumulation, promoting production of neurotrophins, enhancing neuronal glucose uptake, transport of glucose by neurons and regulate synaptic plasticity. They also modulate autophagy dysregulation and endoplasmic reticulum stress, prevent depressive like behavior and spatial memory deficits involved in Alzheimer's disease. Furthermore, proteins such as MT3, ZnT3 balance the high levels of metal ions which otherwise favor the amyloid beta aggregates. S100 family proteins control Ca^{2+} levels and maintain neuronal health. Additionally, larger proteins like humanin, transthyretin inhibit pathological aggregation and protect

neurons from amyloid beta induced toxicity. Thus, neuropeptides and proteins, collectively offer multifaceted neuroprotective potential and offer a long-awaited solution to the Alzheimer's disease.
Keywords- Alzheimer's disease, neuropeptides, proteins, amyloid-beta plaques, neuroprotectives

ICABB26-BM-P61

From Dysplasia to Leukemia: Pathway Convergence and Clonal Selection in MDS to AML Transformation

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Abstract

Myelodysplastic syndromes (MDS) are clonal hematological disorders that result in inefficient synthesis of blood cells and have a clinically significant risk of developing into acute myeloid leukemia (AML), which has a very poor prognosis and is challenging to treat. Despite advancements in cytogenetics and molecular profiling, current risk stratification methods are still not very accurate in predicting the development of leukemia. The transition from MDS to AML is not an instant genetic transformation but a gradual evolution made possible by the survival of the original clones and the selective growth of genetically prepared subclones, as supported by a growing number of genomic and stem cell-resolved studies. A persistent dysplastic clone with altered chromatin states, poor transcript processing, and restricted differentiation will result from the primary damage which often affects RNA-processing and epigenetic regulators. The alterations promote clonal survival and inefficient blood cell synthesis, but they are insufficient to cause leukemia. The disruption of transcription factor networks that follows leads to lineage mixing and limited differentiation. This is an instance in which subsequently acquired mutations in the signaling pathways might arise and give the cells advantages in terms of growth and survival. The gradual decline of the DNA damage response and checkpoint pathways further facilitates the development of genomic instability, which allows subclonal diversification and the rise of aggressive leukemic populations. Over the course of the different disease stages, it is the interaction of pathways, the leading of clones, and the gradual gaining of mutations that decide the transformation and not just the mutation burden. This way of investigating the problem has the potential to enhance the prediction of leukemic transformation, to clarify the risk stratification, to guide the choice of the treatment strategies and still prevent the disease progression in patients with MDS at an earlier stage.

Keywords: Acute Myeloid Leukemia, Myelodysplastic syndrome, Mutations, Progression of Disease

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Ayurgenomics: A New Paradigm for Personalized Medicine

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ABSTRACT

Ayurgenomics integrates the Ayurvedic approach of Prakriti-based classification with genomic and epigenomic science to modify personalized healthcare. Tridosha prakriti framework (Vata, Pitta, Kapha) represents an individual's physiological and psychological base and has been increasingly linked to measurable biochemical, genetic and metabolic signatures. The review shows links between Prakriti types and variations in HLA genes, differences in drug responses (Aspirin Sensitivity) and anesthetic

clearance and distinct gut microbiome patterns. The review also discusses that individuals with different prakriti display differences at genomic, proteomic and metabolomic levels, indicating their potential in precise drug development. Multiple experimental studies highlight scientific validity of prakriti-based classification. Modern tools like SNP analysis, GWAS and epigenetic markers help identify health risks and improve preventive medicine. A strong real-world example showcasing Prakriti assessment combined with advanced genetic testing has been discussed. The researchers identified common gene deletion hotspots, their prakriti type-specific occurrence and correlation with disease severity and CPK levels (example: Kapha-Pitta (KP) and Kapha-Vata (KV)). This demonstrates how prakriti-based grouping can serve as an additional tool to understand variations in disease expression in different individuals. Ayur nutrigenomics, acts as a link between diet and gene, and depicts how food components influence gene expression in different Prakriti types, hence, adding another layer of precision into personalized medicines. Epigenetic studies link diet, stress and lifestyle to DNA methylation differences across doshas. Pitta dosha shows metabolism-linked promoter methylation, while Kapha displays patterns associated with BMI, supporting the molecular basis of constitutional traits. Personalized medications demand models that explain inter-individual variation in disease susceptibility and treatment response. Ayurgenomics offers dual advantage: molecular precision through genomics along with Prakriti, that provides an accessible phenotypic stratification system, enhancing prediction, prevention and individualized interventions.

Keywords: Prakriti; Diet: gene expression; Ayurgenomics; Personalized Medicine; Ayurnutrigenomics

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Redesigning Antibacterial therapy: Phage Antibiotic Synergy in the era of Antimicrobial Resistance

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Abstract

The increasing prevalence of antimicrobial resistance (AMR) worldwide has made the investigation of novel treatment approaches necessary. Using the special mechanisms of bacteriophages in conjunction with traditional antibiotics, phage–antibiotic combination therapy (PACT) has become a powerful antimicrobial strategy for eliminating multidrug-resistant (MDR) pathogens. The limitations of monotherapies are addressed by this synergy, which offers a multimodal strategy to combat stubborn bacterial infections. Several synergistic mechanisms underlie PACT's effectiveness. Bacteriophages target and lyse host bacteria specifically, increasing membrane permeability and damaging the cell wall. This disturbance makes it easier for antibiotics to enter cells, increasing their lethal effect. On the other hand, some antibiotics cause bacterial stress reactions like cell filamentation, which can boost phage adsorption rates and quicken viral replication—a phenomenon called Phage-Antibiotic Synergy (PAS). Furthermore, phages produce depolymerases that degrade the extracellular polymeric substances (EPS) of biofilms, exposing protected bacteria to both phages and chemical agents. This dual approach offers several clinical advantages, including enhanced bactericidal activity, the potential for reduced antibiotic dosages, and the preservation of the host's commensal microbiota due to the high specificity of phages. Importantly, PACT can exploit evolutionary trade-offs; for instance, bacteria developing resistance to phages may become more sensitive to antibiotics (collateral sensitivity), thereby limiting the emergence of pan-resistant strains. Despite its potential, several hurdles remain for widespread clinical adoption. These include the narrow host range of phages, potential neutralization by the host immune system, a

lack of standardized manufacturing protocols, and the scarcity of large-scale Phase III clinical trials. Nevertheless, phage–antibiotic combination therapy represents a transformative shift in clinical microbiology, offering a promising and sustainable alternative to overcome the limitations of traditional antibiotic treatments in the modern era of resistance.

Keywords: Phage Antibiotic Synergy, Antimicrobial resistance, Multidrug resistance, Bacteriophages.

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Probiotic mediated transcriptional regulation of metabolome biosynthesis: A perspective of *Lactobacillus*

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Abstract

Probiotic bacteria are increasingly understood as active metabolic regulators within the gut ecosystem rather than passive commensals. Among them, *Lactobacillus* species have gained particular attention due to their ability to produce a diverse range of metabolites that influence host physiology, including short-chain fatty acids, exopolysaccharides, vitamins, bioactive peptides, and carbohydrate-derived compounds. The biosynthesis of these metabolites is tightly controlled at the transcriptional level, enabling the bacteria to dynamically respond to environmental cues within the gastrointestinal tract. This review examines the current understanding of probiotic-mediated transcriptional regulation of metabolome biosynthesis, with a focused perspective on *Lactobacillus* species. We summarize how global transcriptional regulators, and metabolite-responsive regulatory proteins coordinate gene expression across key metabolic pathways. Emphasis is placed on how external factors such as nutrient availability, pH fluctuations, bile salts, and host-derived signals shape transcriptional responses that ultimately determine metabolite output. Recent advances in transcriptomics and metabolomics have provided critical insights into the link between gene regulation and functional metabolite production, revealing strain-specific regulatory strategies that contribute to probiotic efficacy. This review also identifies key knowledge gaps in transcriptional control mechanisms and highlights future research directions, including the integration of multi-omics data and precise regulatory modulation to optimize metabolite biosynthesis. By integrating evidence from molecular, systems-level, and functional studies, this review provides a framework for the rational development of next-generation *Lactobacillus*-based functional probiotics.

Keywords: Functional probiotics; gut microbiome; *Lactobacillus*; microbial metabolism; regulatory networks; short-chain fatty acids; transcriptional regulation

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Non-Dairy Food-based Bioactives, as Modulators of the Gut–Lung Axis: Molecular Crosstalk and Immuno-metabolic Regulation

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Abstract

The growing disease burden of respiratory diseases, attributed to lifestyle changes, pollution, and post-COVID-19 complications, has brought a paradigm shift in research towards the exploration of the detailed mechanisms of the disease and strategies to alleviate the disease progression. The emerging understanding of the regulation of the gut–lung axis through nutraceuticals has attracted increasing attention as a key regulatory interface linking intestinal physiology with respiratory immune function. Dietary components, particularly non- dairy-based nutraceuticals, are emerging as influential modulators of this axis through their effects on gut microbiota and host molecular signalling. The substrates in the food selectively shape gut microbial communities, leading to enhanced production of microbial metabolites, such as short-chain fatty acids, which act as signalling molecules that influence immune cell programming, inflammatory mediator expression, and epithelial barrier function. These metabolites regulate key molecular pathways involving G-protein-coupled receptors, epigenetic modulation, and cytokine signalling, ultimately affecting pulmonary immune homeostasis. In parallel, non-dairy bioactives directly modulate oxidative stress responses and mucosal integrity, further supporting systemic immune balance. By integrating findings from nutritional science, microbiome research, and molecular immunology, this presentation highlights the potential of non-dairy nutraceuticals as non-pharmacological tools for targeting the gut–lung axis and promoting respiratory health through diet-driven molecular regulation.

Keywords: Non-dairy, Gut-Lung axis, Bioactives, Probiotics

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The Emerging Role of Ferroptosis-Autophagy-Mitophagy in Alzheimer's Disease Pathophysiology and Therapy

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Abstract

Alzheimer's disease (AD) is increasingly recognized as a disorder of disrupted proteostasis and metabolic homeostasis, where oxidative stress and mitochondrial dysfunction converge to accelerate neurodegeneration. Emerging evidence implicates ferroptosis, an iron-dependent form of regulated cell death, as a key driver of inflammatory trigger, leading to oxidative stress and neuronal loss in AD, directly linked to dysregulated autophagy and mitophagy mechanisms. In particular, aberrant ferritinophagy and impaired PINK1/Parkin-mediated mitophagy may amplify labile iron accumulation, mitochondrial ROS generation, and lipid peroxidation, thereby lowering the ferroptosis threshold of vulnerable neurons. To dissect this interplay, we propose an integrated multi-omics framework combining transcriptomic, proteomic, and metabolomic datasets from large AD cohorts with network-based causal inference and single-cell resolution. This strategy enables the identification of concordant and discordant ferroptosis-autophagy signatures across molecular layers, prioritization of causal hubs

such as GPX4, NCOA4, and PINK1, and evaluation of their association with cognitive decline. Connectivity mapping and structural modelling further allow the discovery and validation of candidate therapeutics capable of restoring redox balance and mitophagy flux. Finally, systems-level Ordinary Differential Equation modelling of iron-ROS-lipid peroxide dynamics provides a predictive scaffold for intervention testing. Together, this multi-tiered approach delineates the mechanistic crosstalk between ferroptosis and autophagy pathways in AD and provides a systems-level framework for identifying therapeutic intervention points.

Keywords- Neurodegeneration, Autophagy, Mitophagy, Proteomics, Cognitive decline, Transcriptomics.

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HIF-1α at the Cardio-Psychiatric Interface: Mechanistic Links Between Myocardial Infarction and Affective Disorders

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Abstract

Hypoxia-inducible factor-1α (HIF-1α) is a central hypoxic transcription factor that orchestrates cellular adaptation to oxygen deprivation, making it a compelling integrative target in myocardial infarction (MI) and affective disorders (AD). This review synthesizes experimental and clinical evidence on HIF-1α-mediated signalling at the cardio-cerebral interface and evaluates its therapeutic potential.

In the ischemic heart, HIF-1α activation modulates angiogenesis, glycolytic shift, mitochondrial quality control, and redox balance, thereby limiting infarct size and improving contractile recovery in preclinical models of MI and ischemia-reperfusion injury. Upstream regulators (prolyl-hydroxylase domain enzymes, PI3K/AKT, and inflammatory cues) and downstream targets (VEGF, iNOS, frataxin, CD39/CD73) collectively define a context-dependent cardioprotective versus maladaptive role of HIF-1α during acute ischemia, preconditioning, and chronic remodelling.

Concurrently, hypoxia and cardiovascular dysfunction reshape HIF-1 signalling in mood-relevant brain regions, influencing neuroplasticity, neuroinflammation, and energy metabolism. Altered HIF-1α and target-gene expression have been associated with major depressive and anxiety disorders, while computational and experimental work implicates HIF-1-linked pathways (HIF-1/FoxO, HIF-1/BDNF, and PI3K/AKT) in depression-related cognitive impairment and stress responsivity. By collating evidence from cardiology, neuropsychiatry, and systems biology, the review aims to delineate HIF-1α as a mechanistic bridge between MI and affective pathology, highlight translational opportunities of HIF stabilizers or inhibitors, and outline unresolved controversies and safety concerns surrounding chronic HIF-1α modulation in integrated cardio-psychiatric care.

Keywords: Hypoxia-inducible factor-1α, Myocardial Infarction, Affective Disorders, Chronic Remodelling, Neuroinflammation

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Integrating Ayurvedic Alkaloids into TB Preventive Therapy: Vasicine-Based inhibition of mycobacteria Isocitrate Lyases

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Abstract

Mycobacterium tuberculosis (Mtb) establishes long-term infection by entering metabolically adapted, non-replicating states within nutrient-limited intracellular niches. Under these persistence-associated conditions, frontline anti-TB drugs used in preventive therapy-particularly rifamycins and isoniazid show reduced efficacy, while the emergence of rifamycin- and isoniazid-resistant strains further threatens TB control programs. A central metabolic determinant of mycobacterial persistence is isocitrate lyase (ICL), an essential enzyme of the glyoxylate and methylcitrate cycles that enables survival on host-derived fatty acids and uniquely exhibits both isocitrate lyase (ICL) and methylisocitrate lyase (MICL) activities. Mtb encodes two ICL isoforms, ICL1 and ICL2. ICL2 exists as a continuous protein in some variants such as CDC1551, but as two split proteins in other strains, including H37Rv. Despite its critical role in persistence and virulence, ICL remains untargeted by current TB preventive regimens.

Our previous studies reported the structure function characterization of all ICLs in the Mtb H37Rv strain, followed by the identification of Vasicine, a quinazoline alkaloid derived from the Ayurvedic medicinal plant *Adhatoda vasica*, as a dual inhibitor of ICL and MICL activities (patent filed and under examination). The present study evaluates Vasicine-derived analogues as improved inhibitors using molecular docking and molecular dynamics simulations against ICL1 (H37Rv) and ICL2 (CDC1551). Selected analogues demonstrated stable binding within the catalytic pocket, comparable to or superior to Vasicine. The functional relevance of these findings was validated using a *Mycobacterium smegmatis* dormancy model, where zones of inhibition were compared for rifampicin alone and in combination with selected Vasicine analogues. These results highlight the potential of Vasicine-based scaffolds, in combination with first-line anti-TB drugs, as adjunct candidates capable of enhancing bactericidal activity, shortening treatment duration, and strengthening TB preventive therapy to reduce the risk of reinfection and reactivation.

Keywords: *Mycobacterium tuberculosis*, Isocitrate lyase (ICL1/ICL2), Methylisocitrate lyase (MICL), Vasicine, Vasicine analogues

ICABB26-BM-P69

Emerging Roles of Protein-Lipid Interactions in the Persistence of *Mycobacterium tuberculosis*

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Abstract

Tuberculosis (TB), caused by *Mycobacterium tuberculosis* (Mtb), remains a major global health burden, driven in part by the pathogen's ability to persist within host macrophages. A hallmark of Mtb pathogenesis is its lipid-rich cell envelope and its capacity to adapt metabolically to the nutrient-restricted intracellular environment. Following phagocytosis, Mtb actively subverts host cellular processes, particularly lipid metabolism, to establish a permissive niche for long-term survival. Accumulation of host lipid droplets and the formation of lipid-rich granulomatous lesions are characteristic features of chronic TB infection, underscoring the central role of lipids in disease progression.

Recent studies demonstrate that Mtb persistence is tightly linked to protein-mediated lipid acquisition, storage, and utilization. Host-derived fatty acids and cholesterol are imported and funneled into anaplerotic pathways, including the glyoxylate shunt, enabling efficient carbon conservation under stress conditions. Concurrently, Mtb accumulates intra-bacterial lipid inclusions that support dormancy and antibiotic tolerance. Although lipids are critical determinants of intracellular survival, lipid-centric mechanisms remain underrepresented compared to genomic and proteomic studies. This review synthesizes current evidence on lipid-dependent adaptations in Mtb infection, highlighting how coordinated protein-lipid interactions shape metabolic flexibility, immune modulation, and persistence, and discussing their implications for therapeutic targeting of drug-tolerant and latent tuberculosis.
Keywords: *Mycobacterium tuberculosis*, TB, macrophages, lipids, host immunity, persistence, antitubercular.

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Extraction and characterization of Ergothioneine from *Pleurotus spp*. as a neuroprotective agent

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Abstract

Ergothioneine is one of the medically important compounds found in variety of mushrooms and fungi. It is a thiourea derivative of histidine with a sulphur atom in the imidazole ring, chemically known as 2- mercaptohistidine trimethylbetaine with a molecular weight of approximately 229.30 g/mol. It is a water- soluble and polar molecule acquired in humans through dietary sources, with edible mushrooms such as *Pleurotus ostreatus, Lentinula edodes, Agaricus bisporus, Grifola frondosa, Flammulina velutipes* and also in some members of ascomycetes. The present study focuses on the extraction, quantification, and comparative evaluation of ergothioneine from selected *Pleurotus* species, namely *Pleurotus ostreatus, Pleurotus florida, and Pleurotus djamor*. Ergothioneine was extracted by utilising cultivation and extraction techniques particular to each species. P. florida and P. djamor fruiting bodies were extracted using hot water, whereas P. ostreatus was grown in controlled submerged fermentation conditions. Clarified extracts were purified in each instance by removing proteins and macromolecular contaminants using ethanol precipitation, membrane filtration, and successive centrifugation. Using UV-visible spectrophotometry, the ergothioneine content of the recovered extracts was measured at 257 nm. The absorbance 0.711 for *P. florida*, 0.376 for P. ostreatus, and 0.3064 for P. djamor were recorded in the spectrophotometric analysis. Further the characterization of purified extract of ergothioneine will be performed by Circular Dichroism (CD), High Performance Liquid Chromatography (HPLC), Liquid Chromatography–Mass Spectrometry (LC-MS) and Fourier Transform Infrared Spectroscopy. (FTIR).
Keywords: Oyster mushroom, fermentation, inflammatory, extraction, atherosclerosis, Alzheimer's disease

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Ashwagandha-Enriched Bread Using Baker's Yeast and Lactobacillus

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Abstract:

Ashwagandha fortified functional bread with the mixed fermentation system of Baker's yeast (*Saccharomyces cerevisiae*) and *Lactobacillus* species would be an innovative and novel functional food. Bread represents one of the most popular foodstuffs in the world that has long since developed as a simple source of carbohydrates into a multi-purpose food system to enable nutritional and functional additions. The fermentation of microorganisms is one of the decisive factors of quality in the production of bread: this process directly affects the texture, smell, nutritional qualities, and digestibility. The yeast used in baking (*Saccharomyces cerevisiae*) is the classical organism that provides the leavening, better texture, and good flavor formation during the bread-making. Nevertheless, although yeast improves sensory characteristics, and breakdown of complex material will enhance absorption. By contrast, *Lactobacillus* species or lactic acid bacteria are appreciated due to their probiotic activity. They secrete organic acids and enzymes which make food digestible, improve aroma, decrease the anti-nutritional inorganic like phytic acid, and suppressing microorganisms that cause food spoilage. Incorporation of Ashwagandha which contains withanolides, antioxidants, and anti-stress properties would be an ideal fermented functional food, which would provide a probiotic and adaptogenic bread.

Keywords: Ashwagandha-fortified bread; Probiotic functional food; Saccharomyces cerevisiae; Lactobacillus species; Adaptogenic food formulation; Withanolides; Antioxidants; Phytic acid reduction.

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Exploring the invisible alliance between our gut microbes and global antibiotic resilience

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Abstract

Antimicrobial resistance has emerged as a global health emergency, threatening to reverse decades of medical progress as multidrug-resistant (MDR) pathogens proliferate under the continued overuse of conventional antibiotics. The global quest for sustainable antimicrobial solutions has spotlighted the human gut microbiota as a formidable yet underexplored biological resource. The gut microbiome exerts active control over pathogen interactions, immune modulation, and the evolutionary dynamics of antibiotic resistance.

We highlight the dual role of the gut microbiota as both a key reservoir of antibiotic resistance and a primary barrier against pathogenic colonization. Exposure to antibiotics, whether for treatment, at low doses, or through environmental sources can disturb microbial balance, causing dysbiosis that favors resistant strains and enables opportunistic infections. These disruptions not only support the survival of multidrug-resistant (MDR) organisms but also accelerate the horizontal transfer of antibiotic resistance genes within the gut ecosystem.

Deciphering the intricate networks of microbiome–pathogen interactions, quorum sensing dynamics, and colonization resistance unlocks the potential for precision-driven strategies to combat antimicrobial resistance (AMR). Microbiome-centered interventions, ranging from fecal microbiota transplantation and rationally designed probiotics and prebiotics to bacteriophage therapy, next-generation drug-delivery systems, and robust antimicrobial stewardship, offer transformative alternatives to conventional approaches. By mobilizing the body's own microbial sentinels, this paradigm shifts the focus from indiscriminate pathogen eradication to ecological restoration, enabling resilient, host-compatible solutions to one of the most critical global health challenges of the 21st century.

Keywords: Antimicrobial resistance; microbiome; microbiome–pathogen interactions; quorum sensing; colonization resistance; probiotics; bacteriophage therapy; precision therapeutics

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EXPLORING THE SYNERGISTIC ANTI-BREAST CANCER POTENTIAL OF MARINE-DERIVED BIOACTIVE COMPOUNDS

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Abstract

Breast cancers continue to be among the most common tumors and are regarded as a major therapeutic challenge due to medication resistance and route flexibility. It has recently been determined that the sea is a highly abundant source of new bioactive substances with potential anticancer effects. In addition to the individual usage of these substances, there has been a growing interest in the potential synergistic effects of sea-derived combinations, including medication combos and combinations with other sea chemicals. The most recent data on the use of combinational techniques based on marine resources in the treatment of breast cancer, with an emphasis on in vitro studies and their molecular mechanisms, has been included in this review/experimental summary. Numerous marine species, such as sponges, mollusks, sea cucumbers, and brown algae, produce peptides, alkaloids, macrolides, and sulfated polysaccharides that are extremely cytotoxicto breast cancer cells, particularly the MCF-7 and MDA-MB 231 lines, according to local literature. More significantly, these substances have been shown to enhance the effects of conventional chemotherapeutic medications like as paclitaxel and doxorubicin, resulting in decreased ICβ_0 values. According to the mechanismistic approach, marine-derived combinations affect a number of cell survival pathways, including the induction of mitochondrial-mediated apoptosis, the activation of caspase cascades, the disruption of cell cycle progression, the down-regulation of EGFR/PI3K/Akt signalling, increased production of reactive oxygen species, and the suppression of metastatic markers. Given that redundancy is a major factor in cancer cells' resistance to medication, these polypharmacological compounds may be very helpful in treating breast cancer. Additionally, a number of studies have shown that marine chemicals can lessen breast cancer cells' resistance by reducing the production of anti-apoptotic and drug efflux proteins. Bioanalytical investigations provide light on the crucial role that HPLC profiling, purity assessment, and quantitative analysis play in standardizing marine extracts as well as the connection between chemical patterns and biological activity. Though this strategy is yet largely unexplored, the status of the literature as of right now shows the potential of marine combinations for the treatment of breast cancer. Combination analyses, pathway clarification, standardization, and validation using in-vivo models should be the main topics of future research.

Keywords: Breast cancer; Marine bioactives; Synergy; In vitro; HPLC

Session 1:
Biomedical and Health Innovations
Oral Presentations

ICABB26-BM-OP-01

Comparative Evaluation of Selected Phytocompounds on Proliferation and Migration of Human Ovarian Cancer Cell Lines SKOV3 and PA-1

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Abstract

Ovarian cancer is a leading cause of mortality among gynaecological malignancies, primarily due to delayed diagnosis and the limited effectiveness of existing therapeutic strategies. The search for safer and more effective treatment options has led to increasing interest in plant-derived phytocompounds, which exhibit diverse biological activities with comparatively fewer adverse effects. The present study investigates the comparative effects of selected phytocompounds on human ovarian cancer cell lines SKOV3 and PA-1. The antiproliferative activity of the phytocompounds was evaluated using in vitro cell viability assays, supported by morphological analysis and cell migration-based assays to assess changes in cellular behaviour following treatment. The results demonstrated a significant reduction in cell growth and migratory potential upon phytocompound exposure, indicating their ability to interfere with key processes involved in cancer progression. Overall, this comparative study highlights the inhibitory effects of phytocompounds on ovarian cancer cell growth and underscores their potential as promising candidates for further development in ovarian cancer therapeutics. Further studies are required to elucidate the underlying molecular mechanisms and validate their therapeutic efficacy.

Keywords: Cell migration, Ovarian cancer, PA-1, Phytocompounds, SKOV3

ICABB26-BM-OP-02

Music Therapy and Its Effect on Serum Testosterone Levels among Paramilitary Soldiers under Stress

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Abstract

Testosterone is an androgenic hormone primarily secreted by the gonads under the control of the hypothalamic–pituitary–gonadal (HPG) axis. It is essential for maintaining various physiological and reproductive functions and also influences behavioral traits such as aggression, competitiveness, dominance, and the ability to cope with stress. Circulating testosterone follows a diurnal rhythm, with peak levels in the early morning and a gradual decline as the day progresses. This study was conducted on paramilitary soldiers, a population with very high stress levels, which is a serious concern due to the increasing suicide rates among soldiers. Music was used as a coping mechanism to reduce stress. Serum testosterone was measured as it is an important hormone for activeness and physical performance, and it is known to decrease under stressful conditions, making it a useful marker of stress. The average serum testosterone levels were recorded at 0, 30, 60, 90, and 120 days of music therapy. The result shows that the mean level increased from 484.29 ± 26.42 ng/dL at day 0 to 515.09 ± 41.24, 528.20 ± 55.46, 549.60 ± 71.39, and 554.63 ± 102.74 ng/dL at 30, 60, 90, and 120 days, respectively. A significant increasing trend was observed over time. The study suggests that music is not only a source of entertainment but can also be used as an alternative native and complementary therapy for reducing stress and improving hormonal balance in soldiers.

Keywords: Music therapy; Testosterone; Stress; Paramilitary soldiers; HPG axis; Mental health

ICABB26-BM-OP-03

Differential Gene Expression Analysis Associated with Endoplasmic Reticulum Stress and Angiogenesis from Transcriptomic Database of Breast Cancer.

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Abstract

Breast Cancer remains the most frequently diagnosed malignancy and a leading cause of cancer-related mortality among women worldwide. High-throughput transcriptomic profiling provides an opportunity to uncover gene expression signatures associated with disease onset, progression and potential therapeutic response. This study aimed to identify differentially expressed genes (DEGs) between breast tumor tissues and normal samples, between early and late stage, between normal and early stage, between normal and late stage and also subtype specific. RNA-seq data were retrieved from The Cancer Genome Atlas (TCGA) using the TCGAbiolinks package in R followed by data preparation, grouping and normalization. Differential expression analysis was conducted between tumor and normal samples to identify significantly altered genes. Gene lists related to angiogenesis and endoplasmic reticulum (ER) stress were retrieved from public resources such as MsigDB, KEGG or manually by literature and differentially expressed genes associated with these processes were identified and subjected to functional enrichment analysis. The results were visualized through volcano plots, venn diagrams and heatmaps and subsequently interpreted to understand their biological significance in breast cancer. Analysis of TCGA-BRCA data showed clear gene differences between tumor and normal tissues. Several angiogenesis and ER stress-related genes were upregulated or downregulated in tumors. Enrichment analysis highlighted pathways involved in cell proliferation, hypoxia-adaptation, unfolded protein response and PI3K-AKT signaling. This analysis highlights the molecular interplay between angiogenesis and ER stress pathways in breast cancer. The identified co-expressed genes and enriched signalling networks may serve as potential biomarkers or therapeutic targets, providing deeper insight into tumor adaptation, progression and resistance mechanism in breast cancer.

Keywords: Breast Cancer, Differntially expressed genes, The Cancer Genome Atlas (TCGA), Angiogenesis, Endoplasmic reticulum stress, Unfolded protein response.

ICABB26-BM-OP-04

Mapping the Immuno-Oncologic Interface of Systemic Lupus Erythematosus and Hepatocellular Carcinoma for Drug Repurposing Insights

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ABSTRACT

Hepatocellular Carcinoma (HCC) and Systemic Lupus Erythematosus (SLE) are pre-eminent diseases; however, they have similar immunological characteristics and are caused by inflammation as a result of chronic stimulation by the immune system. An Integrative Computational Framework for Drug Repurposing for HCC and SLE is created to examine the intersecting molecular pathways that lead to these two diseases, as well as the results of drug candidates and their shared mechanism of action(s). The Comparative Toxicogenomics Database (CTD) identified 15 genes common to both diseases, which were subsequently subjected to a systems biology analysis using the Reactome database. This analysis indicated that the IL-4 and IL-13 signaling pathways were predominant in this data set, representing a

possible immuno-oncology connection between these diseases. Subsequently, the Drug Gene Interaction database (DGIdb) was used to map drug-gene interactions to the genes identified in this study; a strong candidate in this regard was Sunitinib, a tyrosine kinase inhibitor. The results of validation using CLC-PRED 2.0 indicated significant cytotoxic effects associated with Sunitinib among a panel of gastrointestinal cancer cell lines. In addition, Droperidol, which was identified using ChemMine based on the structure, was proposed as a co-therapy to ameliorate the adverse effects of Sunitinib based on the results of Protox3.0. This study illustrates a reproducible, systems biology-based methodology to demonstrate the relationship between autoimmunity and cancer through the repurposing of drugs and provides a rationale for precision immuno-oncology.

Keywords- Autoimmune Disease, Cancer, Sunitinib, Drug repurposing, Droperidol

ICABB26-BM-OP-05

AI-Accelerated Discovery of NLRP3 Inflammasome Inhibitors for Chronic Inflammatory Diseases: A Next Generation Approach in Biomedical Innovation

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Abstract

The NLRP3 (NOD-like receptor family, pyrin domain-containing 3) inflammasome is a multiprotein complex involved in the innate immune response that senses cellular stress and pathogen invasion. It consists of NLRP3, the adaptor protein ASC (Apoptosis-associated speck-like protein containing a CARD), and pro-caspase-1. Upon activation, NLRP3 recruits ASC and activates caspase-1, leading to the maturation and release of the inflammatory cytokines IL-1β (Interleukin-1 beta) and IL-18 (Interleukin-18).

NLRP3 is activated by PAMPs (Pathogen-Associated Molecular Patterns) and DAMPs (Damage-Associated Molecular Patterns) such as extracellular ATP (Adenosine Triphosphate), glucose imbalance, and hyaluronan fragments, often through pannexin-1 channels. While essential for host defense, dysregulated NLRP3 activation contributes to chronic inflammatory diseases including type 2 diabetes, Alzheimer's disease, gout, and atherosclerosis, making it an important but challenging therapeutic target.

In this study, in-silico screening of natural compounds was performed to identify potential inhibitors of the NLRP3 inflammasome, a key mediator of chronic inflammatory diseases. The three-dimensional structure of NLRP3 was obtained from publicly available protein databases and used for molecular docking studies with selected bioactive natural compounds. Computational tools was employed to evaluate binding affinity, molecular interactions, and drug-likeness properties of the screened compounds. This computational approach aims to accelerate the early stages of drug discovery by rapidly identifying promising NLRP3 inhibitor candidates. The findings of this work will provide a basis for future in-vitro and in-vivo validation of potential anti-inflammatory therapeutics.

Keywords: NLRP3, PAMPs (Pathogen-Associated Molecular Patterns), Computational tools.

ICABB26-BM-OP-06

Comparative Study of Endo-β-1,4-Mannanases From Novel Bacterial Strains for The Production of Galacto manno oligosaccharides

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Abstract

Prebiotics are compounds including sugar polyols, polysaccharides and oligosaccharides, and resistant starches, and fibers which are non-digestible and should not absorbed by gastro-intestinal tract (GI tract). Galactomannan is a polysaccharide which is made of linear mannose chain and galactose is present as the side branch group. Though it has prebiotic potential, but its usage is limited because of it highly viscous nature. Galactomannan oligosaccharides (GMOs) are the emerging prebiotic which can be used to develop the functional foods for the benefit of human kind. In the presented work we performed a comparative analysis of endo-1,4- β-mannanase enzyme which was produced from novel bacterial strains. The bacterial strains were isolated form the guar fields of Rajasthan and Haryana. The recombinant construct made by inserting gene into pET vectors using recombinant DNA technology. The enzyme was purified with Ni-NTA chromatography. The comparative analysis with biochemical characterization showed that all the enzymes were highly active in the pH 6, their optimal temperature are different but all showed more than 50% activity in the low as well as high temperature (30-90˚C). The RJ 32 showed the optimum activity with 0.1U of enzyme/mg of substrate dosage in pH 6 at 55˚C temperature, RJ 35 optimal activity was found at pH 6 and 50 ˚C with 0.09U of enzyme/mg of substrate and HR 10 showed the optimal activity at pH 6 and 65 ˚C with 0.08U of enzyme/mg of substrate. The endomannanase of the RJ 32 and RJ 35 showed thermal stability with 50% of enzymatic activity upto 7 days and HR 10 upto 12hr. The enzymes were active at high temperatures even though they are not thermophilic strains and isolated from the mesophilic zone; highly stable for longer duration at their optimal temperature. These parameters increase their industrial application.

Keywords: Endo-1,4- β-mannanase, Galactomannan oligosaccharides, Prebiotics, Recombinant DNA technology

ICABB26-BM-OP-07

Mirror Cells: Bridging Action, Cognition, and Empathy

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Abstract:

Mirror neurons are a specialized class of brain cells that fire both when an individual performs an action and when they observe the same action performed by others. First discovered in the premotor cortex of macaque monkeys in early 1990s, extensive research has mapped their presence in the human brain,

predominantly in the inferior frontal gyrus and inferior parietal lobule. Significant advancements include elucidation of mirror cells' role in imitation, language acquisition, emotional resonance, and theory of mind processes. Mirror cells can refer to a hypothetical organism called a mirror life form, made of mirror-image molecules. If they were to be created in released into the nature, then we can take countermeasures such as: Modifying mirror bacteria to be dependent on specific nutrients not found in nature (synthetic auxotrophy). Developing and using mirror-image versions of existing antibiotics (e.g., specific quinolones) that would affect mirror bacteria but not the natural human gut microbiome. Strict physical containment protocols for any research involving mirror biomolecules to prevent accidental release. Developing robust detection systems for mirror organisms to quickly identify their presence in the environment before a widespread issue occurs. Establishing systems for monitoring the purchase of key "mirror" precursor molecules, such as mirror oligonucleotides, to hinder malicious actors.
Mirror Antibiotics/Vaccines: It might be possible to treat human and animal infections with mirror-image versions of antibiotics or vaccines, which would only affect the mirror cells and not natural ones.
Mirror Bacteriophages: Engineering mirror viruses (phages) that could infect and kill mirror bacteria.
Keywords: Mirror cells, Mirror neurons, Mirror image, Environment

ICABB26-BM-OP-08

Bioregenerative Microalgal Systems for Space Medicine and Supplement Production

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Abstract
Long-duration space missions expose astronauts to microgravity, radiation, nutrient imbalance and confined living conditions, leading to muscle atrophy and progressive decline of multiple physiological systems. While short missions depend on pre-packed drugs, this approach becomes impractical for distant or long-term missions due to storage limitations, degradation of pharmaceuticals, and the high cost of repeated resupply. In-situ biomedicine and supplement production therefore becomes essential for sustaining human health during extraterrestrial space missions. Microalgae have emerged as a leading platform for space biomanufacturing because of their rapid growth, minimal resource requirements, high stress tolerance and ability to integrate into closed-loop life support systems. They generate oxygen, remove CO_2 from the spacecraft environment and produce nutrient-rich biomass beneficial for astronaut health. Recent advances in microgravity-compatible photobioreactors, supported by experiments like NASA's Space Algae-2, demonstrate efficient algal growth in orbit. Compact FEP-bag cultures, membrane-based systems and integrated ISS reactors such as PBR@LSR highlight significant progress. Integrating these reactors within Environmental Control and Life Support Systems enables continuous, on-demand production of medicines and supplements, supporting Bioregenerative Life Support Systems (BLSS) for future long term deep-space missions.
Keywords: Microgravity, Muscle Atrophy, Microalgae, Biomanufacturing, Biomedicine, Supplements, Photobioreactors, Bioregenerative Life Support Systems (BLSS), Environmental Control and Life Support Systems (ECLSS)

ICABB26-BM-OP-10

Anti-biofilm potential of Human lactonases against Mycobacterium smegmatis: A novel therapeutic strategy

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Abstract:

Mycobacterium tuberculosis forms complex multicellular biofilms that enhance resistance to host immunity and standard antibiotics, with M. smegmatis widely used as a model organism to investigate these mechanisms. In this study, we investigate a novel therapeutic approach utilising recombinant human lactonases to inhibit biofilm development and enhance antibiotic efficacy. Human Paraoxonases (PONs) and Senescence Marker Protein 30 (SMP30) were recombinantly produced and purified using a bacterial expression platform, followed by biochemical characterization and functional assessments. Both proteins reduced M. smegmatis biofilm formation in a concentration-dependent manner without exhibiting bactericidal activity. Recombinant huPONs were effective at micromolar concentrations, while SMP30 showed activity at nanomolar levels, leading to its selection for detailed investigation. To elucidate and enhance the enzymatic function of its anti-biofilm activity, in silico analysis guided the rational engineering of huSMP30. Molecular docking highlighted three single amino acid substitutions (E18H, N154Q, D204V), which were generated via PCR-based site-directed mutagenesis. These mutant proteins and the wild-type huSMP30 were purified, and the effects on the enzymatic activity and biofilm formation were studied. Among the designed mutants, E18H and D204V showed minimal impact, whereas N154Q markedly improved lactonase activity, catalytic efficiency, and biofilm inhibition. Stability assays confirmed that the proteins remained intact at 37°C for up to four days. Overall, the engineered huSMP30 variant emerges as a promising biofilm-targeting therapeutic candidate with potential to enhance treatment outcomes in mycobacterial infections.

Keywords: Human lactonases, Enzyme-based therapeutics, Comparative analysis, Lactonase activity, Mycobacterium, Biofilm inhibition

ICABB26-BM-OP-11

Comprehensive Phytochemical and Biochemical Profiling of Plant-Derived Compounds with Potential Anticancer Activity Against Lung Cancer

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Abstract:

Lung cancer remains one of the leading causes of cancer-related mortality globally, highlighting the urgent need for safer and more effective therapeutic alternatives. Plant-derived bioactive compounds have emerged as promising candidates for cancer prevention and treatment due to their diverse pharmacological properties. The present study aims to perform a comprehensive phytochemical and biochemical investigation of medicinal plants, including Amaltas (*Cassia fistula L*), Gul-e-Surkh (*Rosa damascena Herrm*), Genda (*Tagetes erecta L*), and Jasmine (*Jasminum sambac* (L) Aiton), to identify the bioactive compounds with potential anticancer activities against lung cancer. This study involves

qualitative and quantitative phytochemical analyses, antioxidant assays, and spectral characterization using Fourier-transform infrared (FTIR) spectroscopy to determine the presence of major functional groups associated with the bioactive metabolites. Furthermore, an in vitro cytotoxic evaluation using the A549 lung cancer cell line was conducted to assess the potential anticancer efficacy of these extracts. This integrative approach provides a scientific rationale for the therapeutic relevance of the selected medicinal plants by identifying key phytochemical constituents, confirming functional groups through FTIR analysis, and demonstrating cytotoxic potential against the A549 lung cancer cell line. The findings lay the groundwork for future molecular and pharmacological studies aimed at developing novel plant-based therapeutics for lung cancer management. The study uniquely combines phytochemical profiling, antioxidant assessment, FTIR-based functional group identification, and in vitro cytotoxic evaluation to establish a comprehensive foundation for exploring natural plant extracts as potential anticancer agents against lung cancer.

Keywords: Cytotoxicity, FTIR, Lung cancer, Natural plants, Phytochemical analysis

ICABB26-BM-OP-12

Production of recombinant Acinetobacter baumannii Carbapenemases

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Abstract:

One of the pivotal global threats emerging today is antimicrobial resistance, which leads to life-threatening infections and restricts the effectiveness of current diagnostic and treatment options. Amongst the most concerning pathogens is Acinetobacter baumannii, a Gram-negative opportunistic bacterium responsible for severe hospital-acquired infections (HAI) and also responsible for high mortality rates. A. baumannii exhibits high resistance to multiple antibiotics, including last-resort carbapenems. The World Health Organization (WHO) has classified the carbapenem-resistant A. baumannii as a critical priority pathogen globally, which enlightens the urgent need for research, discovery, and development effective treatment and diagnostic options. Currently, the methods available for the detection of carbapenem-resistant Acinetobacter baumannii (CRAB) are mostly time-consuming, laborious, and need expensive reagents. Due to the lack of effective diagnostic strategies, there is a high-level urgency of having a quick, cheaper and reliable diagnostic platform that can be used to identify carbapenem-hydrolyzing enzymes with high specificity and sensitivity. In this work, we have expressed and purified key carbapenemases encoded by A. baumannii using E. coli as heterologous host. These carbapenemases were further characterized for their activity using antimicrobial susceptibility test (AST). These purified carbapenemases can be used to develop a rapid, point-of-care diagnostic method for carbapenem resistance in A. baumannii. that will allow preventing and treating the infection in its early stages and enhance the practice of antibiotic stewardship.

Keywords: Carbapenems, Hospital-acquired infections, Acinetobacter baumannii, Carbapenemase, Antimicrobial Resistance, Antimicrobial susceptibilty test, Diagnostic method

ICABB26-BM-OP-13

Thapsigargin Induced Endoplasmic Reticulum Stress and Neurobehavioural Assessment in *C. elegans.*

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Abstract:

Endoplasmic reticulum [ER] stress is generated when misfolded and unfolded proteins are accumulated inside the cell; this stress triggers the unfolded protein response (UPR) to restore the proteostasis. Thapsigargin induces ER stress by affecting the sarco-endoplasmic Reticulum Calcium-transporting ATPase (SERCA) pump. This study aimed to understand the neurodegenerative effect of thapsigargin-induced ER stress in C. elegans by analysing neurobehavioural assay at different concentration and exposure duration. Synchronised early adult C. elegans (N2 wild type) was treated with thapsigargin at 1µg/ml, 5µg/ml and 10µg/ml concentration for 6 hour and 24 hours with untreated controls. Locomotory assay (thrashing and body bend) were conducted on 20 worms per minute at 6 and 24 hours at different concentrations. Each assay was repeated three times. In addition, lifespan assays were also performed at these thapsigargin doses, which revealed a significant reduction in lifespan at 5µg/ml and 10 µg/ml compared with controls, with a gradual, dose-dependent decrease. No significant changes were observed between control and 1µg/ml treated worm at either time point. However, 5µg/ml and 10µg/ml treated worms with thapsigargin shows gradual dose dependent decline in both body bend and thrashing count compared to control and become more prominent at 24 hours compared to 6-hour exposure duration. Thapsigargin causes neurodegeneration in C. elegans by inducing ER stress in both dose and time dependent manner and this observed neurobehavioural essay helps to establish a link between prolonged ER stress and neuro-degeneration.

Keywords: Endoplasmic reticulum stress; Thapsigargin; Caenorhabditis elegans; Neurodegeneration; Lifespan

ICABB26-BM-OP-14

Synergistic Effect of *Bacteroides vulgatus* with *Ginseng* Extract in Treating HFD-induced Hyperlipidaemia

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Abstract

Hyperlipidaemia resulting from a high-fat diet (HFD) is a primary antecedent to cardiovascular disease and metabolic syndrome and represents a growing global health burden. While the medicinal herb Panax ginseng and the gut commensal Bacteroides vulgatus individually exhibit hypolipidaemic and anti-inflammatory properties, their synergistic potential as a targeted synbiotic therapy remains an emerging and underexplored field of interest. This study aims to investigate the combined influence of Bacteroides vulgatus and Ginseng extract on mitigating obesity induced by a high-fat diet. A thorough and systematic literature review was performed to determine the distinct and combined anti-obesity mechanisms of Bacteroides vulgatus and the phytoconstituents found in ginseng extract, with particular emphasis on gut–metabolic signalling pathways.

Our review elucidates a novel mechanistic cascade centred on peripheral serotonin modulation. We identified that Ginsenoside Rg1 acts as a precision modulator, reversing HFD-induced dysbiosis by promoting the re-colonisation of B. vulgatus. This restored bacterial abundance downregulates intestinal Tryptophan Hydroxylase 1 (Tph1), significantly inhibiting the synthesis of peripheral

serotonin (5-HT). The reduction in circulating 5-HT removes the metabolic "brake" on thermogenesis, leading to the upregulation of Uncoupling Protein 1 (UCP1) in brown adipose tissue (BAT) and beige fat. Furthermore, lowered gut serotonin levels hinder the transport of dietary lipids (chylomicrons) into circulation, thereby reducing overall lipid absorption.
The co-administration of Bacteroides vulgatus and Ginseng extract offers a potent, multi-target therapeutic strategy for HFD-induced hyperlipidaemia. Further research should focus on optimising the dosage, assessing safety, and exploring the long-term clinical efficacy in human subjects through controlled trials.
Keywords: *Bacteroides vulgatus*, *Ginseng*, Ginsenosides, Hyperlipidaemia, Serotonin

ICABB26-BM-OP-15

Formation of Students' Aesthetic Culture in the Teaching Process of the "Mushkilot" Section of "Shashmaqom"

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Abstract
In this article, we investigate formation of students' aesthetic culture in the process of teaching the "Mushkulot" section of "Shashmaqom" using listening to music. The main objective of this study is ensuring the student's all-around development and harmoniously shaping their psycho-emotional, cultural-aesthetic, and cognitive potential through a multidisciplinary approach to the music education process. We employ technology for uncovering the aesthetic and expressive potential of "Mushkilot" songs based on art therapy methods, and for effectively organizing the educational process on that basis to foster a positive psycho-emotional state in the student by utilising the psychotherapeutic properties of music. The results indicate that, within the framework of music art therapy, reflection through the musical listening experience ensures emotional understanding, the analysis of one's mental state, and the perception and expression of changes, leading to the introduction of integrated, interactive, and personalised learning technologies, enhances the effectiveness of the pedagogical process, and enables the deeper development of students' aesthetic culture through problem-based learning. These findings provide new insights into the Mushkilot section of the Shashmaqom, with its intricate structure, melodic richness, and profound philosophical content, has great potential not only for musical, but also for spiritual and aesthetic education, and the proposed approach can be applied to organising the learning process at the intersection of music, Psychology, pedagogy, and cultural studies.
Keywords: Mushkulot,psycho-emotional state, Psychology, cognitive potential.

ICABB26-BM-OP-16

Targeting Hyperglycemia-Induced Oxidative Stress in Diabetic Nephropathy Using *Tinospora cordifolia*: A Mechanistic Evaluation

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Abstract
Diabetic nephropathy (DN) is a major microvascular complication of diabetes, marked by impaired metabolism of glucose and increasing renal dysfunction. Early intervention approaches targeting hyperglycemia-induced oxidative damage are crucial for slowing disease progression. The present study explores the therapeutic potential of *Tinospora cordifolia* by examining its phytochemical profile and its functional ability to modulate enzymatic and oxidative pathways relevant to DN.
Comprehensive phytochemical analysis confirmed the presence of bioactive constituents, including phenolic compounds, flavonoids, alkaloids, and diterpenoid lactones. The extract demonstrated

significant inhibition of α-amylase activity, indicating its potential role in regulating excessive glucose release during carbohydrate digestion. Additionally, marked antioxidant activity was observed through established free-radical scavenging and reducing power assays.
The dual modulation of carbohydrate-digesting enzymes and oxidative stress highlights a complementary mechanism by which *T.cordifolia* may protect renal tissue from hyperglycemia-associated injury. By addressing two interconnected pathogenic drivers of diabetic nephropathy, this study strengthens the pharmacological basis for further exploring *T. cordifolia* as a supportive therapeutic candidate. These findings provide a foundation for future investigations at the cellular and molecular level to elucidate its role in renal protection under diabetic conditions.
Keywords: *Tinospora cordifolia*, Diabetic nephropathy, Oxidative stress, α-amylase, Herbal therapeutics

ICABB26-BM-OP-17

Structure–Function Perspectives on SPATR: An Emerging Essential Protein in Malaria Parasites

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Abstract

Malaria remains a major global health challenge due to the emergence of drug-resistant Plasmodium strains and the limited efficacy of existing vaccines, underscoring the need to identify parasite-specific therapeutic targets. In this context, Secreted Protein with Altered Thrombospondin Repeat (SPATR) has emerged as an essential multifunctional protein that links structural features to stage-specific functions across the Plasmodium life cycle. SPATR contains a thrombospondin type I repeat (TSR) domain, a motif widely associated with adhesion, motility, and host cell interactions in apicomplexan parasites.
Beyond its biological significance, SPATR exhibits molecular mimicry with human TSR and epidermal growth factor (EGF) containing proteins, suggesting potential roles in immune modulation and evasion. Current evidence indicates that the TSR domain, together with adjacent conserved regions, contributes to protein localization, secretion and interactions with both host and parasite factors.
Depicting experimental and in-silico structural insights, functional studies of host cell recognition and invasion and emerging data on immunological relevance, this review emphasizes the structure–function relationships underpinning SPATR activity during both mosquito and mammalian stages. It further evaluates SPATR as a potential drug and vaccine target, highlighting opportunities for structure-guided inhibitor development and antibody-based strategies. Collectively, available
evidence positions SPATR as a dual-stage essential protein in Plasmodium development and a promising, though challenging, target for therapeutic and vaccine design.
Keywords: Malaria, Plasmodium, SPATR, TSR, EGF, Immune-modulation

ICABB26-BM-OP-18

Therapeutic uses of venom in cancer

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Abstract

Venoms, previously thought of as only lethal toxins, have now evolved as an important reservoir of bioactive molecules with pharmaceutical applications. They have been used in the development of drugs for cancer, cardiovascular diseases, diabetes, hypertension, multiple sclerosis, and pain etc. These

venoms are obtained from a variety of animals including snakes, bees, scorpions and marine snails. Venoms are rich in various types of peptides and proteins with interesting pharmacological functions. Among these, bee venom are known to affect many major pathways in cancer treatment such as: PI3K/Akt/mTOR, apoptosis signaling pathway (e.g., EGFR and TNF-α, including downstream effectors such as Casp-3, Casp-7, Casp-8, Casp-9, Bcl-2, Bax and Bcl-xL), p38 MAPK pathway, and thus affect the growth, differentiation, invasion, autophagy or migration of cancer cells in lung, breast, cervical and other cancers. Bee venom is known to be anti-inflammatory and immunomodulatory as well and so can be used in case of arthritis and neurologic disease treatment. Ongoing research in this area focuses on isolating, characterizing, and modifying venom peptides to improve safety and clinical applicability. With advances in proteomics, recombinant expression, and nanotechnology-based delivery, these compounds hold promise for developing novel treatments for cancer, cardiovascular disorders, autoimmune diseases, and pain management. The present review aims to highlight the pharmacological significance of venoms and explores their potential as next-generation therapeutic agents.

Keywords: venom, cancer, venom peptide, neurological diseases, cardioprotective peptides, pain management

ICABB26-BM-OP-19

Bacterial Cellulose–Based Three-Dimensional Scaffolds for Biosensing and Sustainable Biomaterial Applications

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Abstract

Bacterial cellulose is a polysaccharide produced by living organisms that has been found to be useful for numerous applications in advanced biomaterials, bioengineering, and biosciences due to its high degree of crystallinity, extremely native-like morphology, excellent mechanical strength, and natural biocompatible properties. This study successfully developed and characterised bacterial-cellulose-based three-dimensional scaffolds for the purpose of creating sustainable platforms for biosensing applications and other biobased materials. The bacterial cellulose was produced by culturing bacteria capable of producing cellulose and isolating the resulting material from organic waste, followed by cultivating the bacteria under controlled fermentation conditions to produce structured matrices of cellulose. The recovery of the bacterial cellulose has been purified and processed into scaffold architectures, with initial structural and physicochemical characterisations performed.

Morphological examination of the scaffolds demonstrated an extensive interconnected porous structure with a high surface area-to-volume ratio, which is critical for optimal mass transport and immobilisation of biological recognition substrates in biosensing applications. Furthermore, the scaffolds demonstrated high water absorption capacity and mechanical stiffness, demonstrating that they are structurally stable when exposed to water. In addition, the fibrillar structure of bacterial cellulose provides functional sites that can be modified or enhanced, as well as allowing for increased compatibility with biosensing interface materials and with biocoatings.

In addition to its biosensing applications, bacterial cellulose can be viewed as a sustainable replacement for polymeric materials produced from fossil or crude oil due to its renewable source and low

environmental impact from both production and disposal (biodegradable). Bacterial cellulose is highly adaptable as it allows for the integration of three-dimensional scaffold design with the production process using both microbial cultivation techniques, thus providing an ideal framework for developing new and innovative applications as they continue to emerge. This work also contributes to the rapidly expanding area of microbial biomaterials and demonstrates the potential use of bacterial cellulose-based scaffold systems for developing eco-friendly biosensing solutions and future forward bioengineered materials.

Keywords: Bacterial cellulose three-dimensional scaffolds; biosensing platforms; sustainable biomaterials; microbial biotechnology

ICABB26-BM-OP-20

Paraoxonase 2: A Critical Axis in Cancer Biology and a Gateway to Targeted Therapies

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Abstract

Paraoxonase 2 (PON2), a member of the lactonase enzyme family, has emerged as a critical determinant in cancer biology. Known for its antioxidant properties and mitochondrial localisation, PON2 plays a central role in maintaining cellular redox balance. However, its overexpression in malignant cells has been increasingly associated with tumour progression, survival under oxidative stress, and resistance to conventional therapies. These attributes position PON2 not only as a biomarker for prognosis and disease monitoring but also as a promising therapeutic target for drug-resistant cancers.

Recent research has highlighted the potential of pharmacological interventions to modulate PON2 activity, with selective COX-2 inhibitors, such as celecoxib, offering intriguing possibilities. By influencing PON2's enzymatic function, these agents may disrupt cancer cell survival pathways and enhance treatment efficacy. This intersection of molecular biology and pharmacology underscores a paradigm shift toward mechanism-driven cancer therapy, where targeting PON2 could complement existing treatment strategies and overcome therapeutic resistance.

This work synthesises current knowledge on PON2's multifaceted roles in cancer, its regulatory mechanisms, and emerging approaches for inhibition. By framing PON2 as a critical axis in tumour biology, we aim to stimulate discussion on innovative strategies for clinical translation. Continued research into PON2-targeted interventions holds the potential to redefine cancer treatment, offering new hope for patients with aggressive and drug-resistant malignancies.

Keywords: Paraoxonase 2 (PON2), Cancer therapeutics, Oxidative stress, COX-2 inhibitors, Cancer biomarkers.

ICABB26-BM-OP-21

Problems Of Preservation, Reconstruction and Restoration of The Historical and Cultural Heritage of Bukhara

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Abstract

The article is devoted to the analysis of the issues of preservation, reconstruction and restoration of the historical and cultural heritage of Bukhara. The historical experience of monument care from ancient times to the Soviet period is considered, achievements and mistakes in the field of restoration in the 20th century are assessed. Particular attention is paid to modern projects implemented with the support of international organizations, as well as current challenges associated with preserving the authenticity of the architectural appearance of the city. The author emphasizes the need for an integrated approach that combines scientific methods, traditional techniques and modern technologies for the effective protection of the cultural heritage of Bukhara.

Also, modern problems of preservation, reconstruction and restoration of the historical and cultural heritage of the city of Bukhara - one of the most important centers of Islamic architecture in Central Asia are considered. Based on the analysis of historical sources, architectural monuments and restoration practices of the 20th-21st centuries, both successful examples of preservation and mistakes leading to the loss of authenticity are identified. Particular attention is paid to the methods and materials used in the restoration of key sites, such as the Lyabi-Khauz and Poi-Kalyan ensembles. The necessity of a comprehensive and scientifically based approach to the protection of cultural heritage in the context of modern urbanization and tourism is emphasized.

Keywords: Bukhara, historical and cultural heritage, restoration, reconstruction, preservation of monuments, UNESCO, architecture, traditional methods, modern restoration. architecture of Central Asia; Lyabi-Khauz; Kalyan minare

ICABB26-BM-OP-22

In Silico Structural Characterization and Virtual Screening of CsaB: A Novel Antibacterial Target in Paenibacillus alvei

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Abstract

CsaB is an enzyme from the Gram-positive bacterium Paenibacillus alvei. It can be a drug target against antibacterial pathogens because it catalyzes the pyruvylation of bacterial cell wall polymers, essential for cell wall integrity and survival. CsaB uses phosphoenol pyruvate to transfer a pyruvyl moiety to cell wall sugar molecules; its inhibition would weaken the bacterial cell wall. As pyruvylation does not occur in humans, CsaB offers selective targeting. We constructed its three-dimensional structure using a homology modeling approach. The protein structure is validated susing saves and molprobity. To begin the molecular docking process ,we needed to identify potential active pockets and ligand-binding sites in the protein structure, so we used CB-Dock 2 to find geometry-based cavity and docking site prediction in protein structure. Additionally, DeepSite is used to perform deep learning–based binding

site analysis. Both tools consistently identified key residues forming the potential active pocket. Furthermore, to prepare a ligand library using molecules that are structurally similar to fosfomycin, as it has a similar structure of phosphoenol pyruvate retrieved from PubChem. Compounds are selected based on 80–90% structural similarity cutoff. The screening identified three lead molecules. The best result was Calcium fosfomycin with the highest binding energy (-10.48kcal/mol). These ligands were optimized for docking using the autodock 4.2 tool using genetic algorithm and Lamarckian genetic algorithm to evaluate binding affinities with the predicted active sites of CsaB. Also protein-ligand complex interactions were thoroughly studied where the interacting residue were Pro, Gln, Tyr, Gly i.e. majorly polar residues.

Keywords: Bacterial pathogenicity, Homology modelling, molecular docking, MD simulation, Binding site prediction.

ICABB26-BM-OP-23

Population Pharmacokinetic Study to Find the Effective Range of Narrow Therapeutic Index drugs

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Abstract

NTI drugs have a small gap between their therapeutic and toxic range, implying that if there is any small change in the drug range it can cause toxic effects which can lead to adverse drug effects. To address this challenge population based pharmacokinetic models can be used to capture inter-individual variability arising from genetics, age, organ function. By integrating these diverse parameters, we can generate a holistic dataset suitable to train a Bayesian based AI model capable of predicting the individualised therapeutic window of such drugs. This data driven Bayesian based framework enables realtime dose adjustment and early detection of toxicity risks, ultimately supporting precision dosing. Given the rising burden of cardiovascular diseases, many of which require lifelong treatment with NTI drugs such as warfarin, digoxin and certain antiarrhythmics, the need for predictive models is more critical. The present study was conducted on a dataset of Tacrolimus NTI drug with 1000+ entries and 14 features, the most important features being blood concentration, clearance level, volume of drug in the blood along with the co-variat information of the patient. Several machine learning models were applied on these datasets and it was observed that the Bayesian model gave the highest accuracy. Optimal dosage range of the drug based on the specific parameters of the patient were obtained. Further studies can be performed on more NTI drugs to find out the specific dosage range. The present study aims to find ways to improve patient safety, reduce drug toxicity and enhance overall effectiveness of cardiovascular therapy.

Keywords: Narrow Therapeutic Index (NTI) drugs, Precision dosing, Individualized therapeutic window, Adverse drug effects, Drug toxicity.

ICABB26-BM-OP-24

Nutrient-Rich Flours from Jackfruit Waste: A Study on Mineral and Vitamin Profiles

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Abstract

Jackfruit is regarded as a great source of carbohydrates, vitamins and minerals and has historically been consumed as a staple food and supplemental food in tropical areas. Jackfruit (Artocarpus heterophyllus Lam.) produces considerable agro-waste in the form of rind, rag, and seeds, which are often discarded despite their nutritional and functional potential. Approximately two-thirds of the fruit biomass consists of seeds, rind, and fibrous rag, frequently treated as agricultural waste. This study systematically evaluates the proximate composition and vitamin and mineral profiles of jackfruit seeds, rind, and rag using standard analytical methods (AOAC, ISO, AACC).

A comprehensive compositional examination measured key macro-minerals (potassium, calcium, magnesium, phosphorus, sodium), trace elements (iron, copper), and vitamins (A, B complex, C, D, E, K). Rind flour had higher calcium and iron than the other two flours; seed flour contained more phosphorus, magnesium, and potassium. Rag flour showed a balanced but overall lower mineral profile except for a relatively high potassium content. Heavy metals (lead, cadmium, and arsenic) remained below detection limits or safe levels, indicating suitability for food use. The findings provide a scientific foundation for utilizing jackfruit waste in value-added flours, transforming an abundant by-product into a nutritionally and economically valuable resource. Valorising these residues as component flours realizes jackfruit's nutritional potential and supports circular bioeconomy initiatives and sustainable food systems.

Keywords: Artocarpus heterophyllus, proximate composition, Biomass, Macro-nutrients, Trace elements, Vitamins, metabolic control.

ICABB26-BM-OP-25

Human Pluripotent Stem Cell-Derived Kidney Organoids for Genetic Renal Disease Modeling and Therapeutic Discovery

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Abstract

Genetic renal diseases pose a major clinical challenge due to limited treatment options and the lack of experimental models that accurately reflect human kidney pathology. Conventional cell culture systems and animal models often fail to capture disease-specific mechanisms at the human level, particularly in the context of complex inherited disorders. In this context, human pluripotent stem cell-derived kidney organoids have emerged as a promising three-dimensional platform that mimics key aspects of renal development, cellular organization, and early tissue patterning. Kidney organoids generated from patient-derived induced pluripotent stem cells or through targeted gene editing have enabled the modelling of several inherited kidney disorders, including autosomal dominant polycystic kidney disease, Alport syndrome, and other monogenic conditions. These models reproduce important disease-

associated features such as cyst formation, tubular defects, and glomerular dysfunction, allowing insights into early pathogenic events, genotype-phenotype relationships, and disease progression mechanisms. Importantly, kidney organoids also provide a human-relevant system for exploring therapeutic strategies, identifying potential drug targets, and assessing drug responses in a controlled in vitro environment. Recent advances in single-cell transcriptomics and molecular profiling have improved the validation and characterization of organoid models by resolving cellular heterogeneity and disease-associated molecular pathways. Although challenges related to tissue maturation, variability, and long-term disease modelling remain, continued refinement of organoid technologies, improved standardization, and integration of bioengineering approaches are expected to enhance their value as scalable platforms for genetic renal disease research and therapeutic discovery.

Keywords: Genetic renal diseases; Kidney organoids; Human pluripotent stem cells; Disease modelling; Therapeutic discovery; Drug screening; Single-cell transcriptomics

ICABB26-BM-OP-26

Multi-Pharmacological Potential of Fenugreek (*Trigonella foenum-graecum*): Experimental and Molecular Insights into Antidiabetic, Antioxidant, Anti-Inflammatory, and Anticancer Activities

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Abstract

Traditional medicinal systems such as Ayurveda and Traditional Chinese Medicine have gained increasing scientific recognition for their role in drug discovery and disease management. *Trigonella foenum-graecum* (fenugreek) is a widely used medicinal plant with well-documented therapeutic potential. The present study and review collectively summarize experimental and mechanistic evidence supporting the antidiabetic, antioxidant, anti-inflammatory, anticancer, anti-obesity, antimicrobial, and wound-healing properties of fenugreek. Phytochemical characterization using high-performance liquid chromatography (HPLC) confirmed the presence of major bioactive constituents, including polyphenols, flavonoids, alkaloids, and saponins. Antidiabetic activity was evaluated through α-amylase inhibition assays, while antioxidant potential was assessed using ABTS radical scavenging, catalase, and other enzymatic antioxidant assays. Anti-inflammatory and anticancer effects were investigated using in vitro wound-healing (scratch) assays and colony formation assays, demonstrating inhibition of cell migration, proliferation, and clonogenic survival. Collectively, these experimental findings suggest that fenugreek modulates key cellular processes related to oxidative stress, inflammation, glucose metabolism, and cancer progression. Our work highlights fenugreek as a multifunctional medicinal plant and emphasizes its potential application in functional foods, nutraceuticals, and complementary therapeutic strategies, while also outlining current limitations and future research directions.

Keywords: Antidiabetic activity, α-Amylase inhibition, Antioxidant, ABTS, Catalase, Wound healing assay, Colony formation assay, HPLC, Anticancer activity, Phytochemicals

ICABB26-BM-OP-27

Mitochondria-Targeted Therapeutic Strategies in Traumatic Brain Injury

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Abstract

Traumatic Brain Injury (TBI) is a leading cause of disability and death globally, with secondary injury processes like oxidative stress, mitochondrial dysfunction, and apoptosis contributing significantly to neuronal loss. Mitochondria play an important role in maintaining cellular energy and redox balance,

making them a potential therapeutic target for mitigating TBI-induced neuronal damage. Excess mitochondrial reactive oxygen species (ROS) damage membranes, harm mitochondrial DNA, and lead to cell death. Mitochondria-targeted therapeutic aims to preserve mitochondrial redox balance and maintain bioenergetic function by reducing oxidative damage and supporting electron transport. Targeted antioxidants, such as MitoQ and the Szeto–Schiller peptide SS-31, can neutralize ROS and stabilize mitochondrial structure, while agents like methylene blue enhance electron transfer within the mitochondrial electron transport chain, restore ATP production, decrease electron leakage at complexes I and III, and limit ROS generation. Together, these strategies show promise in limiting secondary injury, protecting neurons, and improving functional recovery after TBI. However, challenges remain, including optimizing dosing, delivering these therapies effectively to the brain, and confirming their benefits in clinical trials. With further research, mitochondria-targeted therapies have the potential to improve outcomes for patients suffering from TBI.

Keywords: Mitochondria-targeted therapeutics, MitoQ, mitochondrial dysfunction, neuroprotection, oxidative stress, traumatic brain injury.

ICABB26-BM-OP-28

MODULATION OF THE GUT BRAIN AXIS THROUGH PROBIOTIC ENCAPSULATION AS A THERAPEUTIC STRATEGY

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Abstract

Gut -Brain Axis plays a major role in regulating the health by reducing the dysbiosis in the gut which can lead to various neurodegenerative disorders. millions of microorganisms are found in the human gut, which plays a significant role in maintaining health and preventing various diseases. a dysbiosis in the gut microbiota can result in a number of disorders, including Alzheimer's and Parkinson's disease. The Vegas nerve, are an important component of the autonomous nervous system, which acts as a direct conduct between the gut and the brain and plays a part in regulating immune system function, research indicates that this condition can be managed by maintaining an appropriate population of beneficial gut microbiota through consumption of probiotics, prebiotics and postbiotics which can restore the gut microbiota. The mechanism through which the gut microbiota can be restored include consumption of Fiber rich food as they are non -digestible in the upper digestive system and pass as it to the lower digestive system and the beneficial microorganisms present such as *bifidobacterium* and *lactobacillus* ferment the Fiber and produce short chain fatty acids such as butyrate and propionate which contain anti-inflammatory properties and reduce growth of pathogenic microorganisms.As the probiotics have several beneficial effects and they are ingested into the body to treat several disease several study shows that to increase the bioavailability and successful delivery of probiotics into the body to cure the disease include microencapsulation where they are enclosed within micro protective shells and nanoencapsulation where enclosed within nanoparticle as they prevent degradation of probiotics from the acidic pH and enzymes present in the gut this method efficiently helps to integrate probiotics into the target site without degradation.

Keywords: Gut-Brain Axis, Probiotics, Dysbiosis, Microencapsulation, Nanoencapsulation

ICABB26-BM-OP-29

Nutraceutical Approaches to Brain Health and Cognitive Function: Neuroprotective Roles of Functional Mushrooms and Plant-Based Bio actives

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Abstract

Cognitive function depends on coordinated regulation of the brain energy, adapts at the synapse, makes neurotransmitters, and defends itself against oxidative and inflammatory damage. When nutrition falls short or cognitive stress drags on, these systems falter memory slips, focus fades, and mental stamina drops. The present study focuses on designing nutritional supplement by bringing together specific mushrooms and plant metabolites. Brain health supplements step in to support these pathways, delivering nutrients and bioactive compounds known for their neuroprotective effects.

Shiitake and lion's mane mushrooms offer a powerful mix: polysaccharides, ergothioneine, B-complex vitamins, and neuroactive molecules. Together, they boost antioxidant defences, modulate the immune system, and help maintain neurons. Lion's mane stands out for its hericenones and erinacines compounds that ramp up nerve growth factor production and encourage neurite growth, supporting both synaptic health and cognition. Chia seeds bring their own strengths: complete plant protein, essential amino acids, and omega-3s (α-linolenic acid) that keep neuronal membranes flexible, support synaptic signalling, and help regulate neuroinflammation. Spinach adds folate, iron, magnesium, and polyphenols, all key for one-carbon metabolism, oxygen delivery, and fighting oxidative stress in brain tissue. Citrus peel packs in flavonoids and phenolic compounds, which help control oxidative stress and tamp down inflammatory pathways linked to cognitive decline. Put together, the distinct biochemical profiles of these plant and mushroom ingredients work in concert to support neuronal metabolism, synaptic activity, and redox balance. Including them in brain health supplements gives a strong scientific foundation for improving cognitive resilience and preserving neurological health, especially when mental demands are high.

Keywords: Cognitive neurobiology, Neuroprotective nutraceuticals, Nerve growth factor (NGF), Oxidative stress modulation, Neuroinflammation

ICABB26-BM-OP-30

Targeting Extracellular Matrix Remodelling through Phytochemicals: Mechanistic Perspectives in Women's Health

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Abstract

The extracellular matrix (ECM) is not merely a structural scaffold but a highly dynamic and bioactive network that regulates tissue integrity, cell signalling, and hormonal responsiveness. Growing evidence identifies disturbed ECM remodelling as a key pathological driver in several women's health disorders, including polycystic ovary syndrome (PCOS), endometriosis, uterine fibroids, breast and ovarian cancers, pelvic inflammatory diseases, and age-related reproductive tissue degeneration. Abnormal matrix metalloproteinase (MMP) activity, excessive collagen accumulation, disrupted elastin organisation, and persistent low-grade inflammation collectively promote fibrosis, loss of tissue elasticity, impaired cell-matrix communication, and progressive tissue dysfunction.

Plant-derived phytochemicals have emerged as a promising class of multi-functional bioactive compounds capable of restoring ECM homeostasis. Major phytochemical groups such as polyphenols,

flavonoids, anthocyanins, terpenoids, and alkaloids exert regulatory control over MMP expression, transforming growth factor-β (TGF-β) signalling, oxidative stress responses, inflammatory pathways, and fibroblast behaviour. Through these interconnected mechanisms, phytochemicals are uniquely positioned to modulate both ECM synthesis and degradation, supporting balanced remodelling rather than isolated pathway suppression.

This review examines the mechanistic foundations of selected flowers to interact with ECM-associated molecular networks. Particular attention is given to their roles in controlling collagen turnover, limiting pathological fibrosis, influencing epithelial-mesenchymal transition, and reshaping inflammatory microenvironments.

By integrating molecular, cellular, and translational perspectives, this article positions ECM remodelling as a unifying therapeutic framework and highlights phytochemicals as scientifically grounded, system-level modulators with strong potential to advance innovative, women-centred healthcare strategies.

Keywords: Women's Health, Plant-derived phytochemicals, Extracellular matrix, matrix metalloproteinase, ovarian cancers,

ICABB26-BM-OP-31

"Phytochemical Profiling and Functional Validation of *Tinospora cordifolia* Targeting α-Amylase Activity and Oxidative Stress in Diabetic Nephropathy"

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Abstract

Diabetic nephropathy (DN) develops as a consequence of chronic hyperglycemia and sustained oxidative stress, ultimately leading to progressive renal damage. Natural products capable of simultaneously modulating glycemic load and redox imbalance are therefore of increasing interest. In this study, *Tinospora cordifolia*, a widely used medicinal plant in traditional systems of medicine, was investigated for its phytochemical composition and its ability to inhibit α-amylase activity and scavenge free radicals, two key processes implicated in DN progression.

Phytochemical profiling revealed the presence of abundant phenolics, flavonoids, alkaloids, and terpenoid compounds. Functional evaluation demonstrated a concentration-dependent inhibition of α-amylase activity, indicating the potential of the extract to regulate post-prandial glucose levels. In parallel, the extract demonstrated strong antioxidant activity across multiple in vitro assays, indicating a robust capacity to neutralise reactive oxygen species.

The convergence of enzyme inhibitory and antioxidant effects suggests a synergistic mechanism through which *T. cordifolia* may alleviate hyperglycemia-induced oxidative stress, a central driver of renal injury in diabetic nephropathy. These findings provide experimental support for the therapeutic relevance of *T. cordifolia* and underscore its promise as a natural, multitarget intervention for managing early pathogenic events associated with DN. Further cellular and molecular studies are warranted to validate its renoprotective potential.

Keywords: *Tinospora cordifolia*, Diabetic nephropathy, Phytochemicals, α-amylase inhibition, Antioxidant activity

ICABB26-BM-OP-32

Machine Learning-Guided Discovery of Coconut-Derived FtsZ Inhibitors for Antitubercular Therapy: An Integrated In Silico Approach

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Abstract

Tuberculosis, caused by Mycobacterium tuberculosis, presents a huge global health challenge, especially with the emergence and prevalence of the multidrug-resistant and extensively drug-resistant varieties. The Filamenting temperature-sensitive mutant Z (FtsZ) protein, the bacterial tubulin homolog and mediator of cell division, presents a promising target for treatment, given its indispensable nature for the assembly of the Z-ring and the nonexistence of a human ortholog. The present work followed a systematic in silico approach for the prediction of natural products based on coconut as potential inhibitors of FtsZ. Virtual screening using the COCONUT database and machine learning-based prediction of the bioactivity resulted in shortlisting lead candidates based on high predicted values for the pIC_{50} and good binding potential. The electronic properties were predicted using density functional theory (DFT), and pharmacokinetic properties were estimated to be using ADMET screening. 1000 ns molecular dynamic simulation confirmed stable binding for the ligands with good correlation with the RMSD, RMSF, the protein-ligand contact maps, hydrogen bonding, radius of gyration, and solvent exposure studies. Energetic calculations using the MM/GBSA and the QM/MM calculations confirmed favorable binding and electronic compatibility. Principal Component Analysis (PCA) as well as Free Energy Landscape (FEL) mapping confirmed the occurrence of conformational stability, and low-energy pose superimposition justified structural convergence. The optimum potential FtsZ inhibitors based on the double cross-validation across the analyses were the compounds CNP0281420, CNP0277831, and CNP0310586. The present work has been able to validate the potential for therapy from coconut-based scaffolds, besides providing a proven computational lead for the discovery and ranking of natural-product-based antimicrobials.

Keywords: FtsZ inhibitors, Mycobacterium tuberculosis, Molecular dynamics simulation, Coconut natural products, Antibacterial drug discover

ICABB26-BM-OP-33

Bioactive Compounds of *Saccharomyces boulardii* as potential leads against cancer targets revealed by molecular docking and molecular dynamics simulations

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Abstract

Saccharomyces boulardii, a probiotic yeast, is recognised for its advantageous impact on gastrointestinal health and enhancement of general human wellness. This study investigated the impact of bioactive compounds from *S. boulardii* in relation to interrelated gastrointestinal and neurological illnesses, as well as associated malignancies, through the gut-brain axis, utilising network

pharmacology. Of the 116 compounds from S. boulardii (extracellular and/or intracellular) during data mining, 10 were selected based on ADMET analysis. SwissTarget Prediction and SuperPred found 682 distinct human targets linked to these compounds. Gene associated with diseases, after analysis, showed 1,390 related genes associated with targeted illnesses. These illness related genes were sourced from the GeneCards and DisGeNET databases, yielding 115 overlapping genes between anticipated targets and disease categories. STRING and Cytoscape facilitated the analysis of protein–protein and protein-target interactions, revealing 1,174 interactions and demonstrating robust connectivity. The integration with S. boulardii resulted in a network comprising 127 nodes and 1,509 edges. The principal bioactive chemicals comprised phenyllactic acid, tyrosol, 4-hydroxymandelonitrile, and 2-propylpiperidine. Functional enrichment analysis by GO, KEGG, and Reactome identified correlations with the regulation of signal transduction, apoptosis, and oncogenic pathways. Twenty-two primary targets, along with four chosen bioactive molecules, underwent assessment of binding affinity. The foremost four complexes were examined for molecular interactions through molecular dynamics simulations, and free energy assessments indicated robust binding affinities for EGFR-phenyllactic acid (-26.2 kcal/mol), CXCR4-phenyllactic acid (-24.6 kcal/mol), EGFR-tyrosol (-19.0 kcal/mol), and EGFR-4-hydroxymandelonitrile (-18.6 kcal/mol). The findings indicate that bioactive chemicals from S. boulardii interact with human proteins such as ABL1, PTPN11, EGFR, and CXCR4, underscoring their potential in experimental validation.

Keywords: Network Pharmacology; Cancer targets; Molecular Dynamics Simulations; Gut-brain axis; GMX_MMPBSA

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Synthesis and In Vitro Antileishmanial Evaluation of Schiff-Base Metal Complexes against Leishmania donovani

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Abstract

Visceral leishmaniasis (VL) is the most severe and fatal form of leishmaniasis that remains a major public health challenge in endemic regions due to the absence of an effective vaccine and the growing limitations of existing chemotherapeutic agents. These limitations include high toxicity, emerging drug resistance, parenteral administration, prolonged treatment regimens and high cost highlighting the urgent need for safer, more effective and affordable therapeutic alternatives. In the present study, a series of Schiff-base derived compounds and their corresponding metal complexes were synthesized and evaluated for their antileishmanial potential on VL causing Leishmania donovani. All compounds were initially subjected to primary in vitro screening against L. donovani promastigotes, the causative agent of VL, while in silico analysis was performed exclusively on the Schiff-base ligand. A total of 7 compounds were first screened for their in vitro anti-promastigote activity. Two of these compounds exhibited significant antileishmanial activity with visible reduction in parasite growth. The best two compounds exhibiting most potent activity were examined further for IC50 evaluation, toxicity analysis against mammalian host cells and anti-amastigote activity. Against promastigotes, L6 and L7 exhibited significant growth inhibition and demonstrated IC_{50} values of 7.072 and 1.319 µg/mL, respectively. To

assess host-cell safety, cytotoxicity studies were conducted THP-1 derived human macrophages. Compounds L6 and L7 displayed favourable safety profiles, followed by evaluation of their leishmanicidal potential against clinically relevant intra macrophagic form of the parasite. L6 and L7 compounds exhibited pronounced anti-amastigote activity, achieving significant reduction in intracellular macrophagic parasite burden with IC_{50} values of 2.855 and 0.6140 µg/mL, respectively. Overall, these findings highlight Schiff-base derived metal complexes as promising candidates for VL chemotherapy. The potent in vitro efficacy, favourable host cell safety and strong anti-amastigote activity support further mechanistic investigations and in vivo validation.

Keywords: Schiff base, Visceral Leishmaniasis, Metal complex, Leishmaniasis, Leishmania donovani

ICABB26-BM-OP-35

An Integrated Machine Learning–Based QSAR and Virtual Screening Framework for Identifying Potential MurA Inhibitors in Mycobacterium tuberculosis

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Abstract

Antimicrobial resistance in Mycobacterium tuberculosis is becoming more common, which emphasizes the need for new treatment targets. Enolpyruvyl transferases, which are necessary for the formation of Mycobacterium tuberculosis' cell walls, are examined in this work as possible targets. A machine learning-based QSAR model was trained using experimentally confirmed IC_{50} values for known enolpyruvyl and glycosyl transferase inhibitors from ChEMBL. Important molecular characteristics that were found to be important predictors of inhibitory activity were molecular weight, hydrogen bond donors and acceptors, and electrostatic surface characteristics. The discriminative capacity of the model was confirmed by principal component analysis, which showed a clear clustering of active and inactive chemicals. High- confidence hits with strong anticipated binding to MTB enolpyruvyl transferases were given priority by the QSAR model for molecular dynamics research, docking, and subsequent virtual screening. This integrative ML-QSAR and computer- aided drug design pipeline creates a logical framework to speed up the development of new anti-tubercular medicines that target AMR-associated pathways and offers useful insights into structure–activity connections.

Keywords: Mycobacterium tuberculosis, Antimicrobial resistance (AMR), Enolpyruvyl Trans- ferase, Machine learning, QSAR modeling, Virtual screening, Principal component analysis, Drug Discovery.

ICABB26-BM-OP-36

Fungal Bioactives as Potential Antileishmanial Agents

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Abstract

Leishmaniasis is a neglected parasitic disease that continues to impose a substantial health burden in endemic regions, largely due to limitations of available chemotherapy, appearance of resistant strains, association of Leishmania with AIDS and atypical parasite tropism. These challenges highlight the importance to search for promising antileishmanial candidates from natural and eco-friendly sources.

Fungal metabolites have been identified as potential leads for the antiparasitic drug discovery with particular species of versatile soil fungi (SF) capable of producing a broad range of bioactive compounds. Secondary metabolite profile of one such fungus was studied through available literature and fungal metabolite library was subjected to in silico screening against validated drug target(s) in Leishmania parasite. In silico studies showed strong binding affinities and stable interactions of the selected fungal metabolites with critical parasitic target(s). This study emphasizes SF as a promising natural source of anti-leishmanial compounds and highlights the utility of combining in vitro and in silico approaches. Further purification, target validation, and in vivo evaluation are essential to advance these fungal bioactives toward therapeutic development.

Keywords: Leishmania, Leishmaniasis, Anti-leishmanial activity, Fungal bioactives, Secondary metabolites.

ICABB26-BM-OP-37

Effect of probiotics for prevention and treatment of upper respiratory tract infections(URTIs) in children and young adults

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Abstract:

Upper respiratory tract infections(URTIs) are the reason behind numerous deaths worldwide whether caused by viruses or lifestyle related issues like cigarette smoke extract(CSE) or air pollution. It remains a significant source of disease burden in children and young adults. Exposure to fine particulate matter(PM2.5) has a critical role in the development of pulmonary inflammation , oxidative stress and systematic dysbiosis by disrupting the “gut-lung axis”. Despite early evidence for probiotics, applications in curative use remains untapped . Moreover, strain specific evidences that inform about the effective dosage , formulation and study the demographic ranging from children (2-12yr) and young adults (13-25yr). To bridge this gap ,we conducted a meticulous literature search to collect current data that emphasizes the therapeutic and preventive potency of probiotics for URTIs. An adjunctive strategy that would prevent the extensive misuse of antibiotics in the long run. Peer-reviewed articles, systematic reviews and randomized control trials(RCTs) from 2016 -2025 ,were studied to analyze the clinical outcomes which incorporates symptom duration, specific strains, dosage, incubation period and antibiotic consumption rates following probiotic mediation . Key findings of Lactobacillus acidophillus evaluated immunomodulation in RAW264.7 macrophages , assessing cytoprotection in human bronchial epithelial cells (HBEpiC) against cigarette smoke extract as a PM2.5 proxy , and measuring the restoration of intestinal barrier integrity in Caco-2 cells. Daily dosing of Bifidobacterium longum YLGB-1496 lowered URTIs incidences in children which notably reduced the duration of cough and fever . Similarly , lactobacillus rhamnousu GG(LGG) supplementation in milk was found to reduce the risk of acute respiratory infections and aintibiotic prescription in children attending daycare.Bifidobacterium breve M-16V & multi-strain symbiotic approach (Lactobacillus casei + Bifidobacterium lactis + Fructooligosacchraides) persistently indicated the greatest benefits. Conversely single strain administrations demonstrates no significant impact. Systematically , these strains were shown to alleviate immune biomarkers , multiply levels of IgA and IgG while minimizing the levels of pro-inflammatory cytokines like IL-1β and IFN γ . In young adults regular mediation of probiotics showed sustained levels of natural killer cells .These findings established that probiotics interventions are a safe adjunctive strategy for decreasing URTIs.

Keywords:
Probiotics, Upper respiratory tract infections(URTIs), cigarette smoke extract(CSE), Air pollution.

ICABB26-BM-OP-38

Exploiting Cysteine-Induced Metabolic Vulnerability to Restore Antibiotic Efficacy in Multidrug-Resistant Pathogens

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Abstract
The increasing prevalence of multidrug-resistant (MDR) bacterial pathogens poses a serious threat to global public health and necessitates alternative strategies to enhance the efficacy of existing antimicrobial agents. The metabolic state of bacteria has been shown to closely correlate with their susceptibility to antibiotics, prompting growing interest in metabolic modulation as a strategy to overcome antimicrobial resistance. Accumulating evidence supports the use of metabolic modulators as effective antimicrobial adjuvants capable of revitalizing conventional antibiotics. Given that cysteine can influence cellular metabolic states through the induction of reactive oxygen species, it was hypothesized that cysteine may modulate bacterial metabolism and thereby restore antibiotic activity. Accordingly, the present study investigated the potential of cysteine, a key cellular metabolic regulator, as an adjuvant for reinstating antibiotic susceptibility in MDR pathogens. Growth kinetic analyses of ESKAPE pathogens were performed in minimal media in the presence and absence of cysteine, revealing a concentration-dependent inhibitory effect on bacterial growth. Based on these findings, the antibacterial efficacy of cysteine in combination with commonly prescribed antibiotics was further evaluated. Overall, this study highlights the therapeutic potential of combining cysteine with existing antibiotics as a cost-effective and clinically translatable strategy to combat antimicrobial resistance.
Keywords: multi drug resistance; cysteine; Antibiotics; Cysteine Metabolism; Sulfur metabolism

ICABB26-BM-OP-39

Evaluation Of Ubiquitous Plant Species **as a source of Potential Antileishmanial Agents**

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Abstract
Leishmaniasis, caused by Leishmania donovani, is still a serious public health concern, especially in tropical and subtropical climates. Although current chemotherapeutic treatments, such as Amphotericin B (AmB), are effective, they are associated with severe toxicity, a high cost, and the potential for drug resistance. Thus, there is an urgent requisition of more efficacious new drugs that can combat rising drug resistance with improved safety. The present study aims to investigate the antileishmanial potential of selected ubiquitous plant species as safer and more sustainable alternatives to synthetic antileishmanial drugs. In this study, extracts of two common edible plants were prepared by the percolation method using n-hexane and ethanol as extraction solvents, and tested for antileishmanial activity against Leishmania donovani amastigotes. The antileishmanial efficacy was determined using the MTT assay, and the results were compared to the standard medicine, AmB. The experimental data

indicated that the plant extracts exhibited significant antileishmanial activity at the tested concentrations. As appraised by MTT assay, ethanolic fraction of plant 1 (BVE) showed the strongest inhibitory effect, reducing parasite viability to 30.39% and induced significant changes in parasite morphology supporting its potential as a promising candidate for further investigation. The observed activity may be attributed to bioactive phytochemicals such as flavonoids, tannins, and phytosterols present in the plant. This study concludes by highlighting the possibility of ubiquitous plant species as viable sources of antileishmanial agents derived from plants. The results encourage further phytochemical characterization and ex vivo & in vivo studies to create safer, economical, and efficient substitutes for antiquated synthetic leishmaniasis medications.
Keywords: Leishmania donovani, Leishmaniasis, Leishmania, Traditional medicine, Antileishmanial chemotherapy, Plant bioactives.

ICABB26-BM-OP-40

Phytochemical Analysis, Antioxidant Properties, and Anticancer Activity of Citrus limetta Peel Extract on Skin Cancer Cell Line

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Abstract

Citrus limetta peel contains diverse polyphenolic compounds, including flavonoids, coumarins, phenolic acids, terpenoids, tannins, sterols, anthocyanins, and quinones. Among these, flavonoids are considered key bioactive components, particularly for their anticancer properties. This study aimed to perform a comprehensive phytochemical screening of C. limetta peel extracts using various solvents and to evaluate their antioxidant and anticancer activities. Quantitative analyses of phenolic compounds, flavonoids, and tannins were conducted, along with antioxidant activity assessments. Advanced analytical techniques, including TLC, HPTLC, HPLC, and FTIR, were employed to characterize the qualitative and quantitative composition of the extracts. The antiproliferative activity of the extracts was evaluated on A431 skin cancer cell lines using the MTT assay. The qualitative analysis revealed that the ethanolic and methanolic extracts contained various phytocompounds compared to extracts obtained using other solvents. The methanolic and ethanolic extracts exhibited significantly higher phenolic and flavonoid contents, with the ethanolic extract demonstrating superior antioxidant activity. *In vitro* findings suggest that the ethanolic peel extract of C. limetta may serve as a promising source of bioactive compounds with potential anticancer activity.

Keywords: *Citrus limetta* Phytochemical analysis, Quantitative analyses, Antioxidant activity, Anticancer activity

ICABB26-BM-OP-41

Targetable, State-Specific Tight Junction Plasticity in Gastrointestinal Cancers: Insights from Patient-Derived Organoids and Xenografts

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Abstract

Tight junctions (TJs) are multiprotein complexes positioned at the apical domain of epithelial cells that regulate paracellular permeability and maintain apicobasal polarity in the gastrointestinal (GI) tract. In healthy epithelia, TJ organization is dynamically regulated to accommodate epithelial renewal while preserving barrier integrity. In GI cancers, however, TJ components undergo context- and state-dependent alterations in expression and subcellular localization that extend beyond junctional

disassembly and actively influence epithelial plasticity, signaling, and tumor behavior. Dysregulated TJ states are increasingly linked to altered differentiation, invasive potential, inflammatory crosstalk, and therapeutic vulnerability.

This presentation focuses on patient-derived organoids and xenograft-based models that retain native epithelial architecture, lineage heterogeneity, and tumor-specific TJ configurations, thereby overcoming limitations of conventional two-dimensional systems. Application of these models has enabled systematic interrogation of reversible transitions between junctional and non-junctional TJ states and their coupling to pathways governing proliferation, invasion, and treatment response. Collectively, these insights support a unified framework in which state-specific TJ plasticity functions as an active and targetable determinant of GI cancer progression, underscoring the translational value of advanced patient-derived platforms.

Keywords: Tight junctions; gastrointestinal cancer; epithelial polarity; claudins; junctional plasticity; patient-derived organoids; signaling plasticity; tumor heterogeneity

ICABB26-BM-OP-42

Development of a Bioactive Keratin–Moringa oleifera Hydrogel for Wound Healing and Topical Applications

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Abstract

Keratin is a cysteine-rich, biocompatible, film-forming biopolymer widely used in cosmetic, pharmaceutical, and topical delivery systems. Its ability to support cell adhesion and form a moist protective barrier promotes tissue regeneration and enhances wound-healing efficacy. In the present study, keratin was extracted from chicken feathers using an optimized alkaline hydrolysis process and characterized to confirm its suitability as a biocompatible and film-forming biomaterial. A multifunctional keratin-based hydrogel was prepared by optimizing suitable structuring, emulsifying, and stabilizing agents to obtain a stable, hydrated, and skin-compatible matrix. The hydrogel exhibited high moisture retention, good spreadability, and suitable mechanical stability, which are essential properties for effective wound dressing and topical application. To provide additional therapeutic activity, a medicinal plant with well-established antioxidant, anti-inflammatory, and antimicrobial properties was incorporated as a bioactive component. Accordingly, Moringa oleifera extract was prepared and evaluated through qualitative and quantitative phytochemical analyses and antioxidant activity, confirming the presence of bioactive compounds, including polyphenols and flavonoids, with strong free-radical scavenging and antimicrobial properties. The moringa extract was then incorporated into the keratin hydrogel to form a bioactive composite system. Further physicochemical and analytical characterization will be performed, including pH, viscosity, swelling behavior, stability, and structural analysis, to check the suitability of the keratin–moringa hydrogel for topical and wound-healing applications. Skin irritation and wound-healing effects will be studied in the BALB/c mouse model to check biocompatibility and healing performance.

Keywords: Biopolymer matrix, herbal bioactive, antioxidant activity, antimicrobial efficacy, wound-healing, biomedical formulation

ICABB26-BM-OP-43

In Vivo Assessment of Acute and Subacute Toxicity and Antioxidant Activity of Methanolic Ziziphus jujuba (Mill.) Leaf Extract in Male Wistar Rats

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Abstract

The methanolic extract of *Ziziphus jujuba* Mill, a traditional medicinal plant from Morocco, was evaluated for its acute and subacute toxicity in male Wistar rats through an integrated approach combining hematological and biochemical analyses. Plant material was collected in the Taza region, dried away from light, powdered, and subjected to maceration in methanol for extraction.

For the acute toxicity study, animals received a single oral dose of the extract in accordance with OECD Guideline 423, while a control group received distilled water. The subacute toxicity study involved repeated oral administration over 28 days, following OECD Guideline 407. Toxicity assessment included clinical observation, body weight monitoring, food and water intake, as well as hematological and biochemical analyses.

This study provides a comprehensive evaluation of the safety profile of *Ziziphus jujuba* methanolic extract in male Wistar rats, supporting its potential use in therapeutic applications.

Keywords: Ziziphus jujuba; acute toxicity; subacute toxicity; male; Wistar rat; hematology; biochemistry; OECD guidelines

ICABB26-BM-OP-44

Heterogeneity and Carcinogenic Risk in Indian Smokeless Tobacco Products: New Insights

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Abstract

Smokeless tobacco (SLT) products are widely perceived as less harmful than smoked tobacco and are predominantly linked to oral cancer, leading to systematic underestimation of their broader public health impact. In India, where SLT use is highly prevalent and manufacturing remains largely unregulated, major knowledge gaps persist regarding product heterogeneity, tobacco-specific nitrosamine (TSNA) burden, additive use, microbial contamination and carcinogenic mechanisms beyond oral exposure. This comprehensive analysis evaluated five commonly consumed Indian SLT categories - Pan Masala, Khaini, Zarda, Gudaku, and chewing tobacco leaves, using integrated physical, chemical, microbiological, and metagenomic approaches.

Marked inter and intra-product variability was observed in pH (5.03–10.23) and moisture content (7.79%–97.26%), parameters that directly influence nicotine bioavailability, addiction potential, and toxicant exposure. Microbial analyses revealed diverse aerobic, anaerobic, fungal and nitrate/nitrite-reducing bacteria across products, with Pan Masala exhibiting the highest microbial diversity, Khaini supporting predominantly anaerobic communities and Zarda products showing minimal microbial presence. Metagenomic profiling demonstrated dominance of Firmicutes and Proteobacteria, with Bacilli exceeding 94% abundance across products. Species richness ranged from 5–11 per sample,

including several bacteria previously associated with tobacco environments. Chemical analyses showed subgroup-specific TSNA profiles, with NNK predominating in Khaini and NNN in Pan Masala, highlighting differential carcinogenic risk by product type. Nitrate-reducing bacteria-potential contributors to endogenous TSNA formation, were most prevalent in Pan Masala.

These findings demonstrate that SLT products constitute a highly heterogeneous and poorly regulated public health hazard, with product-specific differences in addiction potential, microbial ecology, and carcinogen exposure. Treating SLT as a uniform risk category obscures critical differences relevant to cancer prevention, surveillance, and regulation. Product-specific classification and microbiome-informed risk assessment are essential to strengthen tobacco control policies, improve clinician awareness of multi-site cancer risks, and guide targeted public health interventions in high-burden populations.

Keywords: Carcinogenic risk; Smokeless tobacco; Tobacco-specific nitrosamines (TSNAs); Microbiome; Public health impact

ICABB26-BM-OP-45

Neuroinflammation as a Biological Mechanism Underlying Depression

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Abstract

Depression is a multifactorial disorder traditionally associated with neurotransmitter imbalance; however, recent biological evidence suggests that immune system dysregulation plays a significant role in its pathophysiology. Neuroinflammation has emerged as a critical biological mechanism linking environmental stressors to molecular and cellular changes in the brain. Elevated levels of pro-inflammatory cytokines such as interleukin-6 (IL-6), tumor necrosis factor-alpha (TNF-α), and C-reactive protein (CRP) have been frequently reported in individuals suffering from depressive disorders, indicating a strong association between inflammation and mood regulation.

This research paper examines the role of neuroinflammation in the development and progression of depression, focusing on its impact on neurotransmission, neuroplasticity, and stress-response pathways. Chronic psychological stress activates immune signaling pathways that disrupt the hypothalamic–pituitary–adrenal (HPA) axis, alter serotonin metabolism, and reduce the expression of brain-derived neurotrophic factor (BDNF). These biological alterations impair synaptic connectivity and neural resilience in key brain regions such as the hippocampus and prefrontal cortex, which are essential for emotional regulation and cognitive function. Understanding depression from a biological perspective highlights neuroinflammation as a potential biomarker for diagnosis and disease monitoring. Additionally, targeting inflammatory pathways may offer novel therapeutic strategies that complement conventional antidepressant treatments. This study emphasizes the importance of integrative biological research in redefining depression as a systemic disorder, thereby contributing to improved diagnostic accuracy and the development of more effective treatment approaches.

Keywords: Neuroinflammation; Depression; Cytokines; HPA Axis; Neuroplasticity

ICABB26-BM-OP-46

Understanding Aβ16-22 Conformational Switching in Alzheimer's Disease

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Abstract

Neurodegenerative disorders (ND) such as Alzheimer's (AD) remain a major incurable problem largely due to an opaque mechanistic understanding of pathogenic protein aggregation at the molecular level. While amyloid beta (A**β**)fibrils are the main culprit for AD pathology, recent evidence identifies early oligomers as neurotoxic species. The K16-E22 hydrophobic core governs beta sheet formation, cross-seeding interactions with tau, and nucleation kinetics, making it a critical regulator of A**β** conformational switching. In this study, a rational peptide-analogue strategy was adopted to explore how sequence-level mutations within the K16-E22 segment regulate conformational stability and aggregation. Initially, twenty peptide analogues were designed and screened using PROTPARAM(hydrophobicity) and WALTZ(beta propensity). Following the evaluation of these metrics, five representative analogues were selected to systematically evaluate specific molecular attributes: enhanced hydrophobicity(ALVFFAE: GRAVY +1.957, WALTZ 98.66)), increased β-propensity (KIVFFAE: GRAVVY +1.243, WALTZ 98.327), β-sheet disruption via proline insertion (KLPFFAE: GRAVY +0.314, WALTZ 0), charge density effects (KKVFFAE: GRAVY +0.043, WALTZ 0), and positional charge redistribution without hydrophobicity change (LVFKFAE: GRAVY +1.143, WALTZ 94.31), using the native KLVFFAE(GRAVY +1.143, WALTZ 97.8) sequence as a control. Three-dimensional structures of these selected peptides were generated using PEP-FOLD and validated via QMEAN scoring before molecular dynamics simulations(GROMACS), to link sequence properties to conformational switching pathways. This work aims to pinpoint which molecular feature drives peptides to aggregate and which helps them to resist it. The results of this study are hypothesized to illuminate mechanistic details of disease progression and enable rational design of peptide-based aggregation modulators.

Keywords: neurodegenerative disorders(ND), Alzheimer's disease(AD), amyloid beta(A**β**), in silico analysis, conformational switching.

Session 2:
Environmental Biotechnology and Sustainable Agriculture
Poster Presentations

ICABB26-EA-P01

Plant Growth-Promoting Rhizobacteria (PGPR) as Biofertilizers

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Abstract

Plant Growth-Promoting Rhizobacteria (PGPR) are beneficial soil microorganisms that colonise the rhizosphere and enhance plant growth through various direct and indirect mechanisms. Acting as natural biofertilizers, they improve nutrient availability by fixing atmospheric nitrogen, solubilizing phosphate, and producing essential phytohormones such as indole acetic acid, gibberellins, and cytokinins. In addition to promoting growth, PGPR play a vital role in protecting plants from pathogens and abiotic stresses through siderophore production, antibiotic secretion, and the induction of systemic resistance. The present study focuses on the effectiveness of common PGPR strains, including *Rhizobium, Azospirillum, Azotobacter, Bacillus, and Pseudomonas*, in enhancing plant productivity and soil health. Case studies on rice under water-deficit conditions and tomato cultivation in sandy soils revealed significant improvements in plant height, chlorophyll content, biomass accumulation, and water-use efficiency upon PGPR inoculation. These findings demonstrate the potential of PGPR as a sustainable and eco-friendly alternative to chemical fertilisers. By enhancing nutrient uptake, soil fertility, and crop resilience, PGPR contribute to low-input, climate-smart agricultural practices. Their integration into modern farming systems holds promise for improving crop yields, maintaining soil biodiversity, and supporting long-term environmental sustainability.

Keywords: Plant Growth-Promoting Rhizobacteria (PGPR), Biofertilizers, Rhizosphere, Nitrogen Fixation, Phosphate Solubilization, Phytohormones, Siderophores

ICABB26-EA-P02

Pharmacological potential of holy plants *Calotropis procera* and *Aegle marmelos*

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Abstract

Plants have a special importance in our culture, showing a deep bond with nature, spirituality and healing. Among these *Aegle marmelos* (Bael) and *Calotropis procera* (Aak) are such plants that can be found abundantly across Indian subcontinent and are sacred to Hindu traditions, as they are offered to Lord Shiva during rituals and prayers. Also, very well known for their healing properties in the traditional knowledge of Ayurveda, Siddha and Unani, where they have been used for many years already. *A.marmelos* is used in the treatment of conditions like indigestion, respiratory ailments, diabetes, inflammation and hepatic detox, due to its rich content of secondary metabolites such as alkaloids, tannins, flavonoids and coumarins. It works by up-regulating enzymes such as superoxide dismutase (SOD) and catalase and reducing inflammatory cytokines such as TNF-alpha, IL-1beta and IL-6. It helps in the breakdown of glucose by upregulating enzymes like hexokinase and glucose-6-

phasphate. On the other hand, *C.procera* has been used in traditional medicine in controlled doses for pain relief, wound healing anti-inflammatory effects, even though it is known for its toxicity. It contains cardenolides, triterpenoids, aur flavonoids, which help maintain cell membrane stability, neutralize harmful ROS and block enzymes such as COX and NOS which are responsible for inflammatory conditions. This review aims to highlight the ethnobotanical importance, phytochemical diversity and molecular mechanisms of *Aegle marmelos* and *Calotropis procera*, so that modern drug discovery could benefit with its valuable potential.

Keywords: Ayurveda, Molecular mechanism, Pharmacological potential, Therapeutic application, *Aegle marmelos, Calotropis procera*

ICABB26-EA-P03

Emerging Bioadsorbent Materials for Efficient Removal of Antibiotics and Resistance Genes from Wastewater

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Abstract

The persistent presence of antibiotic residues in wastewater poses a significant environmental and public health threat, contributing to the emergence of antibiotic-resistant bacteria and genes. Conventional wastewater treatment methods often fail to efficiently remove these complex pollutants, necessitating the exploration of sustainable and cost-effective alternatives. Bioadsorbents derived from natural, agricultural, or biological sources have recently emerged as promising materials for antibiotic remediation due to their high surface area, functional group diversity, and biodegradability. This study focuses on recent advancements in the use of bioadsorbents and modified bio-based materials for the removal of antibiotics from wastewater. The superior adsorption efficiency of biochar, chitosan composites, and agricultural waste derived materials in capturing a wide range of antibiotic contaminants such as ciprofloxacin, tetracycline, and sulfonamides. Modifications involving metal impregnation, surface activation, and composite formation have been shown to enhance adsorption capacity and reusability while maintaining environmental compatibility. Additionally, novel biosorbents exhibit potential in simultaneously reducing antibiotic resistance genes, supporting their dual role in pollution control and microbial resistance mitigation. Overall,
bioadsorbent-based treatment technologies offer a sustainable and scalable approach for antibiotic removal, aligning with the goals of green chemistry and circular economy principles. Continued research focused on mechanistic insights, material optimization, and large-scale validation is essential to advance bioadsorbent technologies toward practical implementation in wastewater treatment.

Keywords: *Antibiotic residues, Bioadsorbents, Wastewater treatment, Biochar, Chitosan composites, Antibiotic resistance.*

ICABB26-EA-P04

ACC deaminase producing bacterium *Enterobacter cloacae* ZNP-2 mitigate salinity stress and enhance salinity stress tolerance in wheat plant

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Abstract

Increasing soil salinity adversely affects plant growth and productivity. However, some salt resistant rhizosphere bacteria have the potential to improve plants growth under salt stress. Among ACCD-producing bacteria isolated from the rhizosphere of plants growing in saline desert soil, ZNP-2 was selected based on its ability to produce phytohormone and ammonia, and solubilize phosphate, and further identified as *Enterobacter cloacae*. Furthermore, we evaluated the protective effects of the inoculation of *Enterobacter cloacae* ZNP-2 on morphological and physiological growth parameters, ionic balances, accumulation of osmolytes, and antioxidative defense system under both normal and salt stress conditions.

The presence of *AcdS*, the structural gene for ACC deaminase in *Enterobacter cloacae* ZNP-2 was confirmed by the polymerase chain reaction. Increased salt stress resulted in the accumulation of toxic Na^+content and a decrease in K^+ content, however, inoculation with ZNP-2significantly decreased the level of Na^+(25% to 55%) and improved the K^+content (29% to39%), thereby favoring the K^+/Na^+ratio. Moreover, ZNP-2-inoculated plants showed improvements in biomass (13% to 31%) and chlorophyll contents (25% to 51%) as compared to the un-inoculated plants. ZNP-2 inoculation also improved the various osmolytes in wheat plants to maintain the osmotic balance. The observation implies that ZNP-2 isolate augments salt tolerance in wheat plants by modulating the intracellular level of various osmolytes.

Therefore, the utilization of beneficial microbial isolate as a mechanism for inducing salt tolerance in wheat plants could be used as an effective tool to combat salt stress in plants.

Keywords ACC deaminase. Osmolytes. *AcdS.* IAA. PGPR

ICABB26-EA-P05

PLASTIC EATING MICROBES

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Abstract

Plastic waste is a big problem for nature because it cannot break down in soil and water for decades. This is to make an eco-friendly method to reduce plastic pollution. Scientists discovered that use of plastic eating microbes. These microbes can slowly break down plastic with the help of special enzymes. This idea helps to control the plastics wastage without harming wilderness. Plastic pollution is increased day by day due to excessive use of plastic bottles, bags and other materials, traditional recycling methods are not enough to control plastic pollution. This study helps to easily understand how microbes break plastic. Scientists discovered that bacteria like *Ideonella sakaiensis* that can break down PET [polyethylene terephthalate], which is used in plastic bottles. This study is based on information collected from different scientific reports and research papers. This process is slower than chemical methods, but it's natural and does not produce harmful byproducts. Research results show that plastic eating bacteria can decrease the strength and size of plastic materials. Some microbes can change plastic into CO_2 and

H_2O. This method is safe for controlling plastic waste. Plastic eating microbes are a new idea and helpful solution to plastic pollution. They provide an environmentally friendly method to reduce plastic in nature. However, more research is needed to make this method faster and more suitable for large scale use.

Keywords: Plastic Pollution, Biodegradation, Plastic-Eating Microbes, Enzymatic Decomposition, *Ideonella sakaiensis*, Sustainable Waste Management

ICABB26-EA-P06

Biodegradable Plastics: Promise or Paradox? A Critical Review of Their Environmental Sustainability and Degradation Challenges

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Abstract

An increasing plastic pollution problem has intensified the quest for viable substitutes to conventional plastics, such as Biodegradable Plastics (BDPs). The materials are often marketed as green alternatives that can help cut long-term pollution. However, their supposed low toxicity and consistent biodegradation performance remain uncertain. The present review analyses if BDPs represent an ultimate sustainable solution, or their negative impact will merely transfer from one environmental compartment to another. The review distinguishes bio-based plastics from biodegradable plastics, emphasizing that natural feedstock origin does not guarantee biodegradability. It also provides a condensed explanation of the main BDP categories (polylactic acid, polyhydroxyalkanoates, and starch-based plastics) and their production mechanisms, as well as a critical discussion on their degradation in different disposal environments such as industrial composting facilities, marine systems, or landfills. The effects of the physico-chemical factors on biodegradation efficiency are also studied. Furthermore, the review examines ecological issues linked to microplastic generation, the potential hazards that biodegradable plastic degradation products may pose to ecosystems, and the ongoing challenge of greenwashing within the bioplastics industry. International market trends and life-cycle assessment data are reviewed to estimate the general sustainability and economic viability of BDPs. Findings demonstrate that the environmental benefits of biodegradable plastics depend on proper waste-management systems, reliable biodegradation testing, and increased public awareness. In the absence of these factors, BDPs may fall short of expectations and potentially generate new pollution challenges.

Keywords - Bioplastics, sustainability, Polylactic acid (PLA), Polyhydroxyalkanoates (PHA), Environmental impact, Life cycle assessment (LCA), Greenwashing

ICABB26-EA-P07

Soil microbiome management

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Abstract

Soil Microbiome referes to all the Microorganisms living in soil and there interaction with plants and themselves. These microbes have important role in managing soils fertility, growth of plants and nutrient cycling, disease suppression that's help plants and also microbes helping in growth of plants. Disturbance in the soil microbiome can lead to serious effect on ecosystem balance like Loss of

microbial diversity due to usage of pesticides and fertilizer in an uncontrolled amount. Even tillage , pollution have a serious effect on microbial diversity. Growth of soil borne disease due to reduction in number of beneficial microbes which later cause disease in plants, structure of soil and even decreases it's fertility which later causes slow down in decomposition, making soil nutrition less ,making it difficult for roots to penetrate. As microbes are effected it further causes environmental consequences like production of more greenhouse effect due to incomplete decomposition. There are ways that can be used to maintain soil microbiome. Usage of biofertilizers and pesticides to be minimized for crop cultivation as it harms microbes present in soil. By providing enough moisture to soil microbe's .Water logging and drought can effect microbes so we need to build properly drainage in Waterlogged areas. Encouraging Mycorrhizal and Rhizosphere association as it will improve soil health as well as nutrient cycling. Crop rotation to be used as different plants support different microbes so by practicing soil rotation we can introduce more microbes to soil which promotes diversity as well as reduces buildup of pathogens. Minimizing tillage and ploughing as it disturbs the habitat of soil microbiome.

Keywords: Biofertilizer, Microbiome, Rhizosphere, Tillage

ICABB26-EA-P08

Bioremediation of Heavy Metals: Recent Advances and Future Prospects

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Abstract

The ongoing discharge of untreated wastewater caused by the substantial expansion of industrialization globally has led to widespread heavy metal contamination. Heavy metals (HMs) are very persistent in the environment and gradually accumulate in living organisms through bioaccumulation. Since they are not biodegradable, they can pose severe health risks, including cytotoxicity, mutagenicity, carcinogenicity, developmental disorders etc. Therefore, removal of heavy metals from the environment is very necessary to protect the environment and human life. There are numerous conventional remediation methods, such as chemical precipitation, ion exchange, and membrane filtering etc, but they often result in secondary waste, have high running costs, and are sometimes ineffective. As a result, bioremediation has become a viable option that is both ecologically friendly and scientifically proven, which harnesses the natural detoxification mechanisms of microorganisms. The primary emphasis of this review is to explore the bioremediation mechanism and the growing use of bacterial consortia to enhance performance and demonstrate synergistic metabolic connections and increased resistance when treating heterogeneous contaminated wastewater. Additionally, the review thoroughly examines CRISPR-based technologies that allow scientists to create Genetically Engineered Microorganisms (GEMs) with increased tolerance to toxic environments, and improved metal-binding affinity and capabilities of these microbial systems. The review also covers how the integration of artificial intelligence (AI) and machine learning (ML) can help transform bioremediation through intelligent microbial strain engineering, real-time remediation condition optimization, and predictive modeling of contaminant behavior.

Keywords: Bioremediation, Genetically engineered microorganisms, CRISPR-Cas, Artificial intelligence, Machine learning (ML).

ICABB26-EA-P09

Microbial Biosensors: Detecting Pollution with Living Cells

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Abstract

As environmental pollution continues to threaten ecosystems and human health, scientists are turning to one of nature's smallest creations for solutions — microbes. Microbial biosensors, an emerging innovation in environmental microbiology, use living microbial cells to detect pollutants with remarkable precision and speed. These biosensors function like natural alarm systems, where microorganisms respond to toxic substances by producing measurable signals, such as light, color change, or electrical output. Unlike traditional chemical methods, microbial biosensors are eco-friendly, cost-effective, and capable of continuous monitoring in real time. They can detect contaminants such as heavy metals, pesticides, and industrial waste in soil, water, and air — even at very low concentrations. Moreover, genetically engineered microbes are now being developed to recognize specific pollutants, making detection more accurate than ever before. The application of microbial biosensors holds great promise for achieving environmental sustainability. By combining biology with technology, these living detectors not only help identify pollution early but also guide cleanup efforts more efficiently. In a world striving for green innovation, microbial biosensors represent a powerful example of how life itself can be used to protect life on earth

Keywords: Ecosystem, Biosensors, Eco- friendly, Sustainability, Contaminants

ICABB26-EA-P10

Microbial Fuel Cells: Using Microbes to Generate Electricity

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Abstract

Microbial fuel cells (MFCs) are an emerging bioenergy technology that directly convert organic compounds into electricity, offering lower cost and greater sustainability than conventional wastewater treatment. They use biodegradable substrates instead of refined fuels, reducing sludge production and improving energy efficiency. However, electron transfer and capture inefficiencies significantly limit power output and system performance.

MFCs can generate electricity from diverse substrates, particularly in wastewater treatment, addressing both water pollution and energy scarcity. They also enable simultaneous electricity generation and production of value-added products due to microbial metabolic diversity. MFCs can also serve as biosensors, where current output correlates linearly with biochemical oxygen demand (BOD) or sample toxicity.

Lab-scale studies show MFCs can improve electricity generation, remove COD, produce value-added products, and function as biosensors. However, low power output, closely linked to microbial metabolic activity, remains a challenge. Screening high-performance electrogenic strains and genetic modifications can enhance microbial electricity generation, which depends on the utilization of substrates by microbes. MFCs represent a promising platform for sustainable energy recovery, waste treatment, and biomass valorization.

Keywords: Microbial fuel cells, bioenergy production, wastewater treatment, biosensors, biomass valorization

ICABB26-EA-P11

From Soil to Solution: CAZymes as the Genomic Goldmine for Biocatalysis

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Abstract

The world is in an environmental crisis caused by the drastic increase in global temperatures, which is primarily due to the huge dependence on oil and gas. The most suitable replacement is biofuel obtained through advanced methods from difficult plants like wood and grasses. Nonetheless, those plants are really hard to be processed! The use of strong and specialized tools that are called CAZymes' is very essential in the process to liberate that energy—enzymes that are mainly produced by microbes. They are the basic keys to make renewable energy work.

At present, the scientists are on an expansive treasure hunt for these super-enzymes. They are employing state-of-the-art DNA analysis to survey through different habitats such as fertile forest soils, severe hot springs, and even the complex area of the human gut. This thorough investigation has unveiled a whole hidden universe of microbes and has disproven the theory that the most significant enzyme groups are only found in some places. What is the best part of it, a vast "genomic goldmine" of CAZyme genes that are totally unknown has been uncovered. The enzymes that have not been found yet are our best chance to discover new, very efficient tools for the biofuel industry.

The researchers are making the future through these finds. The researchers are using advanced methods like protein engineering and powerful gene-editing tools to custom-build better, more stable enzymes. This is very important because the power of CAZymes is not only limited to the production of fuel; it also plays a role in human health by assisting the gut microbes with the digestion of carbohydrates coming from the food we eat. This targeted research is accelerating the production of crucial new enzymes that will be necessary for both a clean energy economy and improved human health.

Keywords: CAZymes, Metagenomics, Protein Engineering**,** Lignocellulose, Biofuels, Metabolic Health.

ICABB26-EA-P12

CRISPR/Cas Applications in Enhancing Secondary Metabolite Production in Medicinal Plants

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Abstract

Alkaloids, terpenoids, and phenolics are representative secondary metabolites that contribute to plant defense and confer antioxidant, antimicrobial, and therapeutic activities. Medicinal plants therefore function as natural biofactories of diverse secondary metabolites, although their biosynthesis is stringently regulated by genetic, environmental, and developmental factors that often restrict accumulation to low or highly variable levels. Targeted manipulation of key regulatory genes governing these pathways can be achieved through CRISPR-based metabolic engineering. Artemisinin, a sesquiterpene lactone from *Artemisia annua* L., is a well-established antimalarial drug that also exhibits activity against multiple cancers and a broad spectrum of microbes, including viruses, parasites, and bacteria, yet its inherently low abundance in planta limits reliable production. Artemisinin content can be increased by overexpressing artemisinin biosynthetic genes, overexpressing transcription factors that regulate these genes, or blocking key enzymes in pathways that compete with artemisinin biosynthesis. Recent advances in CRISPR/Cas genome editing, which operates as a programmable molecular scissor system, enable precise modification of genes involved in these secondary metabolic networks, allowing gene knock-ins to elevate desirable products, gene knockouts to eliminate unwanted compounds, promoter and transcriptional regulator editing for fine metabolic tuning, or pathway rewiring to redirect flux toward synthesis of high-value bioactives. A notable case is CRISPR/Cas9-mediated editing of regulatory genes in *A. annua* that disrupt negative regulators of the artemisinin pathway, substantially increasing artemisinin accumulation.. The workflow involves identifying key genes within artemisinin or flavonoid pathways, designing sequence-specific single guide RNAs (sgRNAs), and delivering sgRNA–Cas9 constructs into *A. annua* cells, commonly via seed transformation, where targeted DNA cleavage induces insertions, deletions, or other mutations—such as in the SQS gene—that redirect metabolic resources toward artemisinin biosynthesis; subsequently, edited lines, including kanamycin-resistant plants, are selected and screened for desired genetic changes and elevated metabolite levels. Integration of CRISPR with omics platforms, synthetic biology, and plant tissue culture is poised to accelerate the development of next-generation medicinal crops with superior nutraceutical and therapeutic attributes, enabling sustainable, large-scale production of high-value natural products and advancing plant biotechnology, drug discovery, and precision agriculture.

Keywords: CRISPR/Cas · Secondary metabolites · Medicinal plants · Artemisinin · Sesquiterpene lactones · *Artemisia annua*

ICABB26-EA-P13

Waste into Value Added Products: Recent Advancement and Future Prospects

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Abstract

The Champawat region's forested landscape accumulates large amounts of pine needles yearly, and because of their high resin content and slow rate of breakdown, they are one of the main causes of recurrent forest fires. Unmanaged pine-needle debris causes long-term ecological stress, interferes with nitrogen cycling, and raises the danger of soil erosion also. Moreover, these needles offer a substantial amount of unrealized potential as a renewable source of lignocellulosic biomass. This abundant residue can be turned into value-added products like biochar, fertilizers, or nanomaterials, which has the dual benefit of reducing fire hazards and producing materials that can address soil pollution. According to recent research, pine needles can produce biochar with advantageous physicochemical properties, such as a porous structure, a high carbon content, and the capacity to hold functional groups that facilitate pollutant binding. Pine-needle biomass has also been explored for synthesizing nanomaterials and nano enabled biochars that demonstrate improved surface reactivity and catalytic behavior, leading to efficient removal of emerging pollutants. In agriculture, the use of pine-needle biochar as a soil amendment has shown promise in improving soil pH, nutrient retention, microbial activity, and plant growth. Therefore, the accumulation of pine needles in the Champawat region is the primary focus of this analysis, which also looks at potential commercial opportunities arising from its valorization, including the production of value-added products, nanofertilizers, nanomaterials, and related inventions. These valorization strategies could serve as the basis for scalable, community-focused environmental solutions in places like Champawat, where pine needle accumulation presents ecological and safety issues.

Keywords: Biochar, Fertilisers, Nanomaterials, Nutrient Cycling, Valorization, Sustainability

ICABB26-EA-P14

Micronutrient-Fortified Rice: Addressing Hidden Hunger and Enhancing Pediatric Cognitive Development

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Abstract

Rice an abundant carbohydrate source, is a dietary staple for a large proportion of the global population, yet polished rice lacks essential micronutrients like iron, zinc, and various vitamins necessary for optimal growth and cognitive development in children. Consequently, rice fortification has emerged as a strategic intervention to augment micronutrient content, thereby promoting pediatric health outcomes and cognitive development. Micronutrients are

crucial for growth, immunity and cognitive development in children. Fortifying rice with these critical nutrients offers a sustainable and effective public health strategy to promote optimal brain development and enhance cognitive function among young populations. This review shows that regular consumption of fortified rice can counteract the long-term effects of hidden hunger and support optimal brain

development. The fortification process involves incorporating essential vitamins and minerals into rice grains using methods such as coating, dusting, extrusion and novel techniques offers a practical and scalable solution to micronutrient deficiencies.

Fortified rice enriched with iron and folic acid supports the formation of red blood cells and enhances oxygen supply to the brain, improving concentration and memory. Zinc-fortified rice has been associated with improved neurotransmitter activity, while iodine plays a crucial role in the synthesis of thyroid hormones essential for brain maturation. Additionally, vitamins B9 and B12 contribute to neural connectivity and overall cognitive performance. Growing evidence shows that regular consumption of fortified rice during early childhood improves school readiness, concentration, memory, and overall academic achievement. Therefore, rice fortification stands as a promising and sustainable strategy to combat hidden hunger and support optimal cognitive development in children.

Keywords: Rice fortification, Cognitive development, Micronutrients, Child health, Hidden hunger, Nutritional enhancement

ICABB26-EA-P15

In Vitro Evaluation of Antioxidant Activity in Ethanolic Extracts of *Andrographis alata (vahl) Nees*

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Abstract

Oxidative stress is a major contributor to various chronic diseases, and the search for natural antioxidants has intensified in recent years. This study investigates the in vitro antioxidant potential of ethanolic extracts of Andrographis alata (Vahl) Nees using six standard assays. The results demonstrate dose-dependent antioxidant activity in all assays, with the extract showing significant potential compared to conventional standards. These findings support the use of A. alata vahl nees as a promising natural antioxidant source for potential nutraceutical or pharmaceutical applications. These results suggest that *A. alata* vahl nees possesses significant antioxidant potential, albeit lower than conventional standards (BHA, ascorbic acid, EDTA). The findings support the use of *A. alata vahl nees.*

Keywords: *Andrographis alata vahl nees*, antioxidant activity, natural compounds in vitro assays.

ICABB26-EA-P16

BIOLUMINESCENT TREES

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Abstract

Bioluminescent Trees are an amazing idea in the modern science world because this shows the natural way for plants to produce on their own. These glowing trees can help to reduce the overall consumption of electricity we use on streetlight, parks, and indoor decoration. As the new generation looks for cleaner and more eco-friendly solutions, the idea of light producing trees is both interesting and useful. It is the relation between nature and technology in a unique way, and it offers a new path for natural lighting. The main purpose of studying bioluminescent trees is to understand how natural light is created inside living organisms and how it can be done safely. Many organisms like fireflies, jellyfish, and some fungi produce light naturally through a chemical reaction involving luciferin and luciferase. Scientists are

now trying to insert this light producing genes into plants to see if they can glow on their own without external energy sources. This idea is important because artificial lighting depends on electricity, which costs money and often harms the environment. Scientists then experimented by transferring these genes into plant cells and observing the results. Even though technology is still under development, bioluminescent trees show great promise. They could become a natural lighting option in the future and sustainable environment. With continued research, this idea may one day turn into a practical and eco-friendly solution for lighting our surroundings.

Keywords: Bioluminescent Trees, Luciferin, Genetic Engineering, Synthetic Biology, co-Friendly Technology

ICABB26-EA-P17

Pseudomonas Aeruginosa Strain S8 Isolated from a Potentially Polluted Site Degraded Bisphenol A

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Abstract

Bisphenol A (BPA), an endocrine-disrupting chemical, utilized in a wide range of retail and industrial applications. It's extensive release from the industries and wastewater pollutes the environment. It can persist in water bodies for a long time leading to ecological risks and adversely affecting reproductive and cognitive functions of humans. Therefore, removal of BPA from the environment is essential. Bioremediation, being economically and environmentally friendly, is considered as a preferred alternative over physiochemical approaches. Water samples were collected from a potentially contaminated site. Minimal Salt Media (MSM) was used to provide a controlled growth environment for bacterial growth. Primary culture was prepared; BPA tolerant and degrading bacteria was selected by growing primary culture on MSM agar plates containing different concentrations of BPA. A single colony growing at 50ppm of BPA was selected as BPA tolerant strain. Molecular dentification of isolated BPA tolerant strain using 16S RNA gene sequencing identified it as *Pseudomonas aeruginosa* strain S8. The isolated strain was able to degrade 8 ppm of BPA over an incubation period of 24 days at 37°C as evident by GC-MS analysis. Two putative intermediates were identified during the degradation. Supplementation of glucose did not affect the BPA degradation rate. BPA does not show any significant effect on the total protein content and various physiological enzymes of isolated strain.

These findings indicate that *Pseudomonas aeruginosa* strain S8 may be a suitable strain for the development of BPA bioremediation strategy. The present work may have applications in plastic degradation which is a serious global concern.

Keywords Bisphenol A (BPA); *Pseudomonas aeruginosa* strain S8; Biodegradation, GC–MS analysis; Enzymatic assay,

ICABB26-EA-P18

GDSL Lipases as Regulators of Plant Stress Adaptation

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Abstract

Plant GDSL esterases/lipases (GELPs) are a large, diverse family of SGNH hydrolases that have emerged as important regulators of plant responses to environmental stress. Genome-wide surveys in multiple crops show that GDSL genes form expanded families with stress-, hormone-, and light-responsive cis-elements, and many members are strongly induced under drought, heat and other adverse conditions. Functional studies in rice, cotton, pigeon pea, orchids and pepper demonstrate that individual GDSLs can either enhance or reduce stress tolerance by controlling lipid metabolism, membrane integrity and downstream signalling. For example, specific GDSLs modulate heat tolerance in rice by influencing reactive oxygen species (ROS) levels and antioxidant enzyme activities, while others fine-tune drought responses via changes in cuticular structure, stomatal behaviour and water loss. Additional work links GDSL activity to immune signalling and pathogen resistance through remodeling of galactolipids and other membrane lipids, positioning these enzymes at the intersection of abiotic and biotic stress pathways. Recent reviews highlight that GELPs participate in development, cell-wall and cuticle formation, and plant–environment interactions, but also emphasize that substrate specificity, upstream regulatory networks and systems-level roles of GDSLs under combined stresses remain poorly defined. Overall, current evidence supports a central model in which plant GDSL lipases act as versatile modulators of stress adaptation, translating changes in membrane and surface lipids into ROS balance, hormone signalling and defense outputs. A focused, multi-omics and structural approach to GDSLs in stress-resilient crops such as millets could uncover novel enzymes and mechanisms for breeding or engineering climate-ready varieties.

Keywords: GDSL lipase, SGNH hydrolase, abiotic stress, lipid remodeling, plant stress tolerance, membrane integrity.

ICABB26-EA-P19

Bio-based preservation methods for maintaining quality parameters of fresh fruits

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Abstract

Bio-based preservation techniques use biological substances that occur naturally instead of chemicals to increase the shelf life of the fruits. These techniques have emerged as a promising and eco-friendly way to reduce post-harvest losses and maintain the nutritional value of fresh fruits. Fresh fruits remain metabolically active even after harvest. They continue processes like respiration, ethylene production and transpiration these factors accelerate ripening and spoilage of fruits. Therefore, bio-based preservation is used to slow down this mechanism by using natural materials.

The main bio-based preservation methods are edible coating (Natural Films). These coatings are made from chitosan, aloe vera gel, starch, and protein-based materials and they help reduce moisture loss, respiration rate and also delay ripening. Another preservation method includes active bio-preservatives

(active compound) These active compounds applied directly as washes or incorporated into coatings, such as plant extracts (neem extract, turmeric extract) and essential oil (e.g. Cinnamon, clove, lemongrass). These possess antimicrobial and antioxidant activity, which directly inhibit the growth of pathogenic microorganisms (cause spoilage or toxin production) and reduce oxidative stress thereby, extending the fruit's shelf life. Use of biocontrol agents such yeast and bacteria, they compete with harmful microorganism and help reduce post-harvest diseases.

Using these types of bio-preservation techniques, the quality of fresh fruits can be maintained. Like edible coating act as moisture barriers and reduce transpiration, leading to significantly lower water loss. Edible coating also slows down the cell wall degrading enzymes and reduces the respiration rate, thereby maintaining fruit texture for a longer time.

Thus, these quality parameters can be measured and monitored after the use of bio-based preservation techniques.

Keywords: Active bio-preservatives, Biocontrol agents, Bio-based preservation, Edible coatings, Maintained Quality parameters

ICABB26-EA-P20

CRISPR/CAS9 enabled approach for sustainable agriculture

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Abstract

Rapid growth in population leads to development of various disease and climate change like low rainfall, global warming, biotic and abiotic stress harmful and toxic use of chemicals and fertilizers leads to low agriculture yield and impact the Global Hunger Index (GHI) of India. These problems can also lead to inadequate supply of nutritional food as per global demand. By using CRISPR/Cas 9 (Clustered Regulatory Interspaced Palindromic repeats) can overcome these problems easily. The main aim of this technique is to provide benefits for the farmers in the development and utilization of improved crop varieties leading to increased farm productivity and secure livelihood by using transgenic-free CRISPR/Cas 9 technology.

We can coat our seeds through WASP technology (Water absorbing process) and (PEG Polyethylenglycol) to avoid drought pretreatment of our crops with NACL under water stress. Use of GABA [Y-aminobutyric acid] that improve the germination in seed associated with enhancement in osmotic adjustment, antioxidant metabolism. We can produce genetically modified crops that are heat and pest resistance, use of MET [melatonin] which is a bio stimulant that increase plant tolerance to temperature stress. Agro-MET [agriculture

melatonin], it interacts with phytohormones and gaseous molecule helps to support plant adaptation to temperature stress. It also improves the physiological processes (like photosynthesis, seed germination, and fruit ripening.

Keywords: GHI , CRISPR CAS9, Guide RNA, WASP Technology, GABA, Agro-MET

ICABB26-EA-P21

Engineering Self-Healing Mycelium panels for Space Architecture: Opportunities, Promises, and Challenges

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Abstract

Mycelium-based composites are gaining significant attention as next-generation construction materials because they are lightweight, strong, and naturally effective at absorbing sound and heat. These qualities make them well suited for walls, tiles, and structural panels on Earth, and they are now being explored for use in future space habitats where mass efficiency, insulation performance, and sustainability are essential. In such environments, living fungal materials offer the potential to create multifunctional structures that both protect and adapt.

Recent studies show that several mushroom species, especially members of the genus Pleurotus, exhibit strong physiological responses to audible sound. Experiments using mixed sound frequencies, such as classical music blended with cricket chirping (340–3300 Hz), and discrete tones associated with natural thunder (225–750 Hz), have demonstrated accelerated mycelial growth, earlier developmental transitions, and improved nutrient synthesis. Species including *Pleurotus ostreatus*, *P. eryngii*, *P. cornucopiae*, *Pleurocybella porrigens*, and hybrid strains like Black Pearl have shown growth improvements of 10 to 21%. These responses are linked to calcium-dependent mechano-sensing, membrane restructuring, cytoskeletal adjustments, and stress-activated signalling pathways.

When mycelium is integrated into habitat walls or interior panels, these acoustic responses become functionally valuable. Controlled sound exposure can encourage directional hyphal growth into cracks or stressed regions, allowing the material to repair itself while maintaining excellent thermal and acoustic insulation. Hybrid mushrooms with stable reactions, such as Black Pearl, appear especially promising for engineered self-healing systems. This concept offers substantial promise, including reduced maintenance, enhanced structural resilience, and the ability to create lightweight, regenerative building materials for long-duration missions. However, challenges remain, such as species-specific sensitivity to sound, long-term stability in closed environments, prevention of uncontrolled growth, and integration with spacecraft life-support systems. Addressing these issues will be essential for translating acoustic-responsive mycelium panels into practical space habitat technologies.

Keywords: Mycelium, Regenerative Biomaterials, Self-Healing, Space Architecture

ICABB26-EA-P22

Comparative Evaluation of Natural and Artificial Agents for Sewage Water Treatment

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Abstract

Rapid urbanization has increased sewage generation, creating a need for efficient and eco-friendly treatment methods. Chemical or artificial sewage cleaners are widely used but may pose environmental and health concerns. In contrast, natural plant-based agents such as Moringa oleifera seeds, citrus peels, and other bio coagulants are emerging as sustainable alternatives. The aim of this work is to compare

the efficiency, safety, and practicality of natural plant-based sewage cleaners with conventional artificial chemical cleaners, based on the reported findings of the referenced research study. The comparative analysis was conducted using the research paper as the primary source. The paper evaluated the performance of natural agents (Moringa seeds, lemon/orange peels) and chemical coagulants through parameters such as turbidity reduction, microbial load reduction, pH changes, colour removal, and overall improvement in water quality. The methodology involved assessing treatment performance, analysing experimental results, and reviewing environmental impacts.

Natural plant-based agents demonstrated strong coagulating and antimicrobial properties, significantly reducing turbidity and microbial load. Moringa seeds showed rapid settling of suspended particles, while citrus peels improved clarity and reduced Odor. Artificial cleaners produced faster and more uniform results but were associated with higher chemical residues and potential ecological toxicity. The reviewed data suggests that natural agents are highly effective for primary and secondary treatment stages, whereas chemical cleaners offer high efficiency but at environmental costs. Natural sewage cleaners offer a safe, biodegradable, and cost-effective alternative to artificial chemical agents. While synthetic cleaners provide high immediate efficiency, plant-based agents present sustainable long-term solutions, especially for low-resource settings and environmentally sensitive applications. This comparative review highlights the potential of everyday natural materials as practical sewage treatment agents and emphasizes their advantages over conventional chemical cleaners.

Keywords: Natural coagulants, Moringa, citrus peels, artificial cleaners, sewage treatment, water purification

ICABB26-EA-P23

Synergistic Plant–Microbe Approaches for Sustainable Heavy Metal Bioremediation

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Abstract

Heavy metal pollution poses a major environmental threat due to the persistence and toxicity of metals released from industrial and agricultural activities. This review paper examines the combined potential of plants and microorganisms as a sustainable alternative to conventional remediation methods. Microbial mechanisms—such as biosorption, bioaccumulation, biotransformation, and biomineralization—reduce metal toxicity and enhance their mobility or immobilization in the environment. Complementary phytoremediation strategies, including phytoextraction, Phyto stabilization, rhizofiltration, and phytovolatilization, enable effective uptake and stabilization of contaminants. When applied together, plant–microbe partnerships significantly improve metal absorption, detoxification efficiency, and plant tolerance under stress. Examples include arbuscular mycorrhizal fungi and metal-resistant bacteria facilitating greater nutrient uptake and enhanced phytoextraction in hyperaccumulator species. Overall, synergistic bioremediation offers a cost-effective, eco-friendly, and scalable approach for restoring heavy metal–contaminated sites and holds promise for future environmental management.

Keywords: Heavy metals, bioremediation, phytoremediation, microbial remediation, plant–microbe synergy.

ICABB26-EA-P24

Expanding Controlled Environment Agriculture (CEA) Beyond Horticulture: Constraints and Opportunities for Cereal Crops

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Abstract

CEA has received growing attention as a solution for improving crop production, resource use efficiency, and resilience to climatic stress. However, the majority of research with CEA has focused on horticultural crops, while cereal crops, despite their central role in global food security, remain underexplored within controlled production systems. This review addresses the main constraints and emerging opportunities associated with expanding CEA beyond horticulture to cereal crops. However, high costs of capital and energy, long phenological duration, spatial limitations, and the low economic returns of cereals relative to high-value crops constitute major obstacles in their integration with CEA. Moreover, cereal-specific traits such as plant architecture, root system complexity, and photoperiod sensitivity remain additional challenges to integration into confined environments. Despite these limitations, recent advancements in precision nutrient management, controlled environment conditions, and sensor-based monitoring and automation have made partial or target application possible within CEA systems. These applications include early growth-stage cultivation, hydroponic fodder production, biomass production, controlled phenotyping and stress response research under reproducible environmental conditions. The outputs from these systems have a wide range of applications, such as biomass can be used as bioenergy feedstock or as livestock fodder, while analytical data obtained from phenotyping and stress studies can be integrated into crop improvement and breeding programs. The article highlights that CEA in cereals should be viewed as complementary to traditional field agriculture rather than a substitute. Overall, the incorporation of cereals into CEA systems represents an innovative and complementary research-based approach that supports diverse sustainable controlled-environment applications under future environmental challenges.

Keywords: Controlled Environment Agriculture, Hydroponic systems, Cereal crops,Sustainability.

ICABB26-EA-P25

Tracking Microplastics in Oceans: Environmental Impacts and Advances in AI-Based Detection

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Abstract

Rising accumulation of microplastic debris in marine environments, driven by rapid urbanisation and inadequate global waste-management systems. This growing microplastic pollution poses a major environmental concern due to its long-term ecological and human health impacts. They can also transport a range of hazardous substances, including industrial chemicals and pollutants from urban sources. As a result, microplastic effluents flow into aquatic systems, where they are directly consumed by living organisms, causing significant harmful effects. The extreme resistance of plastics to degradation leads to extensive contamination, including microplastic into marine food webs and coastal

ecosystems. Therefore, the present review mainly focuses on the sources, environmental impacts, and effects of aquatic organisms, along with their advanced detection techniques. Recent advancements in real-time detection, AI-enabled monitoring systems, machine-learning prediction models such as Lagrangian particle-tracking model combined with ocean circulation data, and remote-sensing technologies offer improved capabilities for identifying plastic sources, transport pathways, and accumulation hotspots. Alongside these tools, scalable cleanup approaches, circular-economy practices, and preventive waste-management strategies demonstrate significant potential for reducing plastic leakage and restoring marine environments. Integrating smart sensing technologies with sustainable interventions provides a promising direction for achieving cleaner and healthier oceans.

Keywords: Microplastics, Artificial intelligence, Machine learning, Remote-sensing, Waste-management

ICABB26-EA-P26

Research insights into the Development of Plant extract-loaded Bacterial cellulose composites

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Abstract

Bacterial cellulose (BC) has gained significant attention as a biopolymer due to its high purity, excellent mechanical strength, and unique three-dimensional nanofibrous structure. However, it also has certain limitations, such as low elasticity and insufficient antimicrobial and biological activity, which restrict its direct use in many high-performance domains. Developing in situ composites with plant extracts has emerged as an effective strategy to enhance the physicochemical and biological properties of BC while preserving its structural integrity. In this approach, bioactive plant-derived compounds are incorporated directly into the BC matrix during microbial fermentation, enabling their uniform distribution and strong interaction with the bacterial cellulose fibre network. The presence of plant extracts during BC biosynthesis not only influences fibre assembly but also facilitates the integration of antioxidant, antimicrobial, anti-inflammatory, or therapeutic functionalities without requiring additional chemical modifications. This method ensures better compatibility, reduces post-processing steps, and minimizes the risk of compound degradation that can occur in *ex situ* loading. Mild fermentation conditions support the stability of heat-sensitive phytochemicals and enable their efficient entrapment within the growing BC network. *In situ* BC-plant extract composites demonstrate significant potential for biomedical applications such as wound dressings, drug-releasing membranes, tissue-engineering scaffolds and other domains. As research progresses, *in situ* biosynthesis offers a sustainable and versatile route for creating multifunctional BC-based composites that deliver improved performance and broader application possibilities.

Keywords: Bacterial Cellulose, Composites, Plant extract, Biopolymer

ICABB26-EA-P27

Smart Microbiome Engineering for Climate-Resilient Agriculture: Integrating Bioformulations, Multi-Omics and AI for Drought and Salinity Tolerance

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Abstract

Droughts and salinity caused by climate change are growing risks to the world food supply, which increases the urgency of finding new sustainable solutions to strengthen crop resistance. Smart microbiome engineering is emerging as an option that integrates multi omics technologies, next-generation bioformulations, and artificial intelligence (AI) to develop specific microbial solutions to suit agroecosystems prone to stress. This review outlines mechanistic basis of microbial drought and salinity tolerance such as osmolyte biosynthesis,

ACC deaminase activity, EPS-mediated soil aggregation, antioxidant regulation, and synergistic interactions between keystone taxa, and collectively regulating plant physiological and molecular responses to stress. Recent advances in genomics, transcriptomics, proteomics, metabolomics, and metagenomics provide a systems level understanding of microbial functions; and AI-based computational tools permit predictive modelling of plant-microbe interactions, microbial compatibility, and consortium stability. At the same time, the development of bioformulation science, including encapsulation, controlled-release polymers, nanocarriers, and seed-coating technologies, has enhanced microbial viability and performance in the field. Through the combination of mechanistic understanding with computational analytics and formulation innovations, smart microbiome engineering provides a scalable, precision-based model of the design of climate-resilient agricultural solutions.

Keywords: microbiome engineering, drought tolerance, salinity tolerance, bioformulations, multi-omics, artificial intelligence, climate-resilient agriculture.

ICABB26-EA-P28

From Single Pollutants to Complex Mixtures: Basidiomycete Fungi as Broad-Spectrum Biocatalysts for BTEX and Dye Degradation

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Abstract

Environmental contamination in industrial and urban ecosystems rarely occurs as isolated chemical exposure. Instead, it is dominated by complex mixtures of aromatic hydrocarbons and synthetic dyes that exhibit enhanced persistence and toxicity. Such compositional complexity poses significant limitations for conventional remediation approaches that rely on pollutant specificity or sequential treatment strategies. In this context, basidiomycete fungi emerge as uniquely suited biological systems, owing to their extracellular oxidative enzymatic machinery and broad substrate tolerance. This review explores current advances in the application of basidiomycete fungi for the degradation of BTEX compounds and synthetic dyes under mixed-pollutant conditions, with emphasis on enzymatic adaptability,

co-metabolic interactions, and degradation dynamics. Ligninolytic enzymes, including laccases, manganese peroxidases, and lignin peroxidases, enable non-selective oxidation of structurally diverse

aromatic pollutants, facilitating simultaneous transformation within heterogeneous contaminant matrices. Evidence from research studies indicates that the co-existing dyes and hydrocarbons can stimulate enzyme expression and redox cycling, leading to enhanced degradation efficiency through synergistic interactions. By shifting the focus from single compound degradation to integrated pollutant behaviour, this review highlights the ecological relevance and functional robustness of basidiomycete-based remediation systems. The analysis underscores their potential for deployment in realistic soil and wastewater environments, where pollutant complexity, variability, and co-contamination are unavoidable. Ultimately, basidiomycete fungi are positioned as key biological drivers for sustainable remediation strategies, capable of addressing the multifaceted challenges posed by real-world aromatic carbon compound's generated pollution.

Keywords: Basidiomycete, mixed-pollutants, aromatic hydrocarbons, synthetic dyes, ligninolytic enzymes, BTEX compounds, co-metabolic interactions.

ICABB26-EA-P29

Biopolymer - Encapsulated Biofertilizers for Improved Microbial Survival and Field Performance

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Abstract

This review represents an overview of recent advances in biopolymer-based encapsulated biofertilizer technologies that partially or fully reduce dependence on conventional chemical fertilizer traditionally used to meet the global food demand. The transition from chemical to biologically derived products represents an important step towards a sustainable agricultural approach. Encapsulation protects beneficial microorganisms from environmental stresses; this strategy not only enhances the crop productivity and soil health but also contributes to sustainable and environmentally friendly farming. Bioencapsulation offers a promising approach in reducing the input cost and improving field performance. Encapsulated biofertilizers have a longer shelf life (up to 18-24 months) and can often be stored at normal temperatures, which addresses a major limitation of traditional liquid or powder formulations that require special storage conditions. Various natural and biodegradable polymers are used for encapsulation. Sodium alginate derived from *Macrocystic pyrifera* and chitosan derived from chitin (found in crustacean exoskeletons), it is biodegradable and non-toxic. Sodium beads were found to be more fragile than chitosan; therefore, it is often used in a mixture of both as a coating to improve capsule stability and provide additional antimicrobial properties. Shielding these organisms from biotic and abiotic stresses would otherwise cause rapid viability loss in conventional formulations and providing a safe habitat for beneficial microbial biofertilizer. *Pseudomonas fluorescens*, a gram-negative bacterium, has antagonistic and phosphate-solubilizing qualities is used as a potential biocontrol agent for suppressing plant disease by shielding the roots and seeds from fungal infection. Thus, encapsulated *P. fluorescens* could be superior for promoting soil health and productivity for sustainable agriculture.

Keywords - Biopolymer, Chitosan, encapsulation, biocontrol agents, soil fertility

ICABB26-EA-P30

Novel α-Amylase Resistant to Chaotropic Agents Drives Potato Waste Fermentation for Biofuel Production

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Abstract

The challenging industrial conditions require enzymes that remain active throughout the production of sustainable biofuels. Conventionally, biofuel synthesis from starch is a biphasic process where the enzymatic saccharification of starch is followed by microbial fermentation. However, most α-amylases degrade & lose their activity in the presence of chaotropic agents, such as solvents, surfactants, reducing agents, and chelators, which limits their utilization in an integrated single-step simultaneous saccharification and fermentation (SSF) process.The *Bacillus* strain IBT108 was isolated from the soil of the SAU premises and reported to have a novel α-amylase resistant to chaotropic agents. The robust stability of this novel α-amylase under harsh industrial conditions makes it a game-changer enzyme for the biofuel industry. The 68 kDa protein, with a high specific activity of 734.8 U/mg, was purified via DEAE ion exchange chromatography from a medium containing wheat bran as a cost-effective substrate. The functional characterization of IBT108 α-amylase revealed its strong thermostability, with optimal activity at 70°C and a pH range of 4 to 6.5. Under these conditions, the enzyme retained over 70% of its activity in 1 M organic solvents and 5 mM chaotropic agents, outperforming other commercial α-amylases. *Clostridium acetobutylicum* and *Clostridium butyricum*directly convert waste potatoes using IBT108 α-amylase, yielding a substantial amount of butanol (20.41–23.74 g/L) and hydrogen (3.20–4.38 L/L). This indicates the enzyme's potential to simplify biofuel production, minimise operational costs, and valoriseagro-waste into value-added products. This study positions IBT108 α-amylase as a promising candidate in biorefineries & biofuel industries for the efficient, cost-effective, and sustainable production of next generation biofuels.

Keywords: IBT108 α-amylase, Biofuel, SSF, Waste potato, Wheat bran.

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Biodegradation Potential of Congo Red Degrading Bacteria: Isolation, Characterization and its Optimization

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Abstract

Congo red (CR) is a synthetic azo dye, distinguished by the presence of azo bonds that acts as chromophore, giving it a bright red color and high chemical stability. Owing to these properties, it is extensively employed in many industries. However, its high molecular stability contributes to its persistence in the environment, making it highly resistance to natural biodegradation. Discharge of untreated CR dye into the water bodies leads to environmental contamination and health hazards such as cancer, genetic damage and organ dysfunction. Bioremediation emerges as an effective and economically viable approach for the treatment of dye contaminated effluent.

In this study, congo red dye degrading bacteria was isolated and its degradation potential was evaluated. The water sample was collected and primary culture was prepared. The primary culture was grown on MSM agar plates containing different concentration of dye ranging from 25ppm to 500ppm. Six colonies growing on 200ppm dye were selected as dye tolerant bacteria. Pure cultures of these colonies were prepared and their dye degrading efficiency was calculated in suspension culture containing 50ppm of dye. Out of six, two colonies showing better degradation were selected. Optimization of degradation parameters such as carbon source, pH and temperature revealed that maximum degradation occurred at

pH6 and 37°C in presence of glucose. Colony 1 and 6 showed 99.02% and 96.35% degradation, respectively. Isolated strains were also characterized using various biochemical tests.
The isolated strains may be used for the development of congored dye bioremediation strategy. Efficiency of these strains may also be checked against other dyes and pollutant.
Keywords: Congo red (CR); biodegradation; optimization; biochemical tests.

ICABB26-EA-P32

Recent Advances in Plastic Waste-Derived Electrodes for Microbial Fuel Cells: A Sustainable Approach to Waste-to-Energy Conversion

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Abstract
Plastic waste, especially polyethylene terephthalate (PET), poses a significant threat to the environment due to its long-lasting persistence in nature. Several contemporary studies have focused on recycling PET waste and utilizing the recovered value-added materials for clean energy technology which offers a sustainable solution. This review highlights advances in the fabrication of microbial fuel cell (MFC) electrodes from PET waste emphasising the recovery of terephthalic acid (TPA) through alkaline hydrolysis and its subsequent use as an organic linker in the synthesis of iron-based metal organic framework (Fe-t-MOF). The integration of conductive polymers, namely, polyaniline (PANI) and the creation of the hybrid PANI-Fe-t-MOF nanocomposites have been documented to enhance the electrical conductance, biocompatibility, and electrochemical efficiency. Structural, morphological, and electrochemical characterizations from various studies demonstrate that these hybrid electrodes provide a low-cost and efficient alternative to conventional carbon-based materials while simultaneously offering solutions to the management of plastic waste and fostering the organic, renewable bioenergy value chain. The review concludes with the discussion on current challenges, environmental implications, and future prospects for scaling PET-derived electrode technology towards sustainable bioenergy systems.
Keywords: Plastic waste utilization, Polyethylene terephthalate (PET), Microbial fuel cell (MFC), Bioelectricity generation, Waste-to-energy conversion

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Microplastic Remediation: Recent Advances and Future Prospects

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Abstract
Microplastic pollution has emerged as a critical environmental challenge due to its persistence, and detrimental impacts on ecosystems and human health. Conventional remediation strategies, including physical and chemical approaches, have proven inadequate for large-scale and sustainable removal of microplastics. In this context, genetic engineering offers a transformative avenue for enhancing the efficiency and specificity of bioremediation processes. This review critically explores recent advances in the application of genetic engineering techniques—such as CRISPR-Cas systems, synthetic biology, and metabolic pathway optimization—to develop microorganisms with enhanced plastic-degrading capabilities. Engineered bacteria, algae, and fungal strains have shown promise approach in degrading synthetic polymers like polyethylene terephthalate (PET), polyethylene (PE), and polystyrene (PS) through the overexpression of hydrolases, oxidases, and depolymerases. Furthermore, the integration of synthetic microbial consortia and biofilm engineering approaches has expanded the metabolic versatility and ecological stability of biodegradation systems. The review also discusses the challenges associated with deploying genetically modified organisms in natural ecosystems, including biosafety,

gene transfer risks, and regulatory constraints. By synthesizing current research trends, this paper highlights the potential of genetic engineering to revolutionize microplastic bioremediation and underscores the need for interdisciplinary strategies combining molecular biology, environmental microbiology, and ecological risk assessment to achieve sustainable remediation outcomes.

Keywords: Genetic engineering, Bioremediation, Microplastics, Synthetic biology, CRISPR-Cas, plastic-degrading enzymes, Microbial consortia.

ICABB26-EA-P34

*Withania somnifera (*Ashwagandha) as a Neuroprotective Modulator in Parkinson's disease

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Abstract

Parkinson's disease (PD) is a neurodegenerative disorder that progresses overtime, caused by degeneration of dopaminergic neurons located in the substantia nigra. It is the second most common neurodegenerative disorder, affecting >1.5% of cases worldwide in 65 years population. Medical therapy is the most followed therapy as it focuses on the correction of major factor, that leads to Parkinson's 'Dopamine Deficiency'. Present treatment primarily approaches symptomatic relief instead of preventing neural degeneration. Current evidence points that the pathology of Parkinson might initiate in the gut, where an imbalance in gut bacteria leads to systemic inflammation, mitochondrial dysfunction and misfolding α synuclein. The overproduction of reactive oxygen species activates the α syn cascade than with Lewy bodies leads to neurodegeneration. Ayurveda highlights the importance of gut health and neuro- energetic balance. *Withania somnifera* (Ashwagandha) is a medicinal plant widely used in Ayurveda that supports neural homeostasis and has shown therapeutic potential in disorders involving progressive neuronal degeneration. Ashwagandha compound belonging to a group of steroidal lactones called WITHANOLIDES, with Withaferin A and Withanolide A . Withanolide A has ability to slow the progression of Parkinson's disease and safeguarding dopamine neurons. Enriched with Withanolide A, standardized extracts from Ashwagandha roots can be formulated as nanoparticles for improved delivery to the central nervous system , enabling the compound to work as a targeted therapy that aids mitochondrial function and lowers neurodegeneration.By reducing α-synuclein - driven pathology and re-establishing gutbrain axis homeostasis also, Ashwagandha provides a scientific multi-targeted neuroprotective strategy with the potential to alter the progression of Parkinson's disease. This review merges modern neuropathology with Ayurveda understandings emphasizing the contributions of phytotherapeutic

Keywords: Gut brain axis, mitochondrial dysfunction, α- synuclein, Parkinson's disease, Ashwagandha (Withanolide A)

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High Level of 1,3-propanediol Production From Crude Glycerol by Clostridium Strain BOH3: Critical Roles of Inoculum And Substrate Concentration

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Abstract

Glycerol, the main by-product of biodiesel industry is generated by transesterification of vegetable oils or animal fats.1,3-Propanediol (PDO) functions as an essential chemical across diverse industrial applications. This research investigates the bioconversion potential of a novel wild-type *Clostridium* strain BOH3 for producing PDO from crude glycerol (CG). Initial experiments compared two inoculum preparation strategies for strain BOH3: glucose-based reinforced Clostridial medium (RCM;

medium A) versus glycerol-supplemented modified RCM (medium B). When fermenting 20 g L^{-1} glycerol, medium-A-derived cells produced 5.75 g L^{-1} PDO, accompanied by 3.10 g L^{-1} butanol co-production. In contrast, medium-B-derived cells achieved 11.01 g L^{-1} PDO formation with 2.50 g L^{-1} butyric acid and 1.01 g L^{-1} acetic acid generation, eliminating butanol byproduct formation. Systematic optimisation of batch fermentation parameters established ideal conditions: substrate concentration (80 g L^{-1} glycerol or CG), inoculum age (15 h), and proportion (12.50% v/v) from medium B, initial pH (6.4), and cultivation temperature (39°C). Under these refined conditions, PDO concentrations reached 42.58–47.15 g L^{-1} with conversion yields of 0.65–0.79 mol-PDO/mol-glycerol from CG-based media formulations. Fed-batch cultivation experiments testing 50–80 g L^{-1} initial CG loadings were subsequently conducted to maximise PDO accumulation. The 60 g L^{-1} initial CG concentration proved optimal, supporting total CG consumption of approximately 174 g L^{-1} and generating PDO titers of 103.55–116.45 g L^{-1}. Notably, this configuration achieved conversion yields of 0.72–0.81 mol of PDO per mol of glycerol, establishing a new benchmark for reported conversion efficiencies. Clostridium strain BOH3 demonstrates exceptional capability for high-titer PDO production (>116 g L^{-1}) with outstanding conversion yields (>0.80 mol mol^{-1}) from waste crude glycerol. These performance metrics establish this strain as a viable biocatalyst for industrial-scale production of PDO.

Keywords: 1,3-PDO, Crude glycerol, Clostridium fermentation, waste to energy.

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Biohydrogen production from fruit waste by *Clostridium* strain BOH3

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Abstract

Biohydrogen production is a promising renewable energy strategy that can address environmental issues. Biohydrogon has been produced using *Clostridial* strains from various industrial wastes including agricultural residues and waste waters from food industries. However, fruit waste remains an underutilised substrate despite its rich content of carbohydrates, proteins, amino acids, and essential minerals to support *Clostridia* growth and hydrogen production. In the present study, we evaluated Clostridium strain BOH3 for biohydrogen production due to its strong saccharolytic potential, demonstrated by the production of amylase (0.35 ± 0.08 U mL^{-1}), cellulase (1.22 ± 0.10 U mL^{-1}), xylanase (3.11 ± 0.04 U mL^{-1}), and pectinase (0.72 ± 0.10 U mL^{-1}) during fruit waste fermentation. Two strategies were employed for hydrogen production. In the first approach, fruit waste was pretreated using moist heat (ATH, autoclaving at 121 °C for 15 min) and dry heat (MWH, microwave irradiation at 2.45 GHz for 15 min). These pretreatment methods produced hydrogen in the range of 3118 ± 72 and 2526 ± 80 ml/l from ATH and MWH added media, respectively, with yields of 2.43–2.51 mol H_2 mol^{-1} hexose, while offering the advantage of minimal toxin generation compared to acid hydrolysis. The second strategy used a heterogeneous medium, where the fruit waste was directly supplemented into anaerobic basal medium (ABM). This approach resulted in a higher hydrogen production of 359.97 mL g^{-1} total solids, compared to the previous method. Therefore, this study demonstrates the potential of *Clostridium* strain BOH3 to effectively valorise fruit waste for biohydrogen production, leading to waste reduction and advancing circular and sustainable economy.

Keywords : Biohydrogen, Clostridial fermentation, Microwave pretreatment, Fruit waste

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A synergistic framework for abiotic stress- tolerant crop breeding

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Abstract
The major abiotic stresses that lower crop production are related to water, temperature and salinity. Traditional breeding approaches of crossing and backcrossing for selection of resistance traits have been time consuming, labor intensive and generate undesired genetic load also due to polygenic controle of these charecters. Advance technologies like Genome assisted breeding, omics approaches followed by CRISPR/Cas based targeted genome-editing and nanotech based interventions may help address these limitations. Genome assisted breeding techniques combine molecular breeding for marker-based selection (MAS, GS) of desired characteristics and speed breeding; manipulating environmental conditions (like photoconditions, photocycle) to increase number of crop cycles. High-throughput phenotyping (HTPP) enables rapid screening eliminating phenotyping bottlenecks and accelerating development of climate-resilient, abiotic stress-tolerant crops through continuous rapid phenotypic selection and generational cycling. Omics approach offer a broad molecular basis for understanding plant responses to stresses. Genomics recommend genes and QTLs governing plant stress response using complete genomic sequencing, analyzing SNPs, enabling marker-assisted selection for rapid breeding of stress-tolerant traits. Transcriptomics examines stress-induced gene expression profiles using RNA sequencing, identifying Stress-Response genes, and determining molecular mechanisms for Stress Recognition and Response Pathways. Proteomics determines protein expression of Stress-Tolerance proteins. As heat shock proteins (HSPs) and antioxidants such as (SOD, CAT) that helps to cope plants tolerating abiotic stresses. Metabolomics examines Stress-Induced compounds for osmoprotection (such as Proline, Glycine Betaine), identifying Stress-Tolerant germplasm Biomarkers for screenings. Targeted gene editing approach using CRISPR/Cas methods enables precision gene targeting to fine tune plants ability to fight abiotic stresses by enhancing desirable metabolic components through upregulation of supporting pathways or by downregulating pathways producing inhibitory metabolites to tolerate stress conditions. Together, these omics approaches and precision genome editing enable rapid screening and development of stress-resilient crop varieties. Nanoparticles such as TiO2, ZnO, and Fe2O3 are increasingly used as potential nanofertilizers to enhance the resilience to various abiotic stresses by improving nutrient use efficiency, stimulating the antioxidant production, and reducing the accumulation of reactive oxygen species. Integration of molecular markers, speed breeding, high-throughput plant phenotyping, omics technologies, CRISPR-Cas9 and nanotech interventions create a formidable synergistic breeding pipeline for developing climate-resilient crops that assure future food security.

Keywords: Abiotic Stress Tolerance, CRISPR-Cas9 Genome Editing, Speed Breeding, Omics Technologies, Molecular Breeding

ICABB26-EA-P38

Modulatory Role of Shatavari *(Asparagus racemosus)* on Cancer-Associated Microbiota: A Microbiological Perspective

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Abstract
The development and progression of cancer are currently considered to be multi-factorial processes, in which in addition to genetic and epigenetic alterations they are affected by a host-related microbiota. The impact of dysbiosis in the gut, oral cavity, and reproductive tract has been associated with chronic

inflammation, compromised immune responses, and increased susceptibility to tumorigenesis. This indicates the importance of identification of natural agents that can modulate microbiota as well as exhibit anticancer effect.

Shatavari (Asparagus racemosus) is an acclaimed Ayurvedic medicinal herb and comprises of various phytoconstituents including flavonoids, alkaloids and saponins particularly Shatavarin IV .). These substances exhibit antioxidant, anti-inflammatory, and antitumor activities onlianne.blogspot in cancer cells. Shatavari is also believed to function as a probiotic and prebiotic, helping healthy bacteria such as Bifidobacterium and Lactobacillus. These microorganisms synthesize short-chain fatty acids (SCFAs), which are involved in the anti-carcinogenic pathways. Furthermore, phytochemicals from Shatavari have demonstrated the capability of apoptosis in breast cancer and cervical cancer cell lines.

In addition to its direct anticancer effect, Shatavari's impact on the female reproductive microbiome could lower rates of oncogenic infections such as HPV thereby lowering cancer risk. This dual role—direct cytotoxicity and indirect microbiome modulation—positions Shatavari as a promising candidate for integrative oncology.

This poster will highlight Shatavari's phytochemical mechanisms, its impact on cancer associated microbiota, and its potential as a complementary therapy in cancer prevention and treatment. Future directions include combining Shatavari with probiotics for microbiome specific interventions and exploring Shatavari associated endophytes as novel sources of anticancer metabolites. Together, these approaches may contribute to evidence based, safe, and globally relevant innovations in AYUSH based biomedical research.

Keywords: Shatavari, Cancer, Microbiota, Phytochemicals, Immunomodulation

ICABB26-EA-P39

Microplastics in the Environment: Integrated Perspectives on Sources, Ecological Risks, Degradation Pathways, and Sustainable Management

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Abstract

Microplastics (MPs) have gained recognition as persistent and ubiquitous environmental contaminants due to their extensive distribution, physicochemical stability, and potential ecological and human health implications. Derived from both primary sources, such as industrial additives and personal care products, and secondary sources resulting from the fragmentation of larger plastic debris, MPs are now widely detected in terrestrial, freshwater, and marine ecosystems. This review critically synthesizes recent scientific literature to present an integrated assessment of microplastic sources, classification, environmental occurrence, ecological risks, degradation mechanisms, and management strategies.The ecological and toxicological impacts of MPs are examined with particular emphasis on organismal uptake, trophic transfer, and bioaccumulation, as well as their role as vectors for co-contaminants including heavy metals and persistent organic pollutants. These interactions exacerbate environmental toxicity and raise concerns regarding long-term ecosystem functioning and human exposure through food webs. The review provides a detailed evaluation of degradation pathways, comparing abiotic processes, such as photodegradation, thermodegradation, chemical oxidation, and advanced oxidation techniques, with biotic degradation mediated by bacteria, fungi, and microalgae. Recent advances in microbial consortia, enzyme-based degradation, and biotechnological interventions are highlighted as promising approaches for sustainable microplastic remediation.

Furthermore, current and emerging wastewater treatment technologies, plastic waste management practices, and circular economy-based mitigation strategies are discussed in the context of existing global regulatory frameworks and policy initiatives. By integrating environmental, biotechnological, and regulatory perspectives, this review contributes a comprehensive framework for understanding microplastic pollution and identifies critical research gaps and future directions for effective and sustainable mitigation.

Keywords: Microplastic; Ecological risks; Degradation pathways; Microbial degradation; Abiotic degradation; Regulation and policies.

ICABB26-EA-P40

Cultivated Meat: A Solution to the Global Food Security Challenge

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Abstract

Laboratory-cultured meat (LCM) is the future of meat consumption in the wake of increasing demand for animal proteins and various environmental and food security and ethical concerns. LCM is obtained by isolating muscle cells and pluripotent stem cells and then cultivating them with the use of biocompatible scaffolds to produce muscle tissue. Nowadays, serum-free media with growth factors are used for their production. LCM has several advantages, including the use of little land and water as compared to whole-cut meat. It does not entail the killing of animals and can be formulated with healthier compositions and attributes, such as low saturated fat and high omega-3 fatty acids. Current challenges in this area include effective scaling up of cell proliferation while maintaining stability of the phenotype, reducing dependence on purified recombinant growth factors for support of proliferation in culture, and replicating the texture, taste, and vascularization of whole meats. Other obstacles in this area of development include perfusion of oxygen and nutrients in dense culture, successful harvesting techniques, and approvals of food safety authorities for consumption as meat products. One of the methods which is used to improve the quality of LCM is using the scaffold to support cell growth. One of the scaffolds used for this purpose is Hydrogel-based scaffolds which provide support to the muscle cells and help in the formation of myotubes. Recent pilot-scale work has indicated that chicken and beef LCMs based on porous scaffolds can be similar in qualities to conventional meats in terms of their nutritional properties. The presented review integrates current advancements, limitations, scaling-up and regulatory milestones in LCM to determine its efficiency as a scalable and sustainable counterpart to traditional meat.

Keywords: *Cell-Cultured Meat; Environmental Impact Reduction; Nutritional Tailoring; Consumer Acceptance; Sustainable Production;Bioreactor Scale-up*

ICABB26-EA-P41

Eco-Scaffold: A Water-Efficient, Solid-State Bio-Filter Using Luffa cylindrica for Urban Air Purification

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Abstract

Rapid urbanization in developing nations has led to a critical deterioration in ambient air quality, characterized by hazardous levels of Volatile Organic Compounds and Carbon Dioxide. While microalgal photobioreactors—specifically liquid suspension models—offer a biological solution for carbon sequestration, their large-scale implementation in water-scarce regions is hindered by high evaporative losses, substantial weight loads, and biofouling, where algal overgrowth on reactor walls impedes light penetration. To address these challenges, this study introduces a novel "Solid-State Trickling Bio-Scaffold" designed to overcome these limitations by eliminating the bulk liquid phase. The innovation utilizes the dried, fibrous network of *Luf a cylindrica* (vegetable sponge) as a cost-effective, biodegradable support matrix. A synergistic microbial consortium comprising *Chlorella vulgaris* (for photosynthetic oxygenation) and *Pseudomonas putida* (for hydrocarbon biodegradation) is co-immobilized on the porous Luffa surface. Unlike traditional submerged tanks, this system operates as a trickling filter, by circulating a minimal moisture film to sustain the biofilm. The natural honeycomb geometry of the Luffa sponge provides a high specific surface area for gas-liquid mass

transfer, ensuring direct contact between pollutants and the microbial layer while preventing self-shading. Preliminary assessments indicate that this solid-state design reduces water consumption by approximately 90-95% compared to conventional liquid photobioreactors. Furthermore, the use of agricultural waste (Luffa) as the primary scaffold significantly lowers fabrication costs. This project presents a sustainable, scalable and low-maintenance model for urban air purification, specifically engineered to withstand the unique climatic and resource constraints of the Indian subcontinent.

Keywords: *Luf a cylindrica*, Bio-Scaffold, Trickling Filter, Microbial Consortium, Air Pollution.

ICABB26-EA-P42

Process-Level Optimization Strategies for Enhancing Anaerobic Digestion in Urban Waste-to-Energy Frameworks

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Abstract

The dual challenge of organic waste management and sustainable energy in cities has been intensified by rapid urbanization. Anaerobic digestion-based biogas production is a well-established renewable pathway; however, its adoption in urban centers remains limited due to factors such as long hydraulic retention times, variable methane yields, and operational instability in conventional systems. This study examines process-level strategies that address these limitations and enhance the suitability of biogas for urban applications.

The study reviews advances in feedstock pretreatment, including size reduction and thermal conditioning, which thus improve substrate accessibility and reaction kinetics. It further discusses the role of staged anaerobic digestion and continuous mixing in stabilizing microbial activity and improving gas generation. Temperature regulation within mesophilic and thermophilic ranges is analyzed as a key factor in accelerating digestion too. In addition, process control measures such as pH buffering, alkalinity management, and the use of catalytic or biological additives are also considered for maintaining stable methane production. Physical enhancement techniques, such as ultrasonic agitation, are examined for their ability to intensify the breakdown of complex organic matter. Pressure regulation, biogas purification, digestate recovery, and other downstream considerations are also addressed to ensure operational safety and resource recovery.

By synthesizing these approaches, the study highlights how targeted optimization of the anaerobic processes involved in digestion can significantly improve the rate, reliability, and overall performance of anaerobic digestion systems. The findings underscore the potential of such strategies to support decentralized, efficient biogas production and thus help position biogas as a practical component of integrated waste-to-energy frameworks.

Key words: Anaerobic digestion; biogas production; hydraulic retention time; methane yield; organic waste management

ICABB26-EA-P43

Cultivation practices of Picrorhiza kurroa: Current perspective & future opportunities

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Abstract

The dynamic changes in lifestyle accompanying globalization have driven a rapid increase in hepatic diseases worldwide. As per WHO data (2023), around 4% annual deaths (approximately 2 million annual deaths) were reported due to liver-related diseases, with cirrhosis and hepatocellular cancer being the major causes of it. Also, acute hepatitis causes a smaller number of deaths. The existing medications are beneficial for alleviating disease symptoms, but often with side effects. The growing acceptance of safe alternative therapies has led to medicinal plant-based herbal drugs being used as a potential alternative. Among different hepatoprotective plants, *Picrorhiza kurroa* is a well-known species of the family Scrophulariaceae, widely grown in the South Asian subcontinent, including the

Himalayan regions of China, Pakistan, India, Bhutan, and Nepal. The plant is known for key bioactive compounds, cumulatively called Picroliv or Kutkin. It is a mixture of phytocompounds, such as Picroside I, Picroside II, and Kutkoside, which are, by nature, iridoid glycosides and exhibit strong liver-protective and immunomodulatory effects. Recent studies highlight the key advances in Picroside production using different cultivation strategy including micropropagation, cell suspension culture, and meristem culture. However, the techniques such as hydroponic cultivation are in the initial stage of validations. The recent advancements *Picrorhiza kurroa* cultivation have opened the avenue for the development of herbal formulation using *Picrorhiza kurroa* towards respiratory, anti-inflammatory, neuroprotective, antioxidant and anti-diabetic properties. The review will highlight the key advancements.

Keywords: Picrorhiza kurroa, hydroponics, picroside, therapeutic, hepatoprotective.

ICABB26-EA-P44

Tracing the Ecological Footprint of Pharmaceutical Residues in Nature

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Abstract

Pharmaceutical residues are increasingly recognized as a growing environmental issue due to their sustained presence in soil, water, and biological systems and their potential consequences for ecosystem stability and human health. These residues largely arise from the extensive use of pharmaceuticals, incomplete metabolic breakdown, and improper disposal, enabling active compounds to enter natural systems through wastewater effluents, sewage sludge, and agricultural runoff. Evidence from multiple studies, including reports from river systems such as the Ganges, Yamuna, and the Geum River Basin, indicates the frequent occurrence of pharmaceuticals like diclofenac, sulfamethoxazole, and carbamazepine at concentrations capable of affecting ecological processes, altering microbial communities, and accelerating antimicrobial resistance. Human populations are indirectly exposed through contaminated water supplies and food chains, highlighting the close link between environmental quality and public health. This review study brings together current research on the distribution, ecological impacts, and management of pharmaceutical residues, with particular emphasis on sustainable remediation strategies such as biochar-based adsorption, microbial and algal bioremediation, advanced wastewater treatment technologies including ozonation, reverse osmosis, and activated carbon filtration, as well as preventive approaches like eco-pharmacovigilance that aim to reduce environmental release at the source. The study emphasizes the importance of coordinated scientific innovation and regulatory action to address pharmaceutical pollution while ensuring long-term environmental protection and human well-being.

Keywords: Pharmaceutical residues; Bioremediation; Advanced wastewater treatment; Antimicrobial resistance;eco-pharmacovigilance

ICABB26-EA-P45

Evaluation of The Biodegradation Potential of American Cockroach (*Periplaneta americana*) Gut Microflora for Polyethylene Waste

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Abstract

The environmental persistence of Low density Polyethylene (LDPE), a widely used plastic polymer, presents a major ecological challenge. In this study, the gut of *Periplaneta americana* was investigated as a potential source of LDPE degrading bacteria. The total viable count (TVC) of the gut of was determined to be 4.1*10 6 CFU/g. Four PE degrading bacterial strains were isolated and named as DP1, DP2, DP3 and DP4. Primary screening identified strains DP1 and DP2 as the most efficient isolates,

showing favourable CZ:CS ratio. Morphological, biochemical, and molecular analyses were conducted to characterize the isolates. 16S rRNA gene sequencing identified DP2 as a strain of *Escherichia coli* (with 100% similarity) and DP1 as *Acinetobacter johnsonii* (with similarity of 99.11%). Both isolates were positive for esterase and urease activity, which may contribute to the depolymerization of LDPE. Biodegradation capacity was confirmed by weight loss assays, enzymatic activity, and changes in Polyethylene (PE) film surface morphology. DP1 and DP2 demonstrated 8.4% ± 0.4 and 9.6% ± 0.2 degradation of PE films respectively. Scanning electron microscopy (SEM) imaging revealed surface erosion, holes, and cracks in treated polyethylene films. Substrate degradation ratio analysis showed decrease in PE film weight (8.4% and 9.6%). Chemical structural alterations examined by Fourier-transform infrared spectroscopy (FTIR), which showed emergence of carbonyl and hydroxyl peaks. These findings suggest that PE can be significantly degraded by the gut microbiota of *P. americana*, particularly by *A. johnsonii* strain DP1 and *E. coli* strain DP2 through enzymatic and physicochemical processes.

Keywords: Polyethylene biodegradation, low-density polyethylene (LDPE), plastic-degrading bacteria, *Acinetobacter johnsonii*, *Escherichia coli*

ICABB26-EA-P46

Bridging Micronutrient Deficiencies Through Rice Fortification: A Review on Thiamine and Pyridoxine Fortification in the Indian Context

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Abstract

Micronutrient deficiencies are a major and constant health concern in India. One of the most serious deficits are of thiamine (vitamin B1) and pyridoxine (vitamin B6), influenced by diets where rice is the basis of daily meals for most of the population, and the rest of the diet is very limited or not diverse enough. Post-harvest grain processing practices such as milling, polishing, remove the bran and germ layers where the B vitamins are concentrated in pursuit of improving appearance and taste. This is followed by not up to par storage practices and cooking, where heat exposure damages the levels of B vitamins. Therefore, the fortification of rice with vitamins B1 and B6 offers a sustainable and a promising solution to reintroduce the required levels of the B vitamins in the diets of many.

This review highlights the biochemical role of these vitamins, effects of processing on their retention, and aspects of fortification, including fortificant selection, inclusion levels, and stability.

Also included in this review is the usage of QGIS-based geospatial mapping to identify areas showing high rice dependence as well as insufficiency of the vitamins B1 and B6, helping us visualize at-risk groups and guide implementation.

Overall this review highlights the importance of fortifying rice, a staple grain in India, and the usage of fortifying strategies and geospatial mapping as an effective means to counter malnutrition for at-risk groups.

Keywords: Rice fortification; Vitamin B1; Vitamin B6; Micronutrient deficiency; Grain processing; QGIS; Geospatial mapping

ICABB26-EA-P47

New Bioactive Leads and Target-Species Applications of Biopesticides for Sustainable Crop Production: An Overview of Indian and International Scenarios

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Abstract

Global research on biopesticides as sustainable crop protection solutions has intensified due to the growing environmental hazards and resistance issues connected with chemical pesticides. Compared to synthetic pesticides, biopesticides—which come from natural sources such microbes, plant extracts, and bioactive metabolites—offer target-specific and environmentally friendlier pest control solutions. Driven by local biodiversity and agricultural demands, research in India mostly focusses on native microbial strains (e.g., *Trichoderma*, *Bacillus thuringiensis*), neem-based botanicals, and traditional formulations to preserve staple crops including rice, cotton, and lentils. However, concerns with farmer awareness, regulatory obstacles, and technological limitations continue to limit use. In order to increase efficacy, stability, and species specificity, biopesticide innovation is rapidly using cutting-edge biotechnological techniques, such as microbial consortia, nano-formulations, and RNA interference (RNAi)-based systems. Endophytic bacteria, weed-derived metabolites, and microbial secondary chemicals are examples of emerging bioactive leads that have broad-spectrum pest control potential and improve integrated pest management (IPM) tactics worldwide. Key obstacles to commercialisation are addressed by standardised manufacturing techniques, such as controlled microbial fermentation and formulation protocols, which increase field performance and reproducibility. Comparative analysis shows that biopesticide uptake and sustainability can be strengthened by fusing India's resource-rich biodiversity and low-cost production techniques with cutting-edge international technologies. Accelerating the development and use of efficient biopesticides that lessen reliance on chemicals and promote sustainable agriculture globally requires strategic international cooperation, harmonised laws, and information transfer.

Keywords: Integrated pest management (IPM), Microbial pesticides, Botanical pesticides, Nano-formulations, RNA interference (RNAi).

ICABB26-EA-P48

Niacin and Folate Biofortification of Maize in the Indian Context

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Abstract

Micronutrient deficiencies are a major cause of health related concern in many regions of India where cereal based and predominantly vegetarian diets dominate daily nutrition. Among them B-vitamin deficiencies like Niacin (vitamin B3) and folate (vitamin B9) deficiencies are most widespread especially in communities that depend heavily on maize with limited diversity in diet. Folate deficiency is common in women and young individuals, while insufficient niacin intake is observed in several maize consuming areas due to low bioavailability of this vitamin in untreated grains.

The problem of low bioavailability of these vitamins is compounded by post harvest and processing practices like milling, refining and cooking that rids the grain from a large share of these vitamins before the grain reaches the table. Which results in maize products contributing only a modest fraction of the daily vitamin needs which reinforces long-term nutritional gaps.

Fortification of maize with vitamins B3 and B9 is explored in this review as a sustainable solution to fight vitamin inadequacy of maize grains. It summarizes the existing evidence on the biochemical roles of these vitamins, effects of processing on their retention and technical aspects of fortification including fortificant selection, recommended inclusion levels and stability in flour matrices. Additionally, proposition of the use of QGIS-based spatial analysis to map maize production and consumption along

with deficiency affected regions, identifying priority zones for fortification interventions and policy focus.

Overall this review highlights maize fortification when supported by geospatial mapping and targeted implementation could serve as an effective strategy to counter malnutrition and deficiency dependent health concerns.

Keywords: Maize fortification; Micronutrient deficiency; Bioavailability; Food processing; QGIS; Geospatial mapping

ICABB26-EA-P49

Metagenomic Insights into Plastic-Degrading Compost Microbiomes and Their Implications for Food-Production Soils

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Abstract

Various metagenomic studies have analyzed compost microbes, revealing a variety of microbes with plastic-degrading potential, which is directly relevant to food-production soils. Many newly formed computational tools and software, in combination with multi-omics technologies, has enabled to rapidly identify novel enzymes and protein systems to degrade plastic, through more precise and comprehensive analysis of microbial communities of a targeted metagenome. One such study focuses on the large-scale metagenomic study that catalogs the plastic-contaminated sites analyzes plastizymes, a collection of plastic-active genes, specifically belonging to the class hydrolase and cutinase. Furthermore, a dedicated sequencing of the compost communities has led to identification of a novel enzyme, a cutinase-like hydrolase (MhCulp3), from a compost metagenome, which has the ability to depolyermise the polyester-polurethane ester bonds of the complex polymers. Also, functional annotation reveals plastic-degrading enzyme families and many uncharacterized proteins, suggesting potential biodegradative functions that could be uncovered through targeted biochemical and genetic studies. Additionally, sequencing-based community profiling also demonstrates specific changes in the plastic-driven community shifts. Various compost reactors are enriched by the addition of aliphatic polyesters to enrich several *Actinobacteria*, such as *Pseudonocardia* and *Thermomonospora*, which already possess polyesterase genes. Moreover, the activity of a specific *Thermomonospora spp*. enzyme, Tcur1278, has also been observed to depolymerize and degrade polymers in vitro. Along with this, the addition of specific microplastics leads to the formation of a unique biofilm layer, the plastisphere, and its production is enriched in plastic-clastic bacteria like Proteobacteria spp., whereas overall microbial diversity tends to decrease under heavy plastic load. Collectively, these findings, including the identification of novel enzymes and community shifts in response to plastic, support the view that compost in food-producing soils, especially thermophilic nutrient-rich composts, is a hotspot of polymer-degrading microbes and enzymes.

Keywords: Plastisphere, Plastizymes, Food-producing soils, Metagenomics, Compost

ICABB26-EA-P50

Microbial and Enzymatic Valorization of Agricultural Lignocellulosic Waste for Sustainable Bioproduct Generation

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Abstract

Agricultural lignocellulosic waste, such as rice straw, wheat straw, corn stover, and sugarcane bagasse, represents one of the most abundant renewable bioresources generated globally. Despite its availability,

the complex and recalcitrant structure of lignocellulosic biomass—composed mainly of cellulose, hemicellulose, and lignin—limits its direct utilization. Recent advances in microbial and enzymatic valorization have provided sustainable pathways for converting these agricultural residues into high-value bioproducts, supporting circular bioeconomy principles and sustainable agricultural practices.
This study reviews integrated biotechnological strategies involving pretreatment, enzymatic hydrolysis, and microbial fermentation for efficient lignocellulosic biomass conversion. Microbial consortia, filamentous fungi, and engineered bacterial strains play a pivotal role in degrading complex polymers and improving substrate accessibility. Enzyme systems, including cellulases, hemicellulases, and lignin-modifying enzymes, significantly enhance saccharification efficiency and fermentable sugar release. These processes facilitate the production of diverse bioproducts such as biofuels, biopolymers, organic acids, industrial enzymes, and biofertilizers.
Emerging approaches such as reduce process cost, energy consumption, and environmental impact. Moreover, microbial detoxification strategies address inhibitory compounds generated during biomass pretreatment, improving downstream fermentation efficiency. Overall, microbial and enzymatic valorization of agricultural lignocellulosic waste provides an eco-friendly alternative to conventional waste management, enabling resource recovery, reducing environmental pollution, and enhancing the sustainability of agricultural systems.
Keywords: Lignocellulosic biomass; Agricultural waste; Microbial valorization; Enzymatic hydrolysis; Bioproducts; Sustainable bioprocessing; Circular bioeconomy

ICABB26-EA-P51

Degraded soil converted to functional soil

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Abstract

Soil is one of the most significant repositories for biodiversity. Human activities frequently degrade soil environmental conditions, resulting in a decline in quantity and simplification of animal and plant populations that can withstand stress. Most of these organisms are insects, including Neuroptera, Diptera, Coleoptera, and Lepidoptera. Soil biota are vital to soil function because they are involved in activities such as organic matter breakdown, humus production, and nutrient cycling. Degraded soil loses its natural quality and ability to support healthy plant growth and the ecosystem. The primary causes of soil degradation are erosion, loss of organic matter, urbanisation, and development. Soil deterioration is classified into three types. Physical, Chemical and Biological degradation. Functional soil is healthy soil that can carry out all of its natural activities effectively, including plant development, microbes, animals, and the environment. It promotes plant development, regulates water levels, cycles nutrients, filters pollutants, and stores carbon. Degraded soil is transformed into functioning soil by re-establishing its physical structure, chemical balance, and biological activity, particularly soil microbes. Recent scientific research illustrates how deteriorated soil is being regenerated into functional soil. A 2025 study shows microbial ecosystem techniques to restoration, boosting soil health through biocrusts, Grassland Restoration, Organic amendment's effects on mining-degraded soil, Plant growth-promoting microorganisms for restoration, Microbially induced carbonate precipitation (MICP). As a result Bacteria play an important role in transforming damaged soil into functioning soil, particularly in current restoration procedures. They act as engineers, nutrient recyclers, soil builders, and detoxifiers. Bacteria also aid in precision and AI-based soil restoration, which is achieved through microbiome-based decision systems used in smart agriculture and IoT-based soil management. Another example is Bacteria in Future Technologies: Engineered Microbial Consortia for Experimental CRISPR-Assisted Soil Restoration.
Keywords: Soil biodiversity, Soil degradation, Functional soil, Soil microorganisms (bacteria), Microbial soil restoration

ICABB26-EA-P52

Bioremediation potential of Halophilic and Halotolerant Bacteria in Hypersaline Ecosystem

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Abstract

Hyper-saline environments containing high concentrations of salts (NaCl, Calcium chloride, sodium nitrate) are important as they host extremophiles (ex:-Halobacterium, Halomonas, and Haloferax).The release of untreated wastewaters containing high-salinity and toxic metals leads to environmental pollution and harms aquatic & terrestrial ecosystems.Conventional bioremediation approaches are insufficient to remove contaminant from hyper saline environments. Halophilic & halotolerant microorganisms are used for bioremediation in extreme environments which depend on factors like ionic composition & salt concentration.Halophilic & Halotolerent microorganisms tolerate salt by controlling osmotic pressure in cytoplasm using one of two major strategies including salt in strategy &compatible solute while keeping enzymes active. Recent advances in genetic engineering, such as CRISPR/Cas systems and recombinant DNA technology, enable precise genetic modifications in halophilic microorganisms, improving their metabolic efficiency for the degradation of toxic pollutants in hypersaline environments. Halophilic microorganisms identified as promising agents such as Halomonas and Marinobacter exhibit effective petroleum hydrocarbon degradation and heavy-metal sequestration, while archaeal genera including Haloferax and Halobacterium demonstrate high enzymatic stability under extreme conditions. Ultimately, the combination of resilience to extreme conditions, metabolic diversity, enzyme stability, omics & synthetic biology potential, & cost effectiveness offers a transformative approach to sustainable environmental management in extreme condition. Despite these advances, challenges remain in optimizing genetically tractable strains, limited understanding of genetics, low bioavailability of pollutants,isolation difficulty, biosafety & regulatory issues. Further research is necessary to fully utilize the potential of halophiles in sustainable bioremediation.

Keywords: Extremophiles, Halophiles, Hypersaline Bioremediation, CRISPR/Cas systems, Compatible solutes

ICABB26-EA-P53

PPCPs: Silent Threats in Water Systems

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Abstract

Pharmaceuticals and personal care products (PPCPs) have drawn more attention as a significant class of emerging micropollutants due to their extensive consumption, continuous environmental release, and incomplete removal by conventional wastewater treatment processes. Aquatic environments often contain trace amounts of these substances, which include antibiotics, analgesics, anti-inflammatory medications, preservatives, antibacterial agents, and ultraviolet (UV) radiation filters routinely used in everyday care goods. Due to their persistence and biological activity, these chemicals can adversely affect aquatic organisms, disrupt endocrine systems in wildlife and humans, promote antimicrobial resistance, and offer long-term hazards to human health. Using advanced analytical methods like ultra-high-performance liquid chromatography combined with tandem mass spectrometry (UHPLC-MS/MS), recent studies have shown the ubiquitous presence of several PPCPs in surface water and wastewater effluents. Additionally, compound-specific studies indicates that environmental conditions,

particularly pH, have a considerable impact on the toxicity and bioavailability of personal care product constituents such as UV-filter compounds, thereby increasing their ecological risk. The susceptibility and vulnerability of aquatic microorganisms and trophic interactions to long-term exposure to these new toxins has also been brought to light by ecological risk assessments. With the use of spectrophotometric analysis and physicochemical characterisation of water samples, the current study attempts to investigate the environmental occurrence and distribution of selected pharmaceutical and everyday care product residues in aquatic systems. For the mitigation of PPCPs in water matrices, the study also offers a critical overview of existing risk assessment frameworks and cutting-edge treatment techniques, such as biotechnological and adsorption-based methods. Although UHPLC-MS/MS and other sophisticated techniques offer highly sensitive detection, they are constrained by labour-intensive sample preparation, potential matrix effects, significant sample volume requirements, and a focus on specific substances. As a result, non-target or emerging micropollutants may remain undetected, making such approaches less useful for routine monitoring in resource-constrained laboratories. By integrating experimental data with literature-supported evidence, this study emphasises the urgent need for long-term monitoring and effective remediation strategies to mitigate the persistent threat posed by pharmaceutical and personal care product micropollutants to ecosystem stability and public health.

Keywords: PPCPs, Micropollutants, Aquatic, Ecotoxicity, Remediation

ICABB26-EA-P54

Green Synthesis of MoS_2 Nanostructures: A Sustainable Approach for Developing Biocompatible Lung Cancer Biosensors

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Abstract

Conventional nanomaterial synthesis protocols employing harsh reducing agents and energy intensive fabrication methods present substantial environmental burdens and cytotoxicity concerns that fundamentally constrain their translation to clinical biosensing platforms. This investigation advances a paradigm-shifting green chemistry framework for synthesizing two dimensional molybdenum disulfide (MoS_2) nanostructures utilizing phytochemical-mediated bio reduction, positioning plant-derived polyphenolic compounds as sustainable reducing and stabilizing agents. This biogenic synthesis route circumvents conventional chemical vapor deposition and liquid-phase exfoliation methodologies, operating under ambient conditions with dramatically reduced carbon footprint and hazardous waste generation. Comprehensive physicochemical characterization via UV-visible spectrophotometry, X-ray diffraction crystallography, and high-resolution scanning electron microscopy validated the successful fabrication of few-layered MoS_2 nanosheets with exceptional crystallinity and enhanced surface-to-volume ratios. Literature evidence substantiates that photosynthesized nanomaterials exhibit superior biocompatibility profiles compared to chemically derived counterparts, attributed to organic capping layers that mitigate cytotoxic interactions at the nano-bio interface. The theoretical framework positions green-synthesized MoS_2 as promising signal transduction matrices for electrochemical biosensor architectures targeting clinically relevant lung cancer protein biomarkers. The inherent electronic properties of MoS_2 including high carrier mobility, tenable bandgap, and exceptional electrocatalytic activity coupled with biocompatible surface functionalization, establish a compelling foundation for sensitive, selective diagnostic platforms. This work establishes a scalable, environmentally benign nanofabrication platform that reconciles ecological sustainability with clinical diagnostic imperatives, offering transformative potential for green nanotechnology integration within precision medicine frameworks and advancing the United Nations Sustainable Development Goals in healthcare innovation.

Keywords: Photosynthesis, two-dimensional nanomaterials, molybdenum disulfide, electrochemical biosensing, green nanotechnology, biocompatible transducers, sustainable diagnostics, precision oncology

ICABB26-EA-P55

Antidiabetic Potential of Mushroom Species: Bioactive Compounds and Their Mechanism

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Abstract

Diabetes mellitus is a chronic metabolic disorder in which the body doesn't make enough insulin or become insulin resistant, leading to high glucose level in the body. Type-2 Diabetes poses a serious global health, social and economic challenge and is among the most rapidly growing health issues of the 21st century. Many synthetic hypoglycemic drugs are available commercially for effectively managing diabetes but most of them have several side effects like severe hypoglycemia, weight gain, gastrointestinal problems, cardiovascular risks, kidney and liver toxicity, cancer risks (by some classes of drugs). Synthetic drugs have limited effects on root causes of this disease like oxidative stress, insulin resistance, β-cell degeneration, chronic inflammation. Scientists are now exploring natural products such as mushrooms as functional food as they have various bioactive compounds especially polysaccharides and terpenoids and medicinal properties. The present review focuses on different types of mushroom species which have antidiabetic effects by producing secondary metabolites like polysaccharides, phenolic compounds, terpenoids, dietary fibers and vitamins. In vivo and in vitro studies through research papers shows that these bioactive compounds exhibit their various mechanisms like inhibition of α- amylase, α- glycosidase activity, enhancement of insulin sensitivity, reduction in oxidative stress and inflammation, and improves β-cell functions. The most studied mushroom species showing antidiabetic effects are *Ganoderma lucidum (*Reishi*), Lentinus edodes (*Shiitake*), Agaricus blazei, Grifola frondosa (*Maitake*), Pleurotus pulmonarius (*Oyster mushroom*).* There is still a lack of clinical standardization, insufficient long term human trials, safety concerns, formulation challenges as the challenges. The real life applications for diabetes prevention are still limited. On the basis of studies till now, mushrooms are safe, nutritionally rich and have high therapeutic potentials especially in treatment of diabetes.

Keywords: Medicinal mushrooms, Insulin resistance, Bioactive compounds, Antidiabetic activity

ICABB26-EA-P56

Tracing Antibiotics in Aquatic Ecosystems through Modern Monitoring Approaches

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Abstract

The pervasive presence of antibiotic residues in aquatic ecosystems represents not only an environmental challenge but a growing threat to global human health through the silent amplification of antimicrobial resistance. Recent evidence demonstrates that approximately 9,500 tonnes of human-used antibiotics enter river networks annually exceeding ecological safety thresholds. Systematic surveys across Africa and Chinese river systems consistently reported multiple antibiotics such as ciprofloxacin and amoxicillin in surface waters and wastewaters at concentrations surpassing protective limits.

Advances in analytical detection from high-resolution chromatographic systems to emerging biosensor technologies have fundamentally reshaped our capacity to identify trace contaminants that were previously undetectable yet have significant biological consequences. Advanced techniques such as ultra-fast liquid chromatography–tandem mass spectrometry has significantly enhanced lab monitoring efficiency.They can quantify multiple classes of antibiotic at ng/L sensitivity with run times of only minutes. While mass spectrometry–based platforms are essential for regulatory validation, their limited accessibility due to high cost remains an issue. Biosensing technologies, including surface-enhanced Raman spectroscopy, electrochemical sensors and aptamer-based platforms, offer a transformative pathway toward real-time detection of antibiotics. The integration of artificial intelligence further

enhances these systems by enabling rapid data interpretation, cross-scale surveillance, and predictive assessments of exposure risk. From health perspective, improved and early detection of environmental antibiotics is critical because even trace antibiotic residues exert selective pressure on microbial communities, reducing biodiversity and accelerating the emergence and persistence of resistant bacteria. This is evident from studies which present that approximately 10% of *Escherichia coli* isolates from Sichuan rivers exhibited antibiotic resistance, with more than 5.8% displaying multidrug resistance. Comparable studies in Africa also revealed widespread excess of antibodies concentrations. Contaminated aquatic systems act as conduits for resistance transmission through drinking water supplies, irrigation, and aquatic food chains, thereby linking environmental exposure directly to human and animal health risks. Failure to monitor and control these low-level yet persistent contaminants causes deterioration of clinical antibiotic efficacy and increasing healthcare burdens. Consequently, advances in detection technologies should be viewed as a frontline public health intervention rather than solely an analytical achievement. By linking environmental surveillance with health risk assessment enable early detection and proactive mitigation of antimicrobial resistance protecting long-term human health.

Keywords: Antibiotic residues, Aquatic pollution, Antimicrobial resistance (AMR), UFLC–MS/MS, SERS

Session 2:
Environmental Biotechnology and Sustainable Agriculture
Oral Presentations

ICABB26-EA-OP-01

Curcuma amada Restores Gut Microbial Composition in Pesticide-Stressed *Drosophila melanogaster*

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Abstract

Pesticide exposure is known to disturb gut microbial balance, which affects host physiology, immunity, and metabolism. Chronic low-level exposure to organophosphates in humans has been related to neurological symptoms such as headaches, tremors, paralysis, and dizziness, which are consistent with AChE inhibition in the nervous system; exposure also alters the human gut microbiome. Both occupational and environmental exposures to insecticides and general pesticides considerably alter and damage the gut microbe composition, as measured by various diversity indices. The present study investigated the sex-specific effects of *ethion* exposure on gut microbiota in *Drosophila melanogaster* and evaluated the restorative potential of *Curcuma amada* (mango ginger). The Experiments were performed on control and treated adult flies: (i) Control (untreated), (ii) *Ethion-exposed,* (iii) *C. amada*-treated, and (iv) *Ethion* + *C. amada*-treated. 16S rRNA-based microbiome analysis revealed distinct sex-dependent responses to microbial composition in pesticidal stress. Both male and female *Drosophila* activated common microbial and functional adaptations to cope with pesticide-induced stress. Pesticide stressed female flies exhibited a significant reduction in microbial richness with an increased diversity, which indicates a dysbiotic microbial community with significant functional confusions in metabolic and defensive pathways. In contrast, male flies showed no significant alterations. Supplementation with *C. amada* helped to restore microbial richness in pesticide stressed females, re-establishing near-normal microbial composition and the functional profiles. These findings feature the potential of *Curcuma amada* serving a protective and gut microbiota-stabilising action against pesticide-induced gut dysbiosis. Future studies exploring the basis of these differences could help in getting more clarity regarding personalised approaches to environmental risk and microbiota-targeted interventions.

Keywords: Gut microbiota, *Ethion*, Pesticide, Dysbiosis, Sex-specific response, *Drosophila melanogaster*, *Curcuma amada.*

ICABB26-EA-OP-03

Integrated Biomining and Mycoremediation Approaches for Sustainable Management of Electronic Waste

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Abstract

The rapid increase in electrical and electronic waste (e-waste) due to technological advancement has become a major environmental challenge, as improper recycling and disposal release toxic heavy metals such as lead (Pb), cadmium (Cd), chromium (Cr), mercury (Hg), nickel (Ni), and copper (Cu) into soil and water systems. These metals pose serious risks to ecosystems and human health. Conventional physicochemical remediation methods are often costly, energy-intensive, and ineffective at low metal concentrations, creating a need for sustainable and environmentally friendly remediation strategies.

Mycoremediation and biomining have become viable biological methods for detoxifying e-waste-contaminated areas and recovering metals. Through bioleaching processes involving organic acid generation, chelation, and redox reactions, biomining uses microorganisms, especially fungus, to solubilize and mobilize metals from complicated e-waste matrices. For the efficient removal of heavy metals, mycoremediation uses metallotolerant fungal species including *Aspergillus niger, Penicillium simplicissimum*, *Trichoderma harzianum*, *Rhizopus arrhizus*, and white-rot fungi like *Phanerochaete chrysosporium*.

Fungal remediation operates through integrated mechanisms of biosorption, bioaccumulation, biotransformation, and biomineralization. The fungal cell wall, rich in chitin, glucans, and functional groups such as carboxyl, amino, and phosphate moieties, plays a key role in metal binding, while intracellular sequestration and precipitation as metal oxalates or phosphates reduce metal toxicity. Environmental factors such as pH, temperature, and nutrient availability significantly influence remediation efficiency. Overall, the integration of biomining and mycoremediation offers a cost-effective, eco-friendly, and sustainable strategy for managing heavy metal pollution associated with e-waste.

Keywords: Mycoremediation; E-waste; Heavy metal pollution; Biosorption; Biomining .

ICABB26-EA-OP-04

Metagenomic Analysis Uncovers a Rich Diversity of Bacteriophages in the Yamuna River

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Abstract

Bacteriophages, the most abundant biological entities in aquatic ecosystems, remain largely unexplored despite their potential as natural biocontrol agents against antibiotic-resistant bacteria. Riverine systems, such as the Yamuna River, reflect microbial evolution and genomic adaptation under environmental pressures. In this study, the Yamuna River virome was analyzed through metagenomics to characterize its taxonomic and functional diversity. A total of 28,993 viral sequences were identified across 21 viral classes, with *Caudoviricetes* dominating (49%; n = 14,262), followed by lower-abundance classes including *Pokkesviricetes*, *Revtraviricetes*, *Heriviricetes*, *Leviviricetes*, and *Megaviricetes*. Species-level analysis revealed 8,033 phages (57%) associated with cultivable bacterial hosts, while 6,224 sequences (43%) lacked definitive host classification, indicating the existence of unexplored viral taxa. Importantly, among the 2,642 phages linked to pathogenic bacteria, 544 sequences specifically targeted clinically significant ESKAPE pathogens, including, including, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa* and *Enterobacter* species, highlighting its potential as a reservoir for novel phage-based therapeutics. Systematic exploration and functional characterization of these phages could advance antimicrobial strategies, support ecological monitoring, and inform biomedical applications, emphasizing the importance of continued virome research in aquatic ecosystems.

Keywords: Antimicrobial resistance, Bacteriophages, Caudiviricetes, Metagenomics, Yamuna

ICABB26-EA-OP-05

Production and Characterization of Bacterial Cellulose Produced by Acetobacter aceti MTCC 3246

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Abstract

Bacterial cellulose (BC) is an extracellular polysaccharide produced by certain bacteria, renowned for its high purity, crystallinity, mechanical strength, and biodegradability. In this study, bacterial cellulose was produced using the *Acetobacter aceti* MTCC 3246 bacterial strain under static and agitated fermentation conditions. The culture medium was prepared with suitable carbon and nitrogen sources to promote cellulose synthesis. After the incubation period, the cellulose pellicle formed at the air-liquid interface was harvested, purified through alkali treatment to remove bacterial cells and medium residues, and subsequently washed to neutrality. The yield of bacterial cellulose was calculated on a dry-weight basis, revealing efficient production under the adopted conditions. The purified BC was subjected to comprehensive physicochemical characterization. Fourier-transform infrared spectroscopy (FTIR) confirmed the presence of characteristic cellulose functional groups corresponding to O-H stretching and β-1,4-glycosidic linkages. X-ray diffraction (XRD) analysis indicated a highly crystalline cellulose structure. The combined results confirm that the bacterial strain efficiently produced cellulose with desirable structural integrity and crystallinity. This study establishes the potential of the bacterial strain for the sustainable production of high-quality bacterial cellulose, highlighting its suitability for

advanced applications in biomedical, packaging, and industrial fields.
Keywords: Bacterial cellulose, BC Yield, FTIR, Crystallinity.

ICABB26-EA-OP-06

Metabolite Profiling of Standardized Fermented Chakhao Amubi Rice

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Abstract

Fermentation of the traditional rice variety *Chakhao Amubi* was standardized to characterize its bioactive chemical profile. After optimizing the fermentation process, an ethyl acetate extract of the fermented rice was prepared and analyzed using Gas Chromatography (GC). The GC profile revealed a diverse range of compounds belonging to various chemical classes, including cyclic esters, aromatic diols, heterocyclic aldehydes, alkylated phenols, cyclo alcohols, esters and ester derivatives, saturated fatty acids, ketones, cyclic ketones, monoglycerides, glycerol esters, plant-derived sterols, and triterpenoids. Among the detected compounds, Atraric acid, Catechol, and 1-Monostearin (Stearin, 1-mono-) were identified as prominent constituents, showing the highest peak area % of 5.13, 4.07, and 3.69 respectively. The identified compounds are associated with a wide range of biological and functional properties**,** such as antioxidant, anti-inflammatory, antimicrobial, anticancer, antidiabetic, hepatoprotective, and anti-hypoxic effects. Several compounds also contribute to flavor and fragrance enhancement, bitter taste, and pharmaceutical applications, including antiseptic, insecticidal, and cosmetic uses. It emphasizes that fermented rice has the potential as a functional food ingredient with nutraceutical and therapeutic relevance.

Keywords: *Chakhao Amubi*; Gas Chromatography; ethyl acetate extract; bioactive compounds; nutraceutical.

ICABB26-EA-OP-07

From Assessment to Amendment: Developing Soil Conditioners for Restoration of Peri-Urban Degraded Soils

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Abstract

Rapid urbanization and intensive anthropogenic pressures have led to the degradation of peri-urban soils, resulting in loss of fertility, poor structure, and reduced biological activity. Such soils, often exposed to construction residues, waste dumping, and erratic agricultural practices, demand sustainable rehabilitation strategies to restore their productivity and ecological function. The present study focuses on designing and developing eco-compatible soil conditioners tailored to the physicochemical properties of degraded peri-urban soils. In the preliminary phase, representative soil samples were collected from multiple peri-urban sites characterized by distinct levels of degradation. A comprehensive physicochemical analysis was conducted to assess key soil parameters, including pH, electrical conductivity, organic carbon, texture, bulk density, water-holding capacity, and essential macro- and micronutrients (N, P, K, Ca, Mg, Fe, Zn). The results revealed considerable heterogeneity across sampling locations, indicating structural deterioration and loss of fertility. These findings provide a critical baseline for the formulation of soil conditioners designed to target specific limitations such as

compaction, nutrient deficiency, and water retention. The next phase of the study involves developing composite soil conditioners using a combination of organic amendments and microbial consortium optimized for local soil needs. The conditioners will be evaluated for their efficiency in improving soil structure, nutrient availability, and microbial activity through controlled pot and field experiments. This work aims to establish a framework for site-specific soil restoration strategies in peri-urban ecosystems by linking soil physicochemical diagnostics with the rational design of soil conditioners. The study contributes to sustainable land management practices by promoting circular use of organic residues and enhancing soil resilience under urbanizing landscapes.

Keywords: Peri-urban soils, soil degradation, soil conditioners, physicochemical properties, biochar, sustainable land management

ICABB26-EA-OP-08

Detection of neutrophil elastase inhibitors from plants to combat ulcerative colitis

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Abstract

Ulcerative colitis (UC), an inflammatory bowel disease, distinguished by the chronic inflammation of the gastrointestinal tract. The disease leads to damage of intestinal mucosal structure and immune cell infiltration. Neutrophil are the most prevalent immune cells which are drawn from the blood to inflammatory tissue and aid in the elimination of microbes through phagocytosis by the release of neutrophil extracellular trap (NET). However, the overproduction of NET results in release of neutrophil elastase (NE), which damage the intestinal mucosa and cause UC. NE is endogenously regulated by inhibitors such as elafin, SLPI, serpin A1, serpin A3. During inflammation, an imbalance is established between NE and its endogenous inhibitors that worsen the conditions. UC is a serious disease with incidence rate of 31.5 million cases globally and 5.41 cases per 100,000 people have been documented in India. Available drugs used to treat UC are sivelestat, immunosuppressants and anti-TNF monoclonal antibodies. However, these drugs have certain side effects and limited efficacy. Thus, there is need of an alternative natural therapy with lesser or no side effects and more specific toward NE inhibition. In order to isolate natural NE inhibitor, plants were selected based on their medicinal properties and screened for the presence of NE inhibition activity. Crude protein extracts were prepared and total protein was estimated. Elastase inhibition activity was evaluated in these extracts. *Phaseolus coccineus, Cyamopsis tetragonoloba, Syzygium cumini, Triticum aestivum* and *Psidium gujava* showed more than 60 percent elastase inhibition at 10ug protein concentration. *Phaseolus coccineus* was selected for further isolation of NE inhibitor(s) based on *in-vitro* and *in-silico* studies.

This study showed that different plants exhibit different levels of NE inhibition. These inhibitors may be isolated, characterized and develop into an alternative safer therapy against UC. Further, inhibition kinetics of these inhibitor(s) may help in the development of drug against UC.,

Keywords: Ulcerative colitis, Inflammation, Neutrophil elastase, natural Neutrophil Elastase inhibitors

ICABB26-EA-OP-09

Exploring Multi-Approach Strategies for Efficient Lignin Degradation and Valorisation

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Abstract

Lignin is a complex biopolymer made up of phenolic compounds and provides rigidity and flexibility to plants. It is the major obstacle in the valorisation of biomass due to the complexity in its structure. It is important to degrade lignin, so that we can extract cellulose and hemicellulose which further utilize in the production of bioethanol The goal of this study is to access the relative effective and potential method for sustainable lignin breakdown by various method like acid- mediated (H_2SO_4), nanoparticles-assisted catalytic degradation and biological degradation using fungal isolate AS-3.

Guaiacol assay is a qualitative assay based on the oxidation of guaiacol, which results reddish- brown colouration in the presence of laccase enzyme. In the present study, a ligninolytic fungal isolate which we named AS-3 was screened and selected for its strong laccase activity using guaiacol assay. Crude enzyme was extracted from AS-3 and gives reddish brown colour on guaiacol assay which confirmed the presence of oxidative enzymes. During the crude enzyme preparation, the culture filtrate was separated into two parts, solid and liquid fraction. The liquid fraction contained dissolved lignin and was further analysed for guaiacol assay. The solid residue rich in cellulose and hemicellulose were used for sugar confirmation. To confirm the presence of reducing sugar, the DNS assay was performed. Upon heating the reaction mixture for 10 min colour change from yellow to reddish brown indicates successful detection of reducing sugar.

In addition to the biological methods, copper sulphate nanoparticles were employed as catalytic agents to promote lignin oxidation under light exposure, without the use of any harsh chemical. evaluate lignin depolymerization efficiency through hydrolysis and cleavage of ether linkages. The comparative assessment of these three techniques provides a comprehensive understanding of different degradation mechanisms and their effectiveness under controlled conditions.

Overall, this study highlights the potential of integrating biological, nanoparticle-assisted, and acid-mediated approaches for efficient lignin degradation. Each method offers unique advantages: the biological process provides eco-friendly enzymatic conversion; nanoparticle catalysis enhances reaction rates under mild conditions; and acid hydrolysis facilitates rapid polymer breakdown.

Keywords- Biopolymer, lignin, nanoparticles, eco-friendly

ICABB26-EA-OP-10

In-vitro and in-silico assessment of microplastic degradation by Pseudomonas putida

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Abstract

The present study integrates *In-Vitro* experimentation with *In-Silico* molecular docking to investigate the biodegradation capabilities of *Pseudomonas putida* (pww20) to explore effective methodologies for microplastic removal. Water samples were collected from the Hindon and Yamuna Rivers and quality indicators such as pH, EC, TSS, TDS, and BOD, which are markers of pollution and possible microplastic presence were examined. To further identify and characterize microplastics present in water samples, advanced analytical techniques such as Fourier Transform Infrared Spectroscopy

(FTIR), X-Ray Diffraction (XRD), and Differential Scanning Calorimetry (DSC) were carried out. These techniques validated the chemical composition, crystalline structure, and thermal behavior of microplastic particles detected in water samples. For the biodegradation assessment, *Pseudomonas putida* was cultured in vitro for 21 days in the presence of different microplastic concentrations. In parallel, in-silico docking analyses conducted using PyRx were used to evaluate potential enzyme–polymer interactions that support the microorganism's degradation capability. The combined approach demonstrates a reliable workflow for microplastic degradation to improved aquatic environmental safety.

Keywords: Microplastics; FTIR; XRD; DSC; *Pseudomonas putida; In-vitro* Degradation; Water Analysis; *In-silico* Docking

ICABB26-EA-OP-11

Toxicological Insights into Broflanilide: A Novel Metadiamide Pesticide with Potential Hepato-renal Risks In Mammals

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Abstract

Broflanilide, a meta-diamide insecticide launched in 2021 by Mitsui Chemical Agro Inc., represents a major breakthrough in pest management due to its potent action on insect γ-aminobutyric acid receptors (GABARs). Classified under Group 30 by the Insecticide Resistance Action Committee (IRAC) as a GABA-gated chloride channel allosteric modulator, it represents a major breakthrough in pest control strategies. It provides effective control of Lepidopteran, Coleopteran, and Thysanopteran pests. However, despite its agricultural significance, concerns remain about its impact on non-target organisms, particularly mammals. Recently, it has been demonstrated that Broflanilide exhibits potent chronic metabolic impacts on aquatic species such as Danio rerio, as reflected by moderate bioaccumulation of this pesticide and the induction of detoxification enzymes including CYP450 and GST. In spite of bioaccumulation of these hazardous pesticides in environment, very limited information is available regarding its toxicity in living system and environment.

This review consolidates current evidence on broflanilide's mechanism of action, biochemical alterations, cytogenetic endpoints, and anticipated hepato-renal effects, along with *in silico* insights into its interaction with mammalian GABA-A receptors. By integrating findings from environmental, biochemical, and computational studies, this review bridges critical gaps between pesticide chemistry, mammalian toxicology, and public health. The analysis highlights an urgent need for comprehensive in vivo mammalian studies and risk assessment frameworks to ensure safe regulatory use of broflanilide and to guide evidence-based policy development.

Keywords:

Broflanilide, GABA receptor, hepato-renal toxicity, cytogenetic endpoints, bioaccumulation and in silico toxicology

ICABB26-EA-OP-12

Histopathological analysis and Antioxidant response in freshwater fish upon exposure to clomazone

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Abstract

The histopathological alterations and antioxidant enzyme reactions in the gills and kidney tissues of freshwater fish Channa punctatus, exposed to clomazone during a 28-day period are examined in this work. Upon treatment to Clomazone increasing structural damage was observed, whereas controlled tissues showed normal morphological organization. After 28-days, clomazone treated gills showed curling of secondary lamelle, lamellar fusion, severe epithelial lifting, tissue disarray. Early reactions included hyperplasia, lamellar atrophy, necrosis, and oedema. In kidney constricted renal tubules, enlarged bowman's space, granuloma formation, glomerular dysfunction, necrosis, and eventually widespread necrosis and inflammatory infiltration were observed. Exposure for a prolonged period caused more severe damage suggesting cumulative toxic effects. Biochemical assay showed a time dependent increase in glutathione peroxidase (GPx) and glutathione-S-transferase (GST) activity in both tissues. The gills showed the highest GPx and GST activity, indicating a compensating antioxidant defense mechanism against oxidative stress brought on by the clomazone. Overall, the results show that sub-lethal exposure to clomazone causes significant oxidative stress and histopathological damage in freshwater fish tissues, highlighting their ecological risk to aquatic biota and their ability to disturb physiological homeostasis.

Keywords: Clomazone, Fish toxicity, Glutathione peroxidase, Glutathione-S-transferase, Histopathology

ICABB26-EA-OP-13

Valorization of Agricultural Wastes as Low-Cost Media for Polyhydroxyalkanoates (PHAs) Biosynthesis

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Abstract

The increasing global demand for biodegradable and sustainable packaging materials has intensified interest in polyhydroxyalkanoates (PHAs) as environmentally friendly alternative to petrochemical plastics. However, the high cost of commercial substrates used for PHA production remains a major limitation for large-scale commercialization. The study explores the valorization of agricultural wastes as economically stable nutrient sources for the biosynthesis of PHA. After extracting PHA from bacterial cells dried polymer was dissolved in chloroform to cast PHA film. Vegetable and fruit wastes derived media were hydrolysed and then assessed for microbial growth and PHA production. The highest biomass yield and PHA content were determined in both waste-based media to identify which yielded more efficiently. Afterwards, production was compared with synthetic media, demonstrating that inexpensive agro-wastes can effectively replace refined carbon sources. The prepared film of the extracted polymer was characterised by Fourier-transform infrared spectroscopy (FTIR), confirming the presence of functional groups characteristic of polyhydroxyalkanoates (PHA). Differential scanning calorimetry (DSC) further revealed a melting endotherm within the typical PHB range, indicating

thermoplastic behaviour and moderate crystallinity conducive for film fabrication. Films cast from the purified PHA displayed favourable mechanical integrity and biodegradability under natural conditions, highlighting their applicability in replacing short-life single-use plastics. Overall, the study demonstrates that agricultural residues can be successfully converted into low-cost fermentation media for PHA biosynthesis, significantly reducing production costs while contributing to sustainable waste management. Integrating waste valorisation with microbial biopolymer production leads to circular bioeconomy, and biodegradable PHA films can be prepared from readily available agro-industrial byproducts.

Keywords: Polyhydroxyalkanoates (PHAs), Agricultural wastes, FTIR, DSC, Circular bioeconomy

ICABB26-EA-OP-14

Comprehensive Study of Morphological, Physiological, and Heavy Metal Stress Responses in Forest-Associated Ectomycorrhizal Fungi: Potential for Soil Rehabilitation and Sustainable Land Management

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Abstract

This study evaluates the morphological, physiological, and heavy metal tolerance characteristics of ectomycorrhizal fungi (ECMF) isolates obtained from forest ecosystems. Field-collected ECMF samples, including species from genera such as *Laccaria*, *Tuber*, and *Entoloma*, associated with tree species including *Eucalyptus*, *Pinus*, and *Chir* (*Pinus roxburghii*), were systematically isolated to establish fresh pure cultures. These cultures were subsequently analyzed for microscopic and morphological features to document diagnostic traits. Physiological assays were conducted to assess fungal growth under varying environmental and nutritional conditions, while heavy metal tolerance tests were performed to determine the capacity of isolates to withstand elevated concentrations of metals. The results demonstrated considerable variation among ECMF isolates in growth patterns, hyphal morphology, and stress resilience. Notably, certain isolates of *Laccaria* and *Tuber* exhibited optimal growth under specific culture conditions and showed high tolerance to heavy metals, suggesting their potential for application in soil restoration and ecological rehabilitation. Overall, these findings highlight the utility of integrating laboratory-based morphological and physiological assessments to identify robust ECMF strains with ecological and biotechnological relevance, providing a foundation for their strategic use in forest management, degraded land recovery, and sustainable ecosystem interventions.

Keywords: Ectomycorrhizal fungi (ECMF), Heavy metal tolerance, Soil restoration, Stress resilience, Sustainable ecosystem management

ICABB26-EA-OP-15

Comparative Characterization of Multi-Species Spent Mushroom Substrates and Their Agronomic Potential as Organic Amendments for the Cultivation of Capsicum annuum

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Abstract

Production of mushrooms and mushroom residual material has increased dramatically in the last few decades which causes, the increment in the production of spent mushroom substrate (SMS), the lignocellulosic residual matrix that is left after harvesting mushrooms, has increased at the same rate. Each kilogram of mushrooms produced produces about 3-5kg of SMS which adds to millions of tonnes of biodegradable waste each year. SMS is usually made of semi-decomposing agricultural residues like wheat straw, sawdust, date palm remains, and manure, which makes it a potential useful organic resource, the agronomic potential of which should be systematically studied. The present investigation aims to characterize the physicochemical and biological attributes of SMS derived from seven commercially cultivated macrofungi Pleurotus ostreatus (oyster mushroom), Pleurotus djamor (pink oyster mushroom), Pleurotus eryngii (king oyster mushroom), Hypsizygus marmoreus (Shimeji), Lentinula edodes (shiitake), Hericium erinaceus (lion's mane), and Auricularia cornea (wood ear mushroom) and to examine their influence on the growth performance of Capsicum annuum. Soil SMS mixtures will be formulated at 5%, 10%, 15%, and 20% (v/v), along with a non-amended control. The physicochemical parameters of each SMS type will be quantified using a PUSA STFR Meter, while biological activity will be assessed through enzymatic evaluation. Chilli plants will be monitored for emergence, vegetative growth metrics, chlorophyll content, biomass accumulation, and root system architecture to determine treatment-driven variation.

Keywords: Spent mushroom substrate (SMS), Capsicum annuum, Organic, Sustainability, Physiochemical

ICABB26-EA-OP-16

Development of Plant Extract-Loaded Fungal Chitosan–Polyvinylpyrrolidone Composite Membranes

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Abstract

Fungal-derived chitosan offers a sustainable and eco-friendly alternative to traditional crustacean-based chitosan. It has consistent properties, does not cause allergies, and is sourced renewably. This study, in line with the United Nations Sustainable Development Goals (SDGs 2, 3, 7, and 12) and the "BioE3 Policy," focuses on developing and characterizing composite membranes made from plant extract-loaded fungal chitosan (FC) and polyvinylpyrrolidone (PVP). The goal of adding plant extracts was to improve the membranes' biological functions. PVP enhances their strength, water affinity, and ease of processing.

The study aimed at the fabrication of FC-PVP membranes via solvent casting method and development of plant extract loaded blend membranes. The developed composites were and tested for their physical and thermal properties. Fourier-transform infrared spectroscopy (FTIR) confirmed that intermolecular

hydrogen bonding formed among fungal chitosan, PVP, and bioactive plant components, evident from shifts in absorption peaks. X-ray diffraction (XRD) patterns showed reduction in crystallinity, with increasing concentration of PVP, suggesting the creation of disordered regions with improved diffusion and adsorption. Differential scanning calorimetry (DSC) revealed changes in endothermic transitions and better thermal stability, which suggests good compatibility between the polymers.
The combination of fungal chitosan, PVP, and plant extracts results in a biocompatible, sustainable membrane with greater structural strength, adsorption effectiveness. These findings suggest the potential of fungal chitosan–PVP composite membranes as a promising material for water purification, medical devices, and separation technologies, bridging biotechnology and environmentally friendly.
Keywords-Fungal Chitosan, Plant extract PVP, FTIR, XRD, DSC

ICABB26-EA-OP-17

Novel α-Amylase Resistant to Chaotropic Agents Drives Potato Waste Fermentation for Biofuel Production

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Abstract
The challenging industrial conditions require enzymes that remain active throughout the production of sustainable biofuels. Conventionally, biofuel synthesis from starch is a biphasic process where the enzymatic saccharification of starch is followed by microbial fermentation. However, most α-amylases degrade & lose their activity in the presence of chaotropic agents, such as solvents, surfactants, reducing agents, and chelators, which limits their utilization in an integrated single-step simultaneous saccharification and fermentation (SSF) process.The *Bacillus* strain IBT108 was isolated from the soil of the SAU premises and reported to have a novel α-amylase resistant to chaotropic agents. The robust stability of this novel α-amylase under harsh industrial conditions makes it a game-changer enzyme for the biofuel industry. The 68 kDa protein, with a high specific activity of 734.8 U/mg, was purified via DEAE ion exchange chromatography from a medium containing wheat bran as a cost-effective substrate. The functional characterization of IBT108 α-amylase revealed its strong thermostability, with optimal activity at 70°C and a pH range of 4 to 6.5. Under these conditions, the enzyme retained over 70% of its activity in 1 M organic solvents and 5 mM chaotropic agents, outperforming other commercial α-amylases. *Clostridium acetobutylicum* and *Clostridium butyricum*directly convert waste potatoes using IBT108 α-amylase, yielding a substantial amount of butanol (20.41–23.74 g/L) and hydrogen (3.20–4.38 L/L). This indicates the enzyme's potential to simplify biofuel production, minimise operational costs, and valoriseagro-waste into value-added products. This study positions IBT108 α-amylase as a promising candidate in biorefineries & biofuel industries for the efficient, cost-effective, and sustainable production of next generation biofuels.
Keywords: IBT108 α-amylase, Biofuel, SSF, Waste potato, Wheat bran.

ICABB26-EA-OP-18

Comparative Efficacy of Ricinus communis and Calotropis procera Extracts Combined with Trichoderma Enzymes for Fungal Disease Suppression

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Abstract

Phytobiological extracts of *Ricinus communis* and *Calotropis procera* were investigated in combination with intracellular and extracellular enzyme fractions of *Trichoderma harzianum* for their antifungal activity against the soil-borne plant pathogens *Macrophomina phaseolina* and *Fusarium oxysporum.* Three treatment concentrations (0.128 g/ml, 0.256 g/ml, 0.384 g/ml) were formulated by integrating plant extracts with enzyme fractions and evaluated through in vitro bioassays based on radial mycelial growth inhibition. All extract–enzyme combinations resulted in measurable suppression of fungal growth, showing a concentration-dependent response. At 0.384g/ml, enzyme-fortified *R. communis* formulations achieved approximately 90% inhibition of mycelial growth in both pathogens. In contrast, *C. procera* based treatments at the same concentration produced 65–80% inhibition, depending on the enzyme fraction used. Across all tested concentrations, *R. communis* consistently showed greater antifungal efficacy than *C. procera.* The enhanced inhibitory effect observed in enzyme-enriched treatments suggests a synergistic interaction between plant-derived bioactive compounds and fungal enzymatic activity. These findings demonstrate that higher extract concentrations significantly improve pathogen suppression and support the application of enzyme-fortified phytobiological formulations as an eco-friendly and effective strategy for the management of destructive fungal diseases in agriculture.

Keywords: Ricinus communis, Calotropis procera, Trichoderma harzianum, intracellular enzymes, extracellular enzymes, Macrophomina phaseolina, Fusarium oxysporum, antifungal activity, biocontrol, phytobiological extracts.

ICABB26-EA-OP-19

CRISPR/Cas9-Mediated Knockout of Mycotoxin Genes as a Sustainable Strategy to Suppress Fungal Pathogenicity

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Abstract

Fungi that produce mycotoxins are globally significant threats to agriculture, food, and human health by virtue of their ability to produce toxic secondary metabolites, including aflatoxins, ochratoxin A (OTA), and trichothecenes. The mycotoxins serve as the virulence factors responsible for crop destruction, post harvest wastage, and chronic diseases in public health. The conventional management tool—chemical fungicides, storage treatments, and decontamination strategies—are increasingly limited by concerns for the environment and resistance to chemical management of the fungi. This led to increased enthusiasm for precision molecular approaches, including CRISPR/Cas genome editing techniques, to study and tame fungal species pathogenicity.

In this study, we employed CRISPR/Cas9 genome editing to knockout both structural and regulatory factors that contribute to mycotoxin biosynthesis, aflR in Aspergillus flavus and TRI5 in Fusarium species. We designed guide RNAs to target conserved regions of the genes and used Cas9–

ribonucleoprotein (RNP) complexes delivered by protoplast transformation to generate DNA-free, non-transgenic genome edits. Gene edits were validated by PCR, Sanger sequencing, and loss-of-function phenotypic characteristics.

The edited strains demonstrated reduced levels of toxin production (60–95% reductions), reduced sporulation, a diminished ability to infect host tissues, and downregulated expression of enzymes and biosynthetic pathways involved in downstream events. Importantly, the mutants grow at rates similar to unedited strains, showing that the attenuation of pathogenicity was a direct result of the gene disruption. Conclude that CRISPR/Cas9-mediated gene knockout offers an effective and sustainable strategy to suppress mycotoxin production and fungal pathogenicity.

Keywords: Mycotoxin biosynthesis, Aflatoxin (aflR), TRI5 gene, Aspergillus flavus, Fusarium spp.,

ICABB26-EA-OP-20

COMPARATIVE ASSESSMENT OF PHYTOCHEMICAL PROFILES IN TISSUE CULTURE-RAISED AND FIELD-GROWN BACOPA MONNIERI

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Abstract

The increasing demand for medicinal plants has led to the depletion of natural resources, resulting in reduced availability of several therapeutically important species. *Bacopa monnieri*, a plant of high medicinal value, faces similar challenges due to its growing pharmaceutical demand, which is difficult to meet through conventional cultivation alone. In the present study, tissue culture-raised *Bacopa monnieri* plants were successfully hardened and subsequently subjected to qualitative and quantitative phytochemical analyses to compare their metabolite profiles with those of field grown plants. The results demonstrated that tissue culture-raised plants accumulated significantly higher levels of secondary metabolites, including phenolics, alkaloids, and flavonoids, when evaluated on equivalent biomass basis, enabling greater metabolite extraction from a smaller amount of plant material. A commercial formulation (H1) was included as a reference; although it exhibited strong response in qualitative assays, quantitative analysis revealed lower phenolics and alkaloid contents compared to tissue culture-raised plants. These findings highlight tissue culture as a sustainable and efficient strategy for enhancing metabolite yield and supporting pharmaceutical applications of *Bacopa monnieri*.

Keywords:

Bacopa monnieri; tissue culture-raised; field- grown; phytochemical analysis

ICABB26-EA-OP-21

A remarkable enhancement in hydrogen production from Clostridium beijerinckii G117 by the co- fermentation of crude glycerol and rice bran hydrolysates

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Abstract

The sustainable production of biohydrogen from industrial waste streams presents a promising strategy for advancing clean energy technologies. This study investigates the enhancement of hydrogen production by Clostridium beijerinckii G117 through the cofermentation of crude glycerol, an abundant byproduct of the biodiesel industry, with agro-residual hydrolysates. Although glycerol is a highly

reduced substrate favorable for hydrogen generation, its high concentration and associated impurities significantly inhibit microbial assimilation and limit hydrogen yield. Initially, strain G117 produced ~4400 mL/L hydrogen from 15 g/L CG, but increasing CG concentrations (20–80 g/L) resulted in 34–90% substrate rejection and no proportional increase in hydrogen production. To overcome these limitations, various agro-residual hydrolysates (corn cob, rice bran, sugarcane bagasse, and wheat bran) and metal ions were evaluated as co-substrates and micronutrient supplements. Among them, rice bran hydrolysate (RBH) and ferrous ions (Fe2+) significantly improved glycerol utilization, cellular growth, and hydrogen production. Response Surface Methodology (RSM) coupled with a Central Composite Design (CCD) was employed to optimize medium composition. The optimized medium containing 37.63 g/L CG, 3.65 g/L RBH, and 1.11 mM Fe2+ achieved a favorable redox potential (191.0 ± 1.5 mV), enhanced biomass formation (6.73 ± 0.12 OD600), and a markedly improved hydrogen yield of 17,350 ± 170 mL/L. This optimized process delivered a hydrogen yield of 2.27 ± 0.02 mol H2/mol glycerol utilized, representing the highest yield reported to date for crude glycerol-based Clostridial fermentation. Mass and electron balance analyses confirmed a high process efficiency (82–99%), demonstrating effective carbon and electron recovery. Overall, this study establishes a robust and economically viable co fermentation strategy for maximizing hydrogen production from low-cost industrial and agro-residual substrates, offering significant potential for scalable biohydrogen production systems.
Key words: Biohydrogen, Agroresidues, Clostridium fermentation, waste to energy.

ICABB26-EA-OP-22

Evaluation of Phytocompound and Antibiotic Combinations Against *Pseudomonas fluorescens, Staphylococcus epidermidis, and Acinetobacter baylyi*

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Abstract

Biofilm-associated antimicrobial resistance has significantly reduced the effectiveness of many antibiotics, increasing the need for alternative strategies to improve existing antimicrobial therapies. Plant-derived phytocompounds with antimicrobial properties have emerged as promising antibiotic adjuvants because of their structural diversity and biological activity. The present study aims to evaluate the antibacterial and antibiofilm potential of phytocompounds in combination with antibiotics against *Pseudomonas fluorescens, Staphylococcus epidermidis, and Acinetobacter baylyi*. Antimicrobial and antibiofilm activities were determined by minimum inhibitory concentrations (MICs) and minimum biofilm inhibitory concentrations (MBICs), respectively, for individual agents and their combinations. Antibiotic and phytocompound interactions were evaluated by checkerboard assays with FIC index interpretation. Combination studies showed variable inhibitory responses, with some phytochemical–antibiotic combinations exhibiting greater activity than individual agents. Checkerboard analysis identified both additive and synergistic interaction patterns, depending on the organism and combination tested. Growth kinetic analysis further demonstrated alterations in bacterial growth dynamics in response to selected combinations. Additionally, a preliminary assessment of the mammalian cell line indicated acceptable cellular tolerance within the tested concentration range. This study provides experimental insight into phytochemical–antibiotic interaction patterns and highlights their relevance as a combination-based approach against antimicrobial resistance.
Keywords: Antimicrobial resistance, Phytocompounds, Antibiotic combinations, Biofilm inhibition, Synergistic interactions, Bacterial growth dynamics.

ICABB26-EA-OP-23

Integrating Bioremediation and Soil Health Indicators for Sustainable Land Reclamation

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Abstract

Crude oil contamination brings a serious environmental concern by detoriating soil microbial ecosystems and fertility. There are various conventional methods available, but they only remove pollutants and fail to restore biological properties of soil. This study focuses on a bioremediation method to reclamation of crude oil contaminated soil. Contaminated soils were collected from oil refinery site at Indian Oil Corporation Limited, Panipat and their physicochemical properties, microbial diversity and nutrient content were analysed. By using Bushnell Haas medium indigenous hydrocarbon degrading bacteria were isolated with one percent by volume crude oil as carbon source. The isolates were combined to form consortia and monitored in soil experiments under different parameters control, combined treatment bioaugmentation and bio stimulation. Total petroleum hydrocarbon degradation was analysed using GC-FID and Soxhlet extraction method.Additionally different parameters of soil health such as nutrient content, pH, seed germination and enzymatic activity were monitored continuously. Reduction in TPH percentage were analysed and this study explains that opting for microbial bioremediation together with soil proves to be a sustainable and comprehensive way to restore the contaminated soil and use it for agriculture purposes. This research solves the problem of pollutants, restore soil biological properties, align with the United Nation Sustainable Development Goals (SDGs) 2,12,13,15 and come under National Biofuel and Swachh Bharat Missions of India.

Keywords: Reclamation, Soil health, Bioremediation, Microbial Consortium,SDGs.

ICABB26-EA-OP-24

Antibiotic Resistance In Aquaculture: A Microbiological Assessment Of Fish Farms In Peri-Urban Region Of NCR

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Abstract

Among the food-producing sectors worldwide, aquaculture is remarkably one of the most promising. Over the past 20 years, both aquaculture production and fish consumption per person have increased significantly. The high demand for fish gives rise to intensive fish farming, leading to stocking a large number of fish in lesser spaces of water, which leads to an increase in infectious diseases. The shifting of culture method from semi-intensive to intensive technique and the application of antibiotics to control the disease outbreak are the major trends nowadays which eventually give rise to antibiotic resistivity. In current study, the microbiological environment and antibiotic resistivity of bacteria was assessed in four fish farms in the peri-urban region of Nation Capital Region (NCR). Strains were isolated and characterized by Biochemical test analysis and antibiotic resistance profile study using disc diffusion method. Predominance of antibiotic resistance was observed. Gram-negative bacteria were highly resistant to ampicillin (80%), co-trimoxazole (70%) and Cefotoaxime (50%) and intermediately resistant to ciprofloxacin (60%). Gram-positive bacteria exhibited high resistant to linezolid (76%) and cloxacillin (76%) and 50% showed intermediate resistance to lincomycin, ampicillin and co-trimoxazole. Identification of high resistance strains was further done by 16S rRNA sequencing which identified important fish pathogens such as *Aeromonas veronii*, *Enterobacter*, and *Salmonella*. The current study reveals presence of Pathogenic bacteria with high antibiotic resistance in water samples.

The findings emphasize the necessity of ensuring water source hygiene and enforcing rigorous antimicrobial stewardship protocols within aquaculture practices.

Keywords: Antibiotic resistance, Aquaculture, Aquaculture Water Quality, Fish health, Fish pathogens.

ICABB26-EA-OP-25

Hexavalent Chromium Reduction in Cement Industry Wastewater: Microbial Mechanisms and Bioremediation Perspectives

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Abstract

Hexavalent chromium [Cr (VI)] is a highly toxic and mobile carcinogenic heavy metal, often discharged through a number of industrial processes, one of which is the cement manufacturing sector. The naturally existing trivalent chromium [Cr (III)] in raw materials is oxidized to Cr (VI) during the high-temperature clinker production process. Because of this, cement dust, slurry, and related industrial effluents frequently turn into important sources of chromium pollution. Cr (VI) poses significant risks to aquatic ecosystems and human health due to its high solubility, mobility, and persistence, necessiting the use of efficient and long- lasting remediation techniques. Despite the widespread use of conventional chemical and physical treatment techniques, their practical application is sometimes constrained by high prices, the production of secondary contaminants, and insufficient detoxification.

As an eco-friendly substitute, microbial reduction of Cr (VI) to the less hazardous and poorly mobile Cr (III) has drawn more and more interest. The potential of chromium- reducing bacteria in bioremediation applications is the main topic of this study, which summarizes the literature on chromium pollution resulting from cement industry effluents. The sources of chromium-resistant bacteria that have been identified, their tolerance mechanism, and the metabolic pathways that lead to Cr (VI) reduction are highlighted. Popular analytical techniques for assessing chromium reduction are also included, particularly colorimetric methods based on 1, 5-diphenylcarbazide.

Cement effluents contain native bacterial populations that can withstand high chromium concentrations and efficiently convert Cr (VI) under the right circumstances, according to earlier studies. Significant operational and environmental factors, such as pH, temperature, chromium content, electron donor availability, and oxygen levels, that impact the efficacy of microbial reduction are carefully examined. The development of bioreactor based treatment techniques, comprehension of genetic determinants of chromium resistance, and current advancements in molecular characterisation are also discussed. Overall, the work highlights the need for more research to scale up these biological techniques for the treatment of industrial wastewater and highlights the promise of microbial Cr (VI) reduction as a long-term chromium detoxification method.

Keywords: Cement industry wastewater; Chromium- reducing bacteria; Microbial biotransformation; Bioremediation; Heavy metal detoxification.

ICABB26-EA-OP-26

PET-Degrading Bacteria and the Role of the M5 Motif in PETase-Mediated Degradation

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Abstract

Plastic has been widely used in everyday life and has become a serious environmental problem. Polyethylene terephthalate (PET) is a common type of plastic that can be utilized to make bottles, packaging materials, and textile fibers. Due to their durability, versatility, and low cost, these materials are widely used in every sectors. PET waste accumulation in the environment is becoming a major ecological problem. Conventional methods like landfilling, open burning, and recycling of plastic waste

in the environment produced secondary products that affect the environment and cause problems for living beings. In recent years, PET degradation by bacteria has increased attention as an environmental friendly method for PET waste management. During PET degradation, bacteria use PET as a source of carbon for metabolic processes. Bacteria produce the PETase enzyme, which is known to degrade PET into small monomers. There have been various reports of investigations on PETase i.e engineering, isolation, identification, and characterisation. Several bacteria, including *Ideonella sakaiensis*, *Pseudomonas*, *Bacillus*, *Thermobifida*, and *Rhodococcus,* have been reported to degrade PET. PETase enzymes contain the M5 motif, which has been reported to play an important role in catalytic activity and substrate binding. M5 motif involves tight functional and structural limitations, including the presence of the entire catalytic triad and certain amino acid residues required for substrate binding and enzyme stability. M5 motif was identified as a promising target for improving PETase activity. PET degrading bacteria highlight their importance as a sustainable approach for plastic waste management. These findings support the development of environmentally friendly approaches for PET pollution through microbial and enzymatic processes.

Keywords: Polyethylene terephthalate, PETase, Bacteria, Biodegradation, M5 motif.

ICABB26-EA-OP-27

Nucleoredoxins in Tomato: Molecular Evolution, Structural Features, and Role in Abiotic Stress Tolerance

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Abstract

Nucleoredoxins are a specialized family of thioredoxin-like proteins involved in redox regulation and cellular signaling in plants; however, their molecular evolution and functional relevance in crop species such as tomato remain largely unexplored. In this study, a comprehensive genome-wide analysis of the nucleoredoxin gene family was performed in tomato (*Solanum lycopersicum*) to elucidate their evolutionary relationships, structural features, and potential roles in abiotic stress tolerance. A total of 32 nucleoredoxin genes were identified and systematically characterized based on phylogenetic relationships, gene structure, conserved domain architecture, and chromosomal localization. Phylogenetic analysis classified these genes into distinct clades, indicating both evolutionary conservation and lineage-specific diversification. Analysis of gene duplication events revealed that segmental and tandem duplications have contributed to the expansion of the nucleoredoxin family in tomato. Structural characterization showed the presence of conserved thioredoxin domains along with clade-specific motifs, suggesting functional diversification among family members. Promoter analysis revealed the enrichment of cis-regulatory elements associated with stress responses, hormone signaling, and developmental regulation. Expression profiling using publicly available transcriptomic datasets demonstrated differential and tissue-specific expression patterns of nucleoredoxin genes under abiotic stresses such as salinity, drought, and heat. Several nucleoredoxin members displayed pronounced stress-inducible expression, highlighting their potential involvement in redox-mediated stress adaptation. Overall, this study provides the first comprehensive genome-wide insight into the nucleoredoxin gene family in tomato, revealing their molecular evolution, structural diversity, and potential roles in abiotic stress tolerance. The findings establish a valuable genomic resource and provide a foundation for future functional studies aimed at elucidating nucleoredoxin-mediated redox regulation and improving stress resilience in tomato.

Keywords: Nucleoredoxins; thioredoxins; genome-wide analysis; abiotic stress; tomato.

ICABB26-EA-OP-28

Enhancing paint durability using *Sporosarcina pasteurii*: A critical analysis of urease mediated calcium carbonate precipitation for autonomous crack healing

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Abstract

The development of micro-cracks and the loss of durability in architectural paints can be sustainably tackled through autonomous self-healing coatings. Urease-mediated Microbially Induced Calcium Carbonate Precipitation (MICP), a novel bio-engineering method, has recently gained popularity, mainly due to its ability to exhibit calcite precipitation upon moisture ingress, thereby effectively closing cracks without requiring any external assistance. This work aims to carry out a scientific appraisal of urease-mediated MICP to be applied to self-healing paints, with a particular focus on Sporosarcina pasteurii, being a model bacterium. In order to understand the precipitation of calcium carbonate, viability of microbes in paint mediums and effect of physiochemical parameters such as pH, temperature, nutrient supply, and composition of paints, existing experimental studies are methodically analysed. Limitations in present techniques are identified by analysing significant technological challenges, especially bacterial survivability under extreme coating environments, regulated mineral deposition and stability over the long run. The current research shall also discuss on scale ability of encapsulated forms on healing effect efficiency. This paper presents a novel research-based view on the applied potential of MICP-based self-healing biological paints and describes some future directions for bacterial effectiveness in enhancing the performance of coatings by summarizing recent findings and indicating important research gaps. The following insights are necessary to support the development of robust, sustainable, and innovative coatings.

Keywords Microbially Induced Calcium Carbonate Precipitation (MICP), *Sporosarcina pasteurii*, Self healing paints, Urease activity, Bio-mineralization, Sustainable coatings.

ICABB26-EA-OP-29

"Ecological Impact and Water Quality Assessment at the Sangam During Maha Kumbh 2025: A Multi-Parameter Biomonitoring Study"

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Abstract

Sangam at Prayagraj, a cofluence zone of river Ganga and Yamuna is ecologically sensitive zone. During large religious mass gatherings as Maha Kumbh, millions of pilgrims participate in ritual bathing introducing substantial organic loads, nutrients and microbial contaminants that suddenly alter water quality. This study was targeted to understand the effect of these abrupt pertubations on the Water Quality of river system.

Water samples were collected continuously over seven days, covering two days prior to mass bathing, the mass bathing days, and the post-bathing period. The assessment included key physicochemical parameters such as dissolved oxygen (DO), pH, oxidation–reduction potential (ORP), electrical conductivity (EC), total dissolved solids (TDS), salinity, nitrate, nitrite, ammonia, and alkalinity, along with diatom assemblages as biological indicators of pollution. During the pre-bathing period, most parameters reflected relatively cleaner and less polluted conditions. However, on and after the mass bathing days, several parameters exceeded the permissible limits prescribed by BIS and CPCB, indicating a deterioration in water quality.

Nitrite, Nitrate and ammonia concentrations increased markedly on mass bathing days, indicated nutrient enrichment and organic pollution associated with ritualistic activities. Increased conductivity,

TDS, and alkalinity reflected higher ionic and dissolved pollutant loads from anthropogenic inputs. Variations in ORP and decline in DO suggested enhanced microbial load and increased biological oxygen demand (BOD). These combined changes were reflected in the WQI, which showed a clear shift from Excellent/Good (WQI < 50) during pre-bathing days to Poor (50–100) and Unsuitable (>100) categories on mass bathing days of the Maha Kumbh 2025.

Pollution-sensitive genera of diatoms such as Achnanthes, Achnanthidium, Anomoeonis, and Cyclotella were predominantly recorded during the pre-bathing period, reflecting cleaner water conditions. In contrast, mass bathing days were characterized by the dominance of pollution tolerant genera such as Gomphonema, Navicula, and Nitzschia, indicating elevated organic pollution. The observed shift from sensitive to tolerant diatom taxa corroborated the ecological stress induced by intense anthropogenic pressure during mass bathing events.

Overall, the study establishes that mass bathing during the Maha Kumbh 2025 caused pronounced, short-term deterioration of water quality causing ecologically stressed conditions at the Sangam. The integrated analysis of physicochemical parameters, WQI, and diatom community structure emphasizes the high sensitivity of the confluence river ecosystem and necessity of protection from anthropogenic disturbances. These findings emphasize the need of improved river management strategies, pollution control measures, and sustainable planning of future mass gathering events to safeguard ecological integrity and public health at culturally significant river systems.

Keywords: diatoms, Ganga Kumbh, public health river management, Water Quality.

ICABB26-EA-OP-30

Phylogeny, genetic diversity estimates in Chhattisgarhi, Chilika and Kalahandi buffaloes of Northeast India through the High-density SNP Genotyping

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Abstract

The genetic diversity, population organization, and mating patterns of the Indian buffalo breeds are under-researched although some populations (such as underrepresented in Northeast India) have not been explicitly studied. In this study, we have used the Axiom Buffalo high density SNP genotyping array to examine genetic diversity, estimate the genetic distance, and linkage disequilibrium (LD) and phylogenetic associations among three North East Indian buffalo populations, i.e. Chhattisgarhi, Chilika and Kalahandi. We have used SNP genotyped data of these three buffaloes, and carried out our analysis, including principal component analysis (PCA), phylogenetic tree construction, and LD decay analyses. Findings indicated a strong genetic association and common ancestry of all the three populations as indicated by clustered phylogenetic trees and low genetic distances. Chhattisgarhi buffaloes (the type of buffaloes of the wild type) exhibited a tendency to relate to Chilika and Kalahandi populations of Odisha (eastern India), which indicated historical gene flow as well as similarity. Genome-wide LD also decayed rapidly in small distances, indicating large effective populations. To conserve the biodiversity, these discoveries have an implication for conservation and breeding initiatives concerning the Northeast Indian buffaloes, as they show that these animals are genetically related.

Keywords: Buffalo, SNP array, genetic diversity, phylogenetic analysis, linkage disequilibrium, Northeast India

ICABB26-EA-OP-31

Rancidity-Associated Lipoxygenase (LOX) Gene Family in Finger Millet (*Eleusine coracana*): A Genome-Wide Characterization

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Abstract

Finger millet (*Eleusine coracana*) is a climate-resilient cereal prized for its nutrition—especially calcium, fibre, and micronutrients. Yet once the grain is milled, the flour is much more prone to rancidity: during storage it quickly develops off-odour and off-taste as lipids oxidize. A key driver is lipoxygenase (LOX). In the plant, LOX helps survival under stress by directing lipid-based signaling, but in stored flour the same enzyme chemistry forms lipid hydroperoxides that speed quality loss. To pinpoint LOX genes most relevant to this problem, we carried out a dry-lab, genome-wide analysis using public finger-millet genome/protein databases. LOX candidates were mined, confirmed by conserved LOX domains and catalytic residues, and then characterized for chromosomal distribution, exon–intron structure, conserved motifs, and basic protein properties (length, molecular weight, pI). We added functional context through phylogenetic comparison with grass LOXs, promoter cis-element scanning for seed/hormone/stress regulation, subcellular localization prediction, and synteny analysis to test conservation across grasses. We resolved eight LOX genes (EcLOX1–EcLOX8). They are unevenly distributed across chromosomes and show structural diversification, while retaining the LOX core. Motif combinations differ between members, suggesting specialization. Phylogeny groups EcLOXs into the major cereal 9-LOX and 13-LOX clades and links several genes to orthologs implicated in seed lipid metabolism and stress responses. Promoters are enriched for seed- and stress-responsive elements, localization predictions indicate cytosolic and plastid-associated members, and synteny supports conservation of some loci alongside finger-millet-specific divergence. Overall, this curated LOX catalogue provides high-priority candidates for functional validation and a starting point to improve millet-flour shelf life.

Keywords: finger millet; lipoxygenase; genome-wide; rancidity; shelf life

Session 3:
Multi-Omics Approaches and AI in Biotechnology
Poster Presentations

ICABB26-MOC-P01

From Genome to Cognition: Interfacing Psychological and Neurocognitive Dimensions of Schizophrenia within Genetic and Epigenetic Frameworks

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Abstract

Schizophrenia is a complex neuropsychiatric disorder caused by a multifaceted interaction of genetic vulnerability, epigenetic modifications, and cognitive dysfunction. Affected individuals often struggle with hallucinations, delusions, disorganised thinking, and cognitive impairments that disrupt academic, social, and occupational functioning. Although it has been studied for decades, its underlying causes remain intricate and multifaceted. Recent research indicates that it cannot be fully understood through biological mechanisms alone; instead, it reflects a dynamic interface between neural networks, cognitive processes, and environmental factors. Genome-wide association studies have identified numerous polygenic risk loci, primarily affecting synaptic plasticity pathways, yet translating these findings into psychological or clinical markers remains limited. Despite significant biological insights, gaps in research persist in linking these mechanisms with neuropsychological outcomes. Cognitive impairments appear early and are key predictors of functional disability. However, they are not sufficiently integrated into diagnostic models and treatment plans. Additionally, negative symptoms, metacognitive dysfunction, and cognitive biases pose challenges in measurement and treatment, underscoring a disconnect between neurobiological models and lived experience. Current treatments mainly focus on dopamine-targeting pharmacotherapy, with limited success in addressing cognitive deficits and negative symptoms. Psychotherapeutic approaches show promise but lack precise frameworks based on genetic or epigenetic profiles. Therefore, future directions should involve a shift towards integrated models that connect molecular pathways with cognitive phenotypes, enabling early detection and personalised intervention. Linking genetic and epigenetic findings with psychological factors and neurocognitive rehabilitation may ultimately enhance predictions of disease progression and therapeutic outcomes. Such interdisciplinary frameworks are vital for transforming schizophrenia care.

Keywords: Neuropsychology; Cognitive Deficits; Neural Circuits; Polygenic Risk; Synaptic Plasticity; Personalized Medicine

ICABB26-MOC-P02

Integrative Transcriptomic Analysis Identifies Prognostic and Functional Drivers of MDS-to-AML Transformation

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Abstract

The progression of MDS to AML is primarily characterized through mutational profiling. However, genomic alterations alone do not fully reflect the complex molecular reprogramming driving leukemia transformation. This study aims to identify functional molecular events driving the transition from normal hematopoiesis to MDS and subsequently to AML through comprehensive gene expression profiling. Gene expression datasets (GSE58831, GSE111085, GSE13159, and GSE15061) were retrieved from the NCBI Gene Expression Omnibus (GEO) to identify commonly dysregulated genes associated with progression from normal hematopoiesis to MDS and AML. A defined threshold was applied to determine consistent differential expression across datasets. Functional characterization of genes was performed using DAVID, Enrichr and Metascape for pathway and gene ontology enrichment

analysis. Prognostic significance of candidate genes was assessed using GEPIA2 and UALCAN platforms. Visualization of expression patterns was executed through heatmaps and expression trend plots to delineate overlapping regulatory shifts. Total of 143 genes were upregulated and 374 downregulated in normal vs MDS, whereas 1502 genes were upregulated 1613 downregulated in MDS vs AML. Comparative analysis revealed 21 consistently upregulated and 59 genes consistently downregulated across all datasets. Average LogFC value of genes were used to construct heatmaps which demonstrated that several genes were activated or suppressed in MDS but in exhibited attenuated activity in AML, indicating transcriptional shift during leukemic transformation. The concordance of these genes with prognostic analysis further supports their potential relevance in disease progression and clinical outcomes.The genes identified in this study highlight the molecular continuum linking MDS and AML, reflecting shared pathogenic pathways underlying leukemic transformation. These findings suggest that identified genes may serve as key modulators of disease progression and hold potential as prognostic indicators or therapeutic targets. Further experimental validation warranted to confirm their clinical relevance. This study integrates multiple GEO datasets to describe gene expression patterns driving the transition from MDS-to-AML. It provides novel framework for understanding leukemia progression by tracing sequential molecular alterations. Unlike conventional studies limited to stage wise comparisons, this analysis emphasizes the continuous regulatory reprogramming that drives leukemia transformation and identifies candidate genes with prognostic and therapeutic relevance.

Keywords: Myelodysplastic syndrome, Acute myeloid leukemia, Expression profiling, GEO datasets, Disease progression

ICABB26-MOC-P03

DHA Production from Schizochytrium sp.

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Abstract

Long-chain polyunsaturated fatty acids (LC-PUFAs), comprises of essential omega-3 fatty acids such as docosahexaenoic acid (DHA), with numerous health benefits and prevents health disorders. Since, marine fish source and plant-based source such as flaxseeds used for omega-3 oil production declined, so microalgal sources such as Schizochytrium species have developed as a sustainable alternatives source for DHA production. This study aims to optimize fermentation parameters and nutrient sources in Schizochytrium species to increase the DHA yield. Fermentation optimization was performed by evaluating the effects of different carbon (glucose, glycerol), nitrogen (yeast extract, peptone), and environmental conditions such as dissolved oxygen, pH and temp, aeration, additionally, the use of agricultural and industrial wastes as nutrient substrates, as well as various techniques UV irradiation, ARTP (Atmospheric and Room Temperature Plasma), NTG (N-methyl-N′-nitro-N-nitrosoguanidine), CRISPR Based Editing, Downstream processing for increasing DHA production . Fermentation modes, including batch, fed-batch, and continuous systems, were compared for DHA productivity. Glucose and glycerol served as optimal carbon sources, significantly increasing the DHA accumulation. Peptone and yeast extract were found to be effective nitrogen sources, which further enhances the DHA productivity. Phosphate and salinity modulation also improved yield, while waste materials such as glycerol reduced two-third of the costs. Among fermentation modes, fed-batch fermentation achieved the highest DHA yield, outperforming batch, and continuous systems. Optimization of nutrient composition, waste utilization, and fermentation strategies can significantly enhance the DHA productivity in Schizochytrium, offering a cost-effective and sustainable alternative to fish-based sources and plant-based sources.

KEYWORDS: DHA production; Schizochytrium; fermentation optimization; omega-3 fatty acids

ICABB26-MOC-P04

The Role, Challenges, and Applications of Artificial Intelligence in Tackling ESKAPE Pathogens

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Abstract

The emergence of multidrug-resistant (MDR) ESKAPE pathogens, including Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and Enterobacter spp., poses a critical threat to global health, particularly in hospital-acquired infections. These pathogens can evade multiple antibiotics, leading to increased morbidity, mortality, and healthcare costs. Traditional approaches to drug discovery, diagnostics, and infection control are often slow and insufficient to keep pace with the evolving resistance. Artificial intelligence (AI) offers a promising solution by leveraging computational models to enhance the detection, prediction, and treatment strategies. AI applications in combating ESKAPE pathogens include rapid diagnostics through image recognition and genomic analysis, predictive modeling of antibiotic resistance patterns, drug discovery of novel antimicrobial compounds, and infection surveillance to prevent hospital outbreaks. Machine learning algorithms and deep learning models can be used to analyze large datasets, identify resistance mechanisms, and suggest personalized treatment options, potentially reducing the misuse of antibiotics and slowing the development of resistance. Despite its potential, AI is facing significant challenges in the field. The limited availability of high-quality, standardized datasets, the complexity of resistance mechanisms, and the "black box" nature of many AI models hinder interpretability and clinical adoption. Integration into hospital workflows, data privacy concerns, and ethical considerations further complicates practical implementation. This poster highlights the role, challenges, and applications of AI in addressing ESKAPE. This emphasizes that while AI is not a standalone solution, it can complement traditional methods to accelerate diagnostics, guide effective treatment, and inform infection control strategies. Advancements in data collection, algorithm transparency, and interdisciplinary collaboration are essential for fully harnessing AI's potential of AI against multidrug-resistant bacterial threats. By showing the intersection of AI and microbiology, this study provides insights into innovative approaches for managing and mitigating the impact of ESKAPE pathogens in clinical settings.

Keywords: ESKAPE pathogens, Multidrug-resistant bacteria, Antibiotic resistance, Artificial Intelligence

ICABB26-MOC-P05

Network-Informed Plasmidome Analytics Uncover High-Mobility Resistance Vectors Driving Carbapenem Resistance in Indian Enterobacterales

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Abstract

Carbapenem-resistant Enterobacterales (CRE) are an escalating threat in South Asia, primarily due to plasmid mediated horizontal transfer accelerating the dissemination of β-lactamase genes (blaNDM,

blaOXA-48). Data driven bioinformatics workflow integrating assembly, plasmid reconstruction, annotation, and network-based machine learning was developed to define specific plasmid structures accelerating CRE spread in India. Objective of the study was to Identify key plasmid structures driving CRE spread in India. A total of 214 Enterobacterales genomes were analyzed, comprising sequences from NCBI SRA BioProjects PRJNA692613 and PRJNA8878182, alongwith 27 hospital isolates (Delhi-Mumbai-Hyderabad; 2019–2024). Reads were filtered (FastQCv0.12.1, Trimmomaticv0.40) and assembled via nf-core/bacassv2.2.1 using SPAdesv3.15.5 (k=21,33,55,77). Circular contigs were identified MOB-suite v3.1.0 (mob_recon – min_contig_length 1000-threshold 95), annotated Prokkav1.14.6, and validated via GTDB-Tkv2.3.2. AMR genes were screened using ABRicate v1.0.1 against CARDv3.2.9, ResFinderv4.3 and NCBI AMRFinderPlusv3.10 (>90%identity,>70% coverage). Plasmid–host networks were modeled using NetworkXv3.3, and an XGBoostv2.0.3 classifier (34 features) predicted resistance with 5-fold cross-validation and SHAP interpretability. Assemblies averaged 5.4 Mb (N50: 68,250 bp), with 98.1%≥1 plasmid (mean 3.8 ± 1.6). MOB-suite defined 132 plasmid clusters, dominated by IncFII (27%), IncX3 (18%), ColKP3 (12%), and IncA/C2 (9%). Clusters P_0 (IncFII) and P_1 (IncX3) spanned E. coli, K. pneumoniae, and Enterobacter cloacae. P_0 carried blaNDM-5, tetA, and sul1, flanked by IS26 elements, and exhibited highest betweenness (0.381) and eigenvector (0.76) centralities in the network (734 edges, modularity 0.43). The XGBoost model achieved AUROC = 0.93 ± 0.02, average precision = 0.89, and F1 = 0.87, with plasmid-associated features contributing >70% of model importance. Correlation between plasmid betweenness and resistance probability was $r = 0.72$ ($p < 0.001$); regression explained $R^2 = 0.68$ of phenotypic variance. Temporal stratification revealed post-2022 expansion of P_0/P_1 clusters coinciding with a 1.9× increase in carbapenem resistance. This machine-learning and genomic analysis found two "super-spreader" plasmid clusters responsible for widespread AMR transmission. The pipeline offers a scalable, reproducible model for plasmid-centered AMR surveillance and predictive risk asseessment in clinical microbiology. Developed an integrative genomic–network–machine learning framework to move beyond simple resistance tracking. It identified two high-mobility plasmid clusters of CRE.

Keywords: Carbapenem, Enterobacterales, ResFinder, XGBoost, AMR

ICABB26-MOC-P06

Hybrid Dairy–Plant Protein Foods: Integrating Computational Design, Omics, and Advanced Processing

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Abstract

Hybrid dairy–plant protein systems present a practical way to merge all the advantages of dairy nutrition and technology with the eco-friendly traits of plant proteins. This article consolidates the latest developments in formulation, processing, and computational design that facilitate the production of high-quality hybrid foods. At the molecular scale, molecular docking and molecular dynamics reveal the ligand–protein and protein–protein interactions responsible for gelation, emulsification, and flavor binding; such knowledge assists in the selection of ingredients and the choice of stabilizers. Machine-learning models and chemometric tools correlate composition and processing parameters with textural, nutritional, and sensory characteristics, while no supervised techniques uncover hidden formulation spaces that are helpful for optimization. The combination of proteomics, peptidomics, and metabolomics connects peptide and volatile profiles to functional and sensory endpoints, thereby enhancing predictive capacity and mechanistic understanding. Besides, non

thermal and hybrid processing methods such as high-intensity ultrasound, targeted fermentation with lactic acid bacteria, HPP, and enzymatic treatments lessen plant off-flavors, improve emulsification, and increase digestibility. The latest digital twins make it possible to combine mechanistic models with real-time data for simulation that is aware of the process and planning at the scale of the final product. There are still significant obstacles to be overcome: the availability of heterogeneous and scarce multimodal datasets, the gap between lab and industry, the need for the complex models to be interpretable, and the standardization of protocols along with clinical approval for digestibility and bioavailability. Future research should focus on the development of scalable dual-processing methods, the use of underexploited plant proteins, the application of strong omics-sensory integration, and commercialization studies at the pilot scale aimed at validating both shelf-life and consumer acceptance. The combination of computational design, omics integration, and advanced processing provides a pathway for the development of hybrid functional foods that are nutritious, tasty, and sustainable at the same time.

Keywords: computer design, hybrid dairy, plant protein, omics, functional foods

ICABB26-MOC-P07

ImmunoGate: Dual Logic CAR-T Cell Therapy for Pancreatic Ductal Adenocarcinoma (PDAC)

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Abstract

Pancreatic ductal adenocarcinoma (PDAC) is a cancer having high mortality rate globally. PDAC treatments focussing along CAR-T therapy are majorly due to antigen heterogeneity and off-target toxicity. We developed a Dual Logic Gate CAR-T Designer for PDAC which is a web-based tool that's highly helpful for logic-gate engineering and biomarker-driven antigen selection in order to improve therapeutic precision and to a great extent. We developed ImmunoGate, a Dual Logic Gate CAR-T Designer which is trained on multiple datasets of 1,098 biomarkers by arranging and classifying them according to their oncogenic and tumor-suppressive characteristics, powers the overall working of the system and supports user friendly functions which allow users to dynamically select tumor and healthy cell references under the desired biomarker categories. The comprehensive dataset of 1,098 PDAC biomarkers was curated from MarkerDB **,** cBioPortal PDAC-MSK 2024 cohort**,** and an article from the National Library of Medicine**.** This software recommends the most appropriate logic gate configuration (AND, OR, XOR, or NOT) based on the choices selected by the user to maximize selectivity and specificity and minimize the damage caused to healthy tissue in order to protect it and prevent off-target toxicity. In addition, the platform supports visualization of antigen combination logic by the creation of truth tables for the resulting gate, and designs personalized CAR-T cell schematics corresponding to it. This aims to enhances specificity, reduces off-target effects, and enables personalised CAR design for the treatment of PDAC through the combination of choosen biomarker and optimized boolean logic. This novel step towards establishment of a computational immunotherapy by integrating the current technological advancements and cutting-edge research. ImmunoGate serves as the Dual Logic Gate CAR-T therapy technique that bridges the existing gap between therapeutic development and practical research undertaken in tumor immuno-engineering. The schematic outputs generated will be beneficial for the researchers and clinicians in designing a personalised CAR-T cell as per the immune response of the patient.

Keywords: Pancreatic ductal adenocarcinoma, CAR-T, Logic gate, ImmunoGate, immune engineering.

ICABB26-MOC-P08

Antimicrobial Evaluation of *Carica papaya* Leaf Extract for Dermal Infections: Experimental and Computational Insights

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Abstract

Bacterial and fungal skin infections, such as impetigo, cellulitis, folliculitis, and mycoses, are prevalent across all age groups and are conventionally managed using antibiotic or antifungal therapies. However, the rising concern over antimicrobial resistance has driven increased interest in phytotherapeutic alternatives. Carica papaya (papaya) has emerged as a promising medicinal plant due to its reported anticancer, antioxidant, anti-inflammatory, and antimicrobial properties. This study aimed to conduct a comprehensive phytochemical evaluation of *C. papaya* leaf extract and assess its antioxidant and antimicrobial potential through integrated in silico and *in vitro* approaches.Active-site molecular docking, ADMET profiling, and toxicological assessments were performed to investigate the bioactive constituents and their safety in the human system. The optimised crude ethanolic leaf extract was analysed for key secondary metabolites and subjected to antimicrobial testing against pathogenic bacterial strains (Micrococcus luteus and Bacillus licheniformis) and fungal strains (Rhizopus oryzae, Aspergillus niger, and *Trichoderma* spp.). The extract demonstrated significant antimicrobial activity against all tested microorganisms. Molecular docking studies further revealed favourable receptor–ligand interactions with high binding affinities. Toxicity predictions identified L-ascorbic acid and papain as the least toxic among the evaluated phytocompounds.Overall, the findings support the therapeutic potential of *C. papaya* leaf extract and highlight its suitability for further development as a safe and effective phytotherapeutic agent within pharmaceutical applications.

Keywords: *Carica papaya*; Antioxidant activity; Antimicrobial activity; Molecular docking; Phytochemical analysis.

ICABB26-MOC-P09

Decoding the Microbiota–Host Gene Axis in Neurodegenerative Diseases: A Network-Based Approach

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Abstract

The gut microbiota plays an important role in regulating normal brain function by affecting immune activity, metabolism, and communication between the gut and the brain. Changes in these microbial communities, often described as microbial dysbiosis, have been increasingly linked to neurodegenerative disorders (NDDs). Such changes are thought to contribute to inflammation in the nervous system, changes in metabolic pathways, and gradual loss of neuronal function. Disturbances in the microbiome may also affect the production of metabolites and signaling molecules that influence brain cells and behaviour. In order to study the shared molecular features of NDDs, genes associated with these disorders were gathered from multiple scientific databases. Comparing these genes made it possible to identify a group of "hub genes" that appear repeatedly across different NDDs. These hub genes are likely to be involved in central biological processes, including immune regulation,

responses to cellular stress, mitochondrial activity, and signaling between neurons. Because of their strong connections to many pathways, they may help explain how different neurodegenerative conditions develop and progress. When these hub genes are examined together with host-microbiota interactions, new possibilities emerge. Microbial disturbances in the gut may influence these key genes and the pathways they control, potentially worsening neurodegenerative changes. This suggests that microbiome imbalance could act as a common trigger for molecular disruptions seen across several NDDs. Recognizing these links may help in developing microbiome-based markers for early detection, as well as therapeutic approaches focused on restoring microbial balance and reducing inflammation.

Keywords: Gut microbiota, Immune signaling, Neurodegenerative diseases (NDDs), Microbial dysbiosis, Host–microbiota interactions

ICABB26-MOC-P10

Advances and Challenges of Artificial Intelligence and Machine Learning in Mental Health Care: A Review

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Abstract

The complex etiologies, overlapping symptoms of the disorders, and high degree of diagnostic subjectivity make mental disorders a major global health burden. This review brings together recent findings on how machine learning and artificial intelligence are being used in mental-health research and treatment. Traditional psychiatric assessment diagnoses rely on what clinicians observe and what patients report, which makes early identification and accurate classification difficult. New AI-based approaches aim to overcome these limitations by combining biological data, behavioural information, and digital health records to generate more objective insights. Among the advanced methods studied, deep-learning models have demonstrated notable success in identifying major neurodegenerative disorders.AI-based disease-modelling has also helped in finding new therapeutic targets and speeding up drug-discovery efforts. In recent years, ML and AI offer promising directions for moving psychiatry toward precision medicine by supporting objective diagnosis, individualized treatment planning, and the development of new therapies. Ethical oversight and collaboration across disciplines will be essential to ensure that these technologies are used safely, fairly, and effectively in mental-health care. Privacy - focused methods like federated learning make it possible for different hospitals and clinics to work together without ever sharing sensitive patient information. This helps researchers build better tools for understanding mental health while still protecting people's confidentiality. Despite these significant advances, several challenges still persist.

Keywords: Artificial Intelligence, Machine learning, Mental health, Digital Health, Drug discovery

ICABB26-MOC-P11

Accelerating Advances in Aging and Alzheimer's Disease via AI-driven Research: A Comprehensive Review

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Abstract

Aging is the strongest risk factor for Alzheimer's disease (AD), and its rising global burden reflected in increasing case numbers and recent AD-related deaths reported publicly underscores the need for earlier and more accurate detection methods.Traditional diagnostic approaches, including cognitive assessments, clinician-interpreted neuroimaging, and basic biomarker tests, often lack sensitivity in the earliest stages and rely heavily on subjective judgment. These limitations highlight the necessity for objective, data-driven solutions. Artificial Intelligence (AI), Machine Learning (ML), and computational analytics have emerged as powerful tools to address this gap. AI enables the large, multimodal datasets such as MRI/CT scans, genomic and proteomic profiles, behavioral patterns, and electronic health records. AI-driven diagnostic frameworks have demonstrated the capability to stratify AD stages, forecast longitudinal disease trajectories, and identify prodromal biomarkers with high fidelity. Recent empirical evaluations report classification and prediction accuracies in the range of 85–95%, contingent upon the heterogeneity of input datasets and the complexity of the underlying model architectures. Advancements in explainable artificial intelligence (XAI) have enhanced clinical interpretability by delineating the feature contributions and decision pathways underlying model predictions, thereby improving clinician trust and facilitating integration into diagnostic workflows. This review synthesizes recent advancements in AI-driven methodologies for investigating aging and Alzheimer's disease, with a particular focus on multimodal data integration, deep learning frameworks for early-stage detection, and computational models that characterize disease progression. The current review will also examine the clinical potential of these technologies, ongoing challenges such as data scarcity and interpretability issues, and the current gap between research capabilities and routine clinical use. By integrating foundational concepts, recent progress, and future directions, this review highlights how AI is transforming the understanding of aging-related neurodegeneration and shaping the future of personalized AD diagnosis and intervention.

Keywords: Aging and Alzheimer's disease; Artificial Intelligence; Machine Learning; Prodromal biomarkers; Explainable AI; Neurodegeneration

ICABB26-MOC-P12

Comprehensive Genomic Exploration of *Priestia megaterium* CL1

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Abstract

In this study, we explored the genomic landscape of Priestia megaterium CL1, beginning with the careful isolation of its bacterial DNA and confirmation of its identity through basic biochemical tests. With high-quality DNA in hand, the journey moved to whole-genome sequencing, where the QIASeqDX DNA Kit enabled a seamless one-tube enzymatic digestion, end-repair, and A-tailing of 50 ng of gDNA. Illumina short reads first laid the foundation by forming the preliminary contigs, after which Nanopore long reads helped bridge these fragments into larger scaffolds. To understand where

CL1 fit in the microbial world, ANIb analysis provided its genomic relatedness. The assembled genome was then brought to life through RAST annotation, with Prokka14 sharpening gene predictions. To uncover the functional essence of CL1, predicted proteins were mapped to the UniProt bacterial database using Diamond BLAST for gene ontology, while metabolic capabilities were sketched using the KAAS pathway server. The search for specialized genetic traits led us to identify biosynthetic gene clusters via antiSMASH and evaluate antimicrobial resistance signatures through CARD using BLASTX. The richness of its carbohydrate-active enzymes GHs, GTs, PLs, CEs, AAs, and CBMs added further dimension to its metabolic profile. The broader evolutionary context was revealed through Roary pangenome analysis, identifying both core and accessory genes, while BRIG provided a circular comparative view against related genomes. Plastic-degrading potential was assessed through PlasticDB, and finally, the secretory landscape of CL1 was charted through SignalP v4.1 and SecretomeP v2.0, completing a cohesive genomic narrative of this versatile strain.

Keywords: *Priestia megaterium* CL1; ANIb; RAST; Prokka; Diamond BLAST; KAAS; CARD database; CAZymes; Roary; BRIG; PlasticDB; SignalP; SecretomeP; functional genomics.

ICABB26-MOC-P13

AI-Assisted Approach for Chronic Kidney Disease Treatment

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Abstract

Traditional drug discovery is often slow, expensive, and limited in finding new treatments quickly. This research focused on using artificial intelligence (AI) to find existing drugs that could be reused (repurposed) to treat COVID-19. The goal was to create and test AI-based methods that combine many types of biological and clinical data to identify the most promising treatment options. Chronic kidney disease (CKD) is now widely recognized as a major health problem around the world, and new data-driven technologies are creating fresh opportunities to improve how patients are diagnosed and treated. Recent research shows that machine-learning methods can help spot CKD earlier by analyzing routine clinical and lab information more quickly and accurately than traditional techniques. Many studies also report that these predictive models can estimate how the disease might progress, allowing doctors to identify patients who may need closer follow-up or more advanced care. Deep-learning tools used with kidney ultrasound images have further improved diagnosis by picking up very small changes—like shifts in kidney thickness, texture, or structure—that might be overlooked during a normal examination. Beyond diagnosis, AI-based systems have also been helpful in selecting the most important clinical features, predicting individual risk levels, and even offering diet-related guidance, leading to more personalized care for CKD patients. The central message is that the AI tools are much better in observing kidney problems than old methods. The conventional methods frequently depends on some simple measures. AI models (like ML and DL) can look at huge amounts of information like imaging , demographics all at once . By looking at all this data AL finds the hidden clues Or minute red flags that human doctor or standard formulas will easily miss. Which allows them to find kidney dysfunction before time. AI provide giant exactness risk score, the score tells that the precisely how patient develop the disease. Random forest, XG boost, light GBM act as a group of many different AI models operating together. They each work on the diagnosis and their merge discipline is usually more precise and good then single one will work. Deep learning with imaging CNNs (computational neural networks) provide kidney images or even eye scans . The area under curve (AUC) values of 0.85 to 0.96 and accuracy is nice at differentiating between healthy person or infected one.

Keyword : Chronic kidney disease, Artificial intelligence , drug discovery, covid 19

ICABB26-MOC-P014

In Silico Design and Wet Lab Synthesis of Hybrid Compounds for Potential Therapeutic Applications

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Abstract

The combination of wet lab synthesis and in silico drug design represents an innovative approach in modern pharmaceutical research. Integrating computational methods with experimental approaches, one can design, synthesise, and assess new hybrid molecules with potential therapeutic applications. Bioactive moieties derived from established medicinal drugs were carefully combined using in silico technologies, *viz.,* molecular docking, pharmacophore modelling, and ADMET analysis, to create hybrid compounds with enhanced binding affinity, pharmacokinetic characteristics, and targeted selectivity. The primary characterisation techniques used for structural determination of the most promising candidates are Fourier transform IR, nuclear magnetic resonance (NMR), and mass spectrometry. These candidates were synthesised by employing optimised synthetic pathways. To assess their biological activity and validate computer projections, preliminary *in vitro* tests were conducted. The combined computational–experimental methodology leads to a shortened optimisation process with an improved detection efficiency. The findings indicate that the multifunctional hybrid molecules with exceptional therapeutic potential can be produced by combining logical *in silico* design with wet lab synthesis. This study presents the foundation for creating next-generation medication possibilities that can improve precision medicine and address the limitations of traditional mono-targeted treatments.

Keywords: *In silco*, wet lab, therapeutic, molecular docking

ICABB26-MOC-P015

In-vitro and In-silico Evaluation of Rutin-Mediated Modulation of Oxidative Stress Biomarkers in Idiopathic Parkinson's Disease

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Abstract

Idiopathic Parkinson's Disease (IPD) is one of the most prevalent and progressive neurodegenerative disorders of the central nervous system, characterized by motor dysfunction, tremors and cognitive decline. Although the exact cause of IPD remains unresolved, factors such as oxidative stress, mitochondrial impairment and neuroinflammatory processes are recognized as key contributors to its disease progression. Given that IPD is an age-related and metabolically influenced disorder, oxidative stress plays a major role in its pathogenesis and progression. The lack of curative therapy has intensified the search for natural compounds with neuroprotective and antioxidant potential. Rutin, a polyphenolic flavonoid widely distributed in fruits exhibits potent antioxidant, anti-inflammatory and metal-chelating properties**.** In this study, the antioxidant potential of Rutin was evaluated by analysing oxidative stress biomarkers in Idiopathic Parkinson's Disease (IPD) through both *in vitro* and *in silico* approaches. The venous blood samples from 95 subjects were collected via venipuncture after obtaining informed

consent. The effects of Rutin were assessed against oxidative stress induced by 10mM H_2O_2, evaluated by estimating the levels of malondialdehyde (MDA), reduced glutathione (GSH), superoxide dismutase (SOD) and catalase after co-incubating the erythrocytes in the presence of Rutin (10^{-7}M to 10^{-5}M) and H_2O_2. Molecular docking analysis was also conducted. The etiology of IPD is significantly influenced by neuroinflammation, mitochondrial dysfunction and dopamine (DA) metabolism. Based on the analysed data, the levels of oxidative stress biomarkers were significantly higher in IPD samples compared to the healthy controls. Rutin treatment demonstrated a reduction in oxidative damage markers, supporting its antioxidative potential. This study underscores the therapeutic promise of Rutin as a natural antioxidant capable of mitigating oxidative stress–mediated cellular damage associated with IPD. This study utilizes patient-derived erythrocytes to evaluate Rutin's direct antioxidative potential in IPD, offering a unique translational link between peripheral redox markers and central neurodegeneration.

Keywords: Rutin, Oxidative stress, Idiopathic Parkinsons Disease, Erythrocytes, Biomarkers

ICABB26-MOC-P016

The Role of Computational Chemistry and Cheminformatics in Modern Herbicide Discovery: A Critical Review

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Abstract

Herbicides are prevalent chemical agents that can eliminate unwanted vegetation, including weeds and specific grasses, or inhibit their growth to ensure agricultural productivity is not diminished. The development of herbicides necessitates a meticulous equilibrium between efficacy and safety, similar to that of pharmaceuticals. The majority of pharmaceuticals and herbicides are typically identified through a time-consuming and expensive process of trial and error, which involves the evaluation of the potency of numerous compounds against a target in vitro (High-Throughput Screening). The tools of computational chemistry and techniques of cheminformatics acts as powerful tools which quicken the identification, design, and optimization of novel herbicidal molecules with reduced prices and interval. This comprehensive review addresses the current trends and challenges within herbicidal research along with illustrative examples of the application of classical, cheminformatics, and computational methodologies in herbicide innovation.

A broad literature survey conducted on the published literature in past ten years directing on various computational techniques and cheminformatics tools used in herbicide research including molecular docking, molecular dynamics simulations, ADMET (Absorption Distribution Metabolism Excretion Toxicity) prediction, and machine learning (ML)-based QSAR(Quantitative structure analysis relationship),to evaluate their efficiency and restrictions in herbicide designing. Most drugs and herbicides are usually found through a long and expensive process of trial and error, which entails testing the potency of several compounds against a target in vitro .Computational chemistry and cheminformatics have become very useful tools for quickly finding, designing, and improving new herbicidal compounds at lower costs and with shorter time frames. This review form a bridge between various computational tools and techniques with the herbicide designing in lab and the challenges originated.

Keywords: Computational chemistry; Cheminformatics; Herbicide discovery; Molecular modeling; QSAR; Virtual screening

ICABB26-MOC-P18

Advancing the Microbiome Frontier: State-of-the-Art Technologies

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Abstract

A key domain of oncology is the complex relationship between the microbiota and cancer, which calls for advanced technology to interpret tumor-microbiome interaction. This chapter examines innovative approaches that are transforming cancer microbiome research. High resolution multi-omics techniques allow for the thorough analysis of microbial diversity, functional gene expression, and metabolic contributions to oncogenesis. These techniques include single-cell metagenomics, long-read sequencing, metatranscriptomics, metaproteomics, and metabolomics. Microbe–host interactions and treatment response dynamics are revealed by spatial and temporal resolution technologies like GeoMx Digital Spatial Profiling, 10x Visium, and longitudinal metagenomics. By simulating the tumor microenvironment, organoid systems and microfluidics—such as gut/tumor organoids and organ-on-a-chip platforms—provide functional insights in real time. Microbiome engineering is made possible by phage-mediated delivery, while functional genetic methods such as CRISPR-Cas and transposon-insertion sequencing probe microbial genes that influence carcinogenicity. Microbiome-based biomarkers and treatments, such as live biotherapeutic products and fecal microbiota transplants, have the potential to improve non-invasive diagnostics and tailored interventions. Despite challenges such as reproducibility, geographic bias, and bioethical concerns, the blend of these technologies with human microbiome-atlas projects and real-time biosensors heralds a transformative era for precision oncology, with an emphasis on interoperable and patient-centric research frameworks.

Keywords: Multi-omics, Single-cell metagenomics, Long-read sequencing,, Metaproteomics, Metabolomics, Spatial transcriptomics, Longitudinal profiling, Organoids, Microfluidics, CRISPR-Cas, Biomarkers

ICABB26-MOC-P19

BRCA1 And BRCA2 Gene Dysregulation In Ovarian And Breast Cancer With Respect To DNA Methylation

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Abstract

Breast and ovarian cancers are among the most prevalent malignancies in women worldwide, sharing common genetic susceptibility factors, particularly alterations in the BRCA1 and BRCA2 tumor suppressor genes. While germline and somatic mutations in these genes are well-established drivers of cancer risk, emerging evidence highlights epigenetic dysregulation—especially promoter DNA methylation—as a critical mechanism contributing to BRCA gene silencing in both cancer types. This abstract provides a comparative overview of BRCA1 and BRCA2 methylation patterns in breast and ovarian cancers and their biological and clinical implications. In breast cancer, BRCA1 promoter hypermethylation is frequently observed in sporadic cases, particularly in triple negative breast cancer (TNBC). This epigenetic modification leads to transcriptional repression of BRCA1, impaired homologous recombination-mediated DNA repair, and increased genomic instability, mimicking the phenotype of BRCA1-mutated tumors. In contrast, BRCA2 promoter methylation in breast cancer is relatively rare, suggesting a gene-specific epigenetic regulation. Ovarian cancer, especially high-grade serous ovarian carcinoma, also exhibits BRCA1 promoter hypermethylation at a significant frequency. Similar to breast cancer, BRCA1 methylation in ovarian tumors is associated with defective DNA repair and increased sensitivity to platinum-based chemotherapy and PARP inhibitors. However, ovarian cancers demonstrate a higher prevalence of both BRCA1 and BRCA2 epigenetic alterations compared to breast cancers, indicating broader epigenetic instability. Comparatively, while BRCA1 methylation plays a dominant role in both cancers, its

frequency, tumor subtype association, and therapeutic relevance differ between breast and ovarian malignancies. Understanding these cancer specific methylation patterns enhances risk stratification, prognostic evaluation, and personalized therapeutic strategies. Overall, BRCA1 and BRCA2 methylation represents a crucial epigenetic mechanism driving tumorigenesis and treatment response in breast and ovarian cancers.

Keywords: BRCA1, BRCA2, DNA methylation, epigenetics, promoter hypermethylation, breast cancer, ovarian cancer, tumor suppressor genes, gene silencing, BRCAness phenotype

ICABB26-MOC-P20

Tobacco-Induced Epigenetic Dysregulation in Oral Cancer

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Abstract

Oral squamous cell carcinoma (OSCC) is the most common form of oral cancer, accounting for over 90% of cases, and remains a major cause of cancer-related mortality worldwide. Tobacco consumption is one of the primary etiological factors, with more than 60 toxic compounds capable of inducing cellular and molecular damage. Increasing evidence highlights that beyond genetic mutations, tobacco exerts its carcinogenic effects through profound epigenetic alterations. These include aberrant DNA methylation, dysregulated histone modifications, and altered miRNA expression, collectively disrupting the regulation of tumor suppressor genes and oncogenes. Such epigenetic deregulation promotes initiation, progression, and therapy resistance in OSCC. Histone-modifying enzymes and DNA methyltransferases emerge as key mediators in this process, linking tobacco exposure to chromatin remodelling and gene silencing. Moreover, epigenetic signatures shaped by tobacco toxins hold potential as biomarkers for early diagnosis, prognosis prediction, and therapeutic stratification. Emerging epigenetic therapies, such as DNMT and HDAC inhibitors, demonstrate the ability to reverse abnormal modifications and restore normal gene expression, offering novel avenues for OSCC management. This review consolidates current knowledge on tobacco-induced epigenetic mechanisms in OSCC and underscores the importance of epigenetic biomarkers and epi-drugs in overcoming therapeutic resistance. Understanding this interplay not only provides mechanistic insights but also opens translational opportunities for precision medicine in oral cancer.

Keywords*: Oral squamous cell carcinoma (OSCC), Tobacco carcinogenesis, Epigenetic alterations, DNA methylation and histone modifications, Epigenetic therapy*

ICABB26-MOC-P21

AI-Driven Antimicrobial Discovery: Harnessing Artificial Intelligence to Combat Antimicrobial Resistance

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Abstract

Resistance against antimicrobials has become one of the most serious global health threats, which results in difficulty in treating various infections. It also reduce the efficacy of the all major conventional antimicrobial arsenal and has lead to increase in mortality, morbidity and overall healthcare costs. Therefore, there is an urgent need for new antimicrobials. However, Traditional practices are time consuming, cost intensive and rely on tedious screening and optimization search procedures. This acts as a limitation for keeping up with the rapidly evolving and adapting mechanisms of MDR bacteria. For search and identification of antimicrobials, Artificial intelligence (AI) and ML (machine learning) have emerged as potential tools to overcome the limitations of drug discovery. AI based models can assist in the identification and selection of novel antimicrobial candidates by utilizing available biological and chemical datasets. Similarly, different features like amino acid composition, molecular descriptors and

structural attributes can be utilized to identify active compounds from millions of compounds that lack the anticipated biological activity. Furthermore, different models can be used to assess toxicity and stability profiles of various antimicrobial compounds that have been shortlisted. Recent developments in deep learning and structure based approaches could additionally help in efficiently screening of data libraries, optimization of shortlisted compounds and probability of resistance development. However, AI based dataset bias, interpretability of model and general applicability remains important challenges. These issues could be addressed by robust dataset curation, while considering the checkpoints for bias and transparent modelling strategies for reliable prediction. Overall, the integration of AI based methodologies could offer an efficient framework, which could be utilized in combination with the traditional antimicrobial discovery to address the escalating global burden of antimicrobial resistance.

Keywords: Artificial Intelligence, Antimicrobial Resistance (AMR), Drug Discovery, Machine Learning

ICABB26-MOC-P22

In Silico Discovery of Anti-Breast-Cancer Leads from Eucalyptus *globulus* and *Corymbia citriodora*

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Abstract

Breast cancer remains a primary global health challenge, affecting approximately 2.3 million individuals annually with significant impacts in nations such as China, the USA, and India. Luminal A breast cancer is characterized by estrogen-receptor-positive and HER2-negative status and is the most commonly occurring cancer type. The current study employs an integrated computational framework incorporating network pharmacology, molecular docking, ADMET profiling, and Monte Carlo simulations to identify potent anti breast-cancer phytocompounds from *Eucalyptus globulus* and *Corymbia citriodora* leaf extracts. By screening a library of 100 phytochemicals against eight pivotal biomarkers of luminal A breast cancer namely AKT1, BRAF, BRCA2, CTNNB1, FGFR2, PR, PTEN, and PTPN11, the research identified several high-affinity leads. Notably, molecular docking revealed that β-sitosterol exhibited superior binding energy against the BRAF protein, while eucalyptin and myricetin demonstrated strong interactions with FGFR2, outperforming standard drug benchmarks. Subsequent ADMET and toxicity evaluations confirmed the favorable pharmacokinetic profiles and safety of these candidates. Furthermore, these interactions were validated with Monte Carlo simulations A significant reduction in RMSF peaks, particularly in the catalytic loops or activation segments, indicates that the phytochemical effectively binds the biomarker into a stable, non-functional conformation. These simulations confirmed the conformational stability and reliability of the predicted complexes, showing that β-sitosterol and myricetin provide more uniform stabilization than their synthetic standard counterparts. These findings suggest that β-sitosterol and myricetin serve as promising scaffolds for novel therapeutic development, providing a robust foundation for future in vitro and in vivo oncological validation of these botanical species.

Keywords:- Breast cancer; Luminal A; Eucalyptus globulus; Corymbia citriodora; Molecular Docking; ADME and Toxicity analysis; Monte Carlo.

ICABB26-MOC-P23

Ribosomal Stress and p53 Pathway Regulation in Prostate Cancer

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Abstract

Ribosome biogenesis is a tightly regulated and energy-intensive cellular process essential for protein synthesis and cell growth. Disruption of this process triggers a conserved response known as ribosomal or nucleolar stress, which acts as an important tumor-suppressive mechanism largely mediated through activation of the p53 pathway. Prostate cancer is characterized by uncontrolled proliferation, altered

ribosome production, and frequent dysregulation of p53 signaling. In this case ribosomal stress represents a critical regulatory axis influencing tumor progression and therapeutic response. Under normal physiological conditions, ribosomal proteins assemble efficiently with ribosomal RNA within the nucleolus, while p53 levels are maintained at low concentrations through MDM2-mediated ubiquitination and proteasomal degradation. Oncogenic signaling, nutrient limitation, or inhibition of ribosome biogenesis disrupts nucleolar integrity, causing the release and accumulation of free ribosomal proteins such as RPL5 and RPL11 in the nucleoplasm. These proteins bind to and inhibit MDM2, leading to stabilization and activation of p53. Activated p53 initiates transcriptional programs that promote cell-cycle arrest, senescence, apoptosis, and suppression of cellular growth. Transcriptomic and ribosome-profiling studies further demonstrate that p53 activation is accompanied by inhibition of the mTOR pathway, resulting in reduced ribosomal protein translation and global attenuation of protein synthesis. Prostate cancer cells commonly exhibit enhanced ribosome biogenesis and increased translational capacity to sustain rapid growth. Structural alterations of the nucleolus and overexpression of ribosome biogenesis regulators correlate with aggressive disease and poor prognosis. Pharmacological or genetic inhibition of ribosome biogenesis can induce ribosomal stress and activate p53 in tumors retaining wild-type TP53, involving nucleolar disorganization, decreased rRNA synthesis, and RPL11-dependent MDM2 inhibition. Moreover, ribosomal stress can also activate p53-independent pathways, particularly in TP53-mutant prostate cancers, where ribosomal proteins modulate oncogenic factors such as c-Myc and E2F-1 to suppress proliferation and induce apoptosis. These mechanisms highlight ribosomal stress as a promising therapeutic target in prostate cancer management strategies clinically.

Keywords: Ribosomal stress, Ribosome biogenesis, Nucleolar stress, Prostate cancer, p53 signaling pathway, MDM2 inhibition, Ribosomal proteins (RPL5, RPL11), mTOR pathway, Translational control, TP53 mutations

ICABB26-MOC-P24

Yeast Cell Lines as a Model System to Study DNA Methylation Mechanisms Relevant to Asthma

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Abstract

DNA methylation is a key epigenetic modification involved in the regulation of gene expression and has been strongly implicated in the pathogenesis of asthma. Aberrant methylation of promoter regions in immune and airway-related genes contributes to dysregulated cytokine expression, Th2-skewed immune responses, and chronic airway inflammation. However, studying the direct mechanistic effects of DNA methylation in mammalian systems is challenging due to cellular complexity and the presence of multiple interacting epigenetic regulators. To address these limitations, yeast cells, particularly *Saccharomyces cerevisiae*, provide a simplified and highly controllable experimental model. Yeast naturally lacks endogenous DNA methylation and DNA methyltransferases, creating an epigenetically neutral background. By engineering yeast to express mammalian DNA methyltransferases such as DNMT1, DNMT3A, or DNMT3B, targeted CpG methylation can be introduced into the genome. In asthma-related epigenetic studies, promoter regions of key asthma-associated genes, including IL4, IL13, IFNG, CHI3L1, and PI3, can be cloned upstream of reporter genes to directly assess the effects of promoter methylation on transcriptional activity. Inducible expression systems allow controlled modulation of methylation levels, enabling precise analysis of methylation-dependent gene repression. Bisulfite sequencing and reporter assays facilitate confirmation of methylation patterns and quantification of transcriptional changes. Studies using DNMT-expressing yeast have demonstrated methylation distributions resembling mammalian systems, indicating that DNA sequence context and chromatin organization influence methylation outcomes even in the absence of native methylation readers. Although yeast cannot replicate immune signaling pathways, it serves as a cost-effective and genetically tractable platform to dissect fundamental principles of DNA methylation. This approach

provides mechanistic insights into how promoter methylation may regulate asthma-associated genes and supports the use of yeast as a complementary model for epigenetic research in asthma.
Keywords: DNA methylation, yeast model, DNMT, promoter regulation, epigenetics, asthma genes

ICABB26-MOC-P26

Environmental Influences on DNA Methylation and Their Role in Asthma Pathophysiology

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Abstract
Asthma is a chronic inflammatory airway disease resulting from complex interactions between genetic susceptibility and environmental exposures. Increasing evidence highlights DNA methylation as a critical epigenetic mechanism through which environmental factors influence gene expression and asthma development. Environmental exposures such as air pollution, tobacco smoke, allergens, and occupational irritants can induce stable changes in DNA methylation patterns, particularly in genes involved in immune regulation and airway inflammation. Air pollutants, including particulate matter ($PM_{2.5}$ and PM_{10}), nitrogen dioxide (NO_2), and ozone, have been associated wwith differentialmethylation of asthma-related genes in blood, airway epithelial cells, and immune cells. These methylation changes affect key pathways involved in Th1/Th2 immune balance, cytokine production, and airway remodeling. Promoter methylation alterations in genes such as IL4, IL13, IFNG, FOXP3, CHI3L1, and SERPINE1 contribute to enhanced inflammatory responses and impaired immune tolerance observed in asthma patients. Importantly, early life and prenatal exposures can produce persistent epigenetic modifications, increasing the risk of asthma later in life. DNA methylation also acts as a mediator linking environmental exposure to clinical outcomes such as asthma severity, lung function decline, and disease control. Epigenome-wide association studies have identified exposure-sensitive methylation signatures that partially explain the relationship between pollution exposure and asthma symptoms. These findings suggest that DNA methylation not only serves as a biomarker of environmental exposure but also plays an active role in disease pathophysiology. Understanding environmentally induced epigenetic changes provides valuable insights into asthma prevention and management and highlights DNA methylation as a potential target for personalized therapeutic strategies. The present study reviews current evidence linking environmental exposures to DNA methylation changes involved in asthma pathogenesis. It summarizes how pollutants and allergens induce epigenetic modifications in immune and airway-related genes, influencing inflammation and disease severity. The review also highlights DNA methylation as both a mechanistic mediator and a potential biomarker for exposure related asthma risk and progression.
Keywords: asthma, DNA methylation, environmental exposure, air pollution, epigenetics, immune regulation

ICABB26-MOC-P27

Recent Advancements in Cancer Reversal Technology

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Abstract
Cancer remains one of the foremost challenges in global healthcare, driven by intricate genetic and epigenetic modifications that destabilize normal cellular homeostasis. Traditional treatment modalities chemotherapy, radiotherapy and targeted therapies focus on eradicating malignant cells but often result in toxicity, therapeutic resistance and recurrence. Emerging research introduces a paradigm shift through cancer reversion wherein malignant cells are reprogrammed to restore normal physiological functions instead of being destroyed. This innovative concept hinges on manipulating gene expression patterns, intracellular signaling cascades and the tumor microenvironment to reverse malignancy. Systems biology tools, including attractor landscape analysis, provide a mechanistic framework to

identify molecular tipping points that govern tumor progression and reversion. Concurrently, advancements in molecular editing, proteomics, and chemical biology offer promising avenues to induce this transformation. Collectively, these developments herald a new frontier in oncology—one focused on restoring cellular equilibrium and achieving durable, non-toxic cancer therapies.

Keywords: Cancer reversion, Tumorigenesis, Systems biology, Attractor landscape, Molecular reprogramming.

ICABB26-MOC-P28

Computational Network-Based Identification of Heavy Metal Associated Hub Genes and Pathways in Neurodegenerative Disorders

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Abstract

Neurodegenerative disorders (ND) are emerging as a global health burden, and growing evidence suggests that environmental factors play a vital role in disease onset and progression. Heavy metals such as mercury, cadmium, chromium, lead, and arsenic constitute a major public health concern due to their persistence, bioaccumulation, ability to cross the blood–brain barrier, and capacity to disrupt neuronal homeostasis. To address this research gap, we applied a systems level computational network biology framework to determine the common genes and pathways linking heavy metals exposure to the development of ND. The data were obtained from the Comparative Toxicogenomics Database (CTD), resulting in a set of 101 human genes commonly involved in heavy metals exposure as well as ND like Parkinson's disorder, Alzheimer's disease, Amyotrophic lateral sclerosis, Multiple Sclerosis, and Autism spectrum disorder/attention deficit hyperactivity disorder. Protein–protein interaction networks were generated using STRING and analysed in Cytoscape using Maximal Clique Centrality (MCC) index to identify key regulatory hub genes. Network analysis revealed an interactome characterized by top 10 prominent hub genes. Functional enrichment analysis demonstrate that the hub genes are significantly associated with regulating immune-inflammatory response, oxidative stress response, apoptosis, synaptic dysfunction, and metabolic regulation. Together, our study established a mechanistic framework linking heavy metals exposure might specifically impact overlapping of biological pathways across ND and offer a rational basis for biomarker discovery, environmental risk assessment, and therapeutic target prioritization.

Keywords: Neurodegenerative disorders, Protein–protein interaction, STRING, network analysis, Biomarker

ICABB26-MOC-P29

In-Silico Elucidation of Agarwood Phytochemicals as Multi-Target Modulators of Alzheimer's Disease

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Abstract

Alzheimer's disease (AD) is a chronic neurodegenerative disorder in which multiple factors contribute to pathogenesis, including amyloid-β aggregation, tau hyperphosphorylation, oxidative stress, neuroinflammation and synaptic dysfunction. Due to the poor efficacy of single-target agents in current therapeutics, multi-target interventive therapeutic approaches from natural sources are required for intervention. Methania (Seed of Withania somnifera) and Agarwood (Aquilaria spp.) have long been known for their neuroprotective and anti-inflammatory effects but their molecular mechanisms in AD are poorly understood. Here, the network pharmacology approach (an integrated in-silico systems-based strategy) is used to target and find possible cure-active phytoconstituents that could serve to interfere with AD-associated targets. Phytochemical analysis of Methania and Agarwood was done, which we got from curated databases and we screened them based on drug likeness and pharmacokinetic parameters. We predicted putative molecular targets using target prediction platforms

and also did intersection with AD-related genes, which we obtained from disease-specific databases. We constructed protein protein interaction networks to identify key regulatory hubs and then did Gene Ontology and pathway enrichment analysis to better understand biological relevance. We did molecular docking studies of major AD-associated
proteins, which include acetylcholinesterase, β-secretase, and glycogen synthase kinase-3β, to determine binding affinity and interaction stability. Also we did ADMET and toxicity profiling to assess pharmacological feasibility. The analysis found various phytoconstituents with strong binding affinities and favorable pharmacokinetics. They can also affect multiple pathways relevant to AD, including neuroinflammation, oxidative stress, and synaptic signaling. Overall, this analysis provides computational support for Methania and Agarwood as potential multi-target therapeutics for Alzheimer's disease and provides a helpful basis for future experimental tests and improved methods for drug delivery.

KEYWORDS: Alzheimer's disease; Methania (*Withania somnifera*); Agarwood (*Aquilaria* spp.); in silico studies; network pharmacology; molecular docking

ICABB26-MOC-P30

Computational Insights into Synergistic Neuroprotective Effects of Quercetin and Fisetin in Alzheimer's Disease

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Abstract

Alzheimer's disease (AD) is a complex neurodegenerative disorder driven by the interplay of amyloid-β accumulation, tau hyperphosphorylation, oxidative stress, neuroinflammation, and synaptic dysfunction. The multifactorial nature of AD limits the effectiveness of conventional single-target therapies, necessitating the exploration of multi-target and combination-based therapeutic strategies. Quercetin and fisetin are naturally occurring flavonoids known for their antioxidant, anti-inflammatory, senolytic, and neuroprotective properties; however, their synergistic mechanisms in AD remain inadequately characterized. The present study employs an integrated in-silico systems pharmacology approach to elucidate the synergistic therapeutic potential of quercetin and fisetin against Alzheimer's disease.

Putative molecular targets of quercetin and fisetin were predicted using target prediction platforms and intersected with AD-associated genes retrieved from disease-specific databases. Protein–protein interaction (PPI) networks were constructed to identify key regulatory hubs, followed by Gene Ontology and pathway enrichment analyses to uncover biological processes and signalling pathways relevant to AD pathology. Molecular docking studies were performed against major AD-related targets, including acetylcholinesterase, β-secretase, glycogen synthase kinase-3β, cyclin-dependent kinase 5, and NF-κB, to evaluate binding affinities and interaction stability. Furthermore, ADMET and toxicity profiling were conducted to assess pharmacokinetic feasibility and safety.

The integrated analysis revealed that quercetin and fisetin collectively modulate multiple AD-relevant targets and pathways, including oxidative stress response, neuroinflammation, amyloid processing, and synaptic signalling, demonstrating a complementary and synergistic mode of action. These findings provide strong computational evidence supporting the quercetin–fisetin combination as a promising multi-target therapeutic strategy for Alzheimer's disease and establish a rational foundation for future experimental validation and nano-enabled co-delivery approaches.

Keywords: Alzheimer's disease; quercetin; fisetin; synergistic neuroprotection; in-silico studies; molecular docking

ICABB26-MOC-P31

Empirical Analysis of Deep-CNN Models for Ultrasound based Computer Aided Diagnosis System

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Abstract
Due to non-invasive nature, real-time imaging capability and cost effectiveness ultrasound imaging is extensively used for lesion assessment. However, low contrast, speckle noise and variability in lesion appearances makes automated lesion classification from ultrasound imaging very challenging. Deep convolutional neural networks (CNNs) have shown promising results in this direction. But, there is a lack of unified studies that systematically analyze both pre-processing strategies and CNN architectures within a single experimental framework. This paper presents a comprehensive review and empirical analysis of ultrasound based lesion classification, focusing on the impact of image pre-processing and the performance of deep CNN models. First, an ablation study is conducted to assess pre-processing techniques in order to identify their individual and combined effects on classification performance. Subsequently, an empirical evaluation of multiple CNN architectures is performed, encompassing a shallow CNN baseline as well as state-of-the-art deep models such as VGG, Inception, ResNet50, Xception, MobileNet and EfficientNet. All experiments are conducted using a common pre-processing pipeline and a consistent evaluation protocol to ensure fair comparison. Experimental results demonstrate that with appropriate pre-processing the deeper and more parameter-efficient CNN architectures achieve superior results. In particular, ResNet50 and EfficientNet attain nearly 90% classification accuracy; while F1-scores remain around 88%. The study provides practical insights into effective pre-processing strategies and CNN model selection and offers valuable direction for the development of robust ultrasound based computer aided diagnosis systems.
Keywords: Deep CNN models, ResNet50, EfficientNet, Computational diagnosis

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AI-Enabled Identification of Plasma Lipid Biomarkers Associated with Non alcoholic Fatty Liver Disease Progression

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Abstract
Nonalcoholic Fatty Liver Disease (NAFLD) progression from early stages of steatosis and nonalcoholic steatohepatitis (NASH) to advanced cirrhosis often remains clinically unnoticed until severe liver damage has occurred. Therefore, identification of such biomarkers that define the progression of NAFLD has become quite critical for timely diagnosis and effective therapeutic interventions. In the present study, a dataset consisting of plasma-based lipid signatures of steatosis, NASH and cirrhosis patients was obtained from Metabolomics Workbench. The dataset was further curated and labeled by putting steatosis & NASH samples together in the early-stage NAFLD category and assigning cirrhosis samples to the late-stage NAFLD category. Multiple machine learning-based classification models were trained and evaluated on this dataset, including Logistic Regression, Random Forest, HistGradient Boosting, Gradient Boosting, Support Vector Classifier, KNeighbors and Gaussian Naïve Bayes. The performance of each model was assessed using five-fold cross-validation, where KNeighbors outperformed every classifier by achieving mean accuracy of 0.947, mean precision_macro of 0.941, mean recall_macro of 0.948, mean f1_macro of 0.943 and mean ROC-AUC of 0.951 across folds. Subsequently, the trained KNeighbors classifier was interpreted using explainable artificial intelligence (xAI), following which SHapley Additive exPlanations (SHAP)-based importance ranking integrated with log2 fold change analysis led to the identification of 20 most significant lipid biomarkers involved in the progression of NAFLD from early to late stage. Among these, PC (36:4), PC (38:4) and PC (38:5) emerged as the most influential lipids with

relatively lower concentrations in late-stage NAFLD and these phosphatidylcholine species are well established NAFLD associated biomarkers, thereby validating the biological significance and precision of the model. In contrast, PE (36:2p), PI (36:3) and PI (36:1) emerged as novel lipid biomarkers involved in NAFLD progression with relatively higher concentrations in late-stage NAFLD. Collectively, this xAI-enabled lipidomics framework identified plasma lipid biomarkers with potential for non-invasive NAFLD progression monitoring.

Keywords: Nonalcoholic Fatty Liver Disease; Artificial Intelligence; SHAP; Lipid Biomarkers

ICABB26-MOC-P33

Phytochemicals as modulators of PrP^{c}–PrP^{sc} conversion: targeting misfolding and oligomerization pathways

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Abstract

Prion diseases are fatal neurodegenerative disorders, affecting about 1 to 2 people per million each year worldwide. A staggering 85 to 90% of these cases are identified as sporadic Creutzfeldt–Jakob disease. Once symptoms appear, the disease progresses quickly, with a median survival time of only 6 to 12 months. Highlighting the aggressive nature of prion-related issues. These disorders arise when the normal cellular prion protein (PrP^{c}) changes it's shape into a harmful β-sheet-rich form (PrP^{sc}). This misfolding leads to a series of harmful processes which include oligomerization and amyloid aggregation which ultimately cause irreversible damage to neurons. Despite a lot of research, there are currently no approved therapies that can modify the disease and the treatments currently available only address symptoms and not the disease.Some synthetic anti-prion compounds have shown promise in lab tests but have not succeeded in clinical settings due to challenges like poor ability to cross the blood-brain barrier, toxicity and insufficient for prevention of early misfolding.

Recent experimental and computational research has brought to light the multifaceted role of phytochemicals as potential modulators in the conversion pathways of PrP^{c} to PrP^{sc}. Natural polyphenols including epigallocatechin-3-gallate (EGCG), curcumin, resveratrol, and tannic acid, along with flavonoids like quercetin and luteolin have shown a significant ability to lower PrP^{sc} levels in prion-infected cell models.These compounds play a crucial role in keeping the natural α-helical structure of PrP^{c} intact which prevents the formation of harmful β-sheets.This further leads to disruption of the toxic oligomeric intermediates, boosting the body's ability to clear out these proteins through proteasomal and autophagic processes. Alkaloids like berberine and terpenoids such as ginsenosides offer neuroprotection by lowering oxidative stress and reducing neuroinflammation. These findings highlight phytochemicals as fascinating, low-toxicity options for addressing early-stage prion-related issues.

Keywords: Prion diseases, PrP^{c}–PrP^{sc} conversion, protein misfolding and aggregation, oligomerization, amyloid formation, phytochemical modulators, polyphenols and flavonoids, EGCG, curcumin, neuroprotection, disease-modifying therapeutics

ICABB26-MOC-P34

Target-Class Enrichment Mapping of Neuroactive Phytochemicals for Neurocognitive and Neurobehavioral Modulation

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Abstract

Traditional Indian ethnomedicine has long relied on specific medicinal plants to enhance cognition and manage complex neurobehavioral conditions. While these traditional practices are well documented, bridging the gap between ancient botanical knowledge and modern molecular pharmacology remains a significant challenge. Most contemporary research tends to focus narrowly on isolated bioactive

compounds or specific disease linked proteins. However, this "one-drug-one-target" approach often fails to capture the multi-target synergy inherent in herbal medicine. In this study, we propose a systemic, target-family level framework to investigate whether plants traditionally used for cognitive health exhibit non-random, evolutionary preferences for specific pharmacological target classes. We curated a diverse library of phytochemicals from public ethnopharmacological databases and mapped them to their known or predicted human protein targets. These targets were then categorized into major pharmacological families including G-protein coupled receptors (GPCRs), enzymes, ion channels, kinases, and transporters. By employing statistical enrichment analysis against a broad background set of general medicinal plants, we identified distinct "pharmacological fingerprints" unique to neuroactive flora.

Our results shift the analytical lens from individual molecular interactions to broader functional themes, providing a more holistic interpretation of how these plants interact with the human neuro-proteome. This approach not only validates traditional ethnomedicinal knowledge through a computational lens but also offers a scalable, data-driven strategy for prioritizing plant-derived scaffolds in the development of next-generation neurotherapeutics. By identifying these enriched target classes, we provide a clearer roadmap for future experimental validation in neuropharmacology.

Keywords : Ethnopharmacology; Cognitive enhancement; Neurobehavioral modulation; Medicinal plants; Phytochemicals; Pharmacological target classes; Target-class enrichment analysis

ICABB26-MOC-P35

Identification Of Conserved T-Cell Exhaustion Biomarkers In Lung And Breast Cancer Through Integrated Transcriptomic Analysis.

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Abstract

Breast cancer is the most common cancer among women, while lung cancer remains one of the leading causes of cancer-related deaths worldwide. One of the major challenges in cancer treatment is T-cell exhaustion, a condition in which T cells gradually lose their ability to eliminate tumor cells after prolonged antigen exposure within an immunosuppressive tumor microenvironment. This phenomenon contributes significantly to the variable responses observed in patients receiving targeted therapies and immune checkpoint inhibitors. However, the conserved molecular mechanisms underlying T-cell exhaustion across different cancer types are still not well understood. In this study, we aimed to identify conserved biomarkers associated with T-cell exhaustion in breast and lung cancer. We analyzed eight publicly available microarray datasets from the Gene Expression Omnibus (GEO), including four lung cancer datasets (GSE10072, GSE18842, GSE19804, GSE32863) and four breast cancer datasets (GSE10780, GSE42568, GSE65194, GSE70947). Differentially expressed genes between tumor and normal groups were identified. T-cell exhaustion scores were calculated using single-sample gene set enrichment analysis (ssGSEA), and gene modules associated with these scores were identified using Weighted Gene Co-expression Network Analysis (WGCNA). Key genes were further prioritized using the Maximal Clique Centrality (MCC) method, and further biological pathways were explored through functional enrichment analysis. Additionally, survival analysis was performed to evaluate their clinical relevance and identify potential therapeutic candidates. Further we applied Random Forest and LASSO to identify key genes linked to disease progression followed by evaluating their diagnostic potential using ROC analysis. Immune cell infiltration was examined using ssGSEA to understand the relationship between immune cells and gene expression. Statistical tests were applied to confirm the significance of the observed differences and associations. This study provides insight into shared molecular mechanisms of T-cell exhaustion in lung and breast cancers and highlights immune-related biomarkers that may support future immunotherapy-based research and treatment strategies.

Keywords: T cell exhaustion, Microarray, Lung cancer, Breast cancer, Biomarkers

ICABB26-MOC-P36

Systematic Mapping of Phytochemical-miRNA-Transcription Factor Networks Using AI-Powered Literature Mining for Precision Therapeutics

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Abstract

Plant-derived bioactive compounds modulate gene expression through interactions with microRNAs and transcription factors, forming complex regulatory networks. However, this knowledge is fragmented across the literature, hindering the development of evidence-based, targeted phytotherapeutic interventions.

This study systematically organized evidence on plant compound–microRNA–transcription factor regulation using AI-assisted literature mining and network analysis to create a centralized knowledge base supporting the rational development of precision botanical therapeutics.

AI-assisted PubMed searches (2015–2024) identified studies on plant-derived bioactives and gene regulatory molecules. About 50 key compounds were analyzed for effects on microRNAs and transcription factors, with networks built in Cytoscape and pathway associations examined using STRING and KEGG.

Approximately 300 validated molecular interactions spanning inflammatory conditions, metabolic disorders, and cancer-related mechanisms were identified. Network topology analysis identified multi-target compounds with high centrality scores, indicating broad regulatory influence. The systematic analysis also revealed significant knowledge gaps related to lesser-studied compounds, tissue-specific microRNA regulation, and dose–response relationships.

The analysis identified ~300 validated molecular interactions across inflammatory, metabolic, and cancer pathways, highlighting multi-target compounds with broad regulatory influence and revealing key gaps in understudied compounds, tissue-specific microRNA regulation, and dose–response relationships.

Keywords: Phytochemicals, gene expression, regulation, microRNAs, transcription factors, network pharmacology, precision therapeutics.

ICABB26-MOC-P37

LUCA: Molecular Signatures of the First Cellular Life

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Abstract

All living organisms belonging to Bacteria, Archaea, and Eukarya are believed to have evolved from a single ancestral cell known as the Last Universal Common Ancestor (LUCA). Information about LUCA has been obtained by studying genes, proteins, and metabolic pathways that are conserved across all domains of life. Modern approaches such as comparative genomics and evolutionary analysis suggest that LUCA was not a simple or primitive form, but a fully functional, free-living, DNA-based cell.

LUCA is thought to have possessed a complete genetic and protein-synthesis system, including DNA replication and repair machinery, ribosomes, transfer RNAs, and aminoacyl tRNA synthetases that together operated the universal genetic code. Studies reconstructing ancestral gene sets indicate that LUCA contained hundreds of conserved proteins involved in essential cellular processes such as information transfer, amino acid and nucleotide metabolism, and energy production. The presence of membrane-bound ATP synthase suggests that LUCA generated energy using chemiosmotic mechanisms similar to modern cells.

Metabolic evidence points toward an anaerobic and autotrophic lifestyle, with LUCA likely relying on hydrogen as an energy source through NiFe hydrogenases. Core metabolic pathways such as

glycolysis, gluconeogenesis, parts of the tricarboxylic acid cycle, and carbon fixation via the Wood–Ljungdahl pathway were probably present, while pathways linked to oxygen-based or methanogenic metabolism were absent. Estimates of LUCA's genome size, comparable to modern prokaryotes, support the idea of a relatively complex ancestor. By summarizing the conserved molecular features of LUCA, this study helps connect core molecular biology concepts with evolutionary history and illustrates how modern genomic tools can be used to explore the earliest stages of life on Earth.

Keywords: Last universal common ancestor (LUCA); comparative genomics; ancestral proteome reconstruction; chemiosmotic energy metabolism; early carbon fixation pathways; evolutionary bioinformatics; single-cell evolution models; origin of life studies.

ICABB26-MOC-P38

MALBAC in Disease Diagnostics: From Single-Cell Genomics to AI Enabled Precision Medicine

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Abstract

Multiple Annealing and Looping Based Amplification Cycles (MALBAC) has emerged as a next-generation whole-genome amplification (WGA) technique that enables comprehensive genomic profiling from single cells and ultra-low DNA inputs. Conventional diagnostic approaches often face challenges such as amplification bias, allelic dropout, and limited sensitivity when analyzing rare or heterogeneous cell populations. MALBAC overcomes these limitations through quasi-linear amplification, providing uniform genome coverage and improved reproducibility. As a result, MALBAC has found broad applications across multiple disease domains, including inherited genetic disorders, cancer, neurodegenerative diseases, and reproductive abnormalities. In oncology, MALBAC-based single-cell sequencing facilitates the investigation of tumor heterogeneity, clonal evolution, and therapeutic resistance. In reproductive medicine, its application in preimplantation genetic testing (PGT) enables accurate detection of chromosomal aneuploidies and pathogenic variants, contributing to improved clinical outcomes. Additionally, MALBAC has been applied in neurological and infectious disease research to identify rare mutations and low-frequency variants with high precision.

Recent advances have focused on integrating MALBAC-generated datasets with artificial intelligence (AI) and machine learning driven analytical frameworks to address the complexity of large-scale genomic data. AI-assisted pipelines improve noise reduction, amplification bias correction, variant detection, and pattern recognition, thereby enhancing diagnostic accuracy and predictive capability. The convergence of MALBAC, next-generation sequencing, and AI-powered bioinformatics platforms supports personalized disease profiling and precision medicine approaches. Despite ongoing challenges related to scalability, standardization, and cost, MALBAC represents a transformative diagnostic strategy that bridges experimental genomics and clinical application.

Keywords: MALBAC; whole-genome amplification; single-cell sequencing; artificial intelligence; disease diagnostics; precision medicine.

ICABB26-MOC-P39

Single-Cell Genomics: Redefining Cellular Identity

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Abstract:

Bulk genomic and transcriptomic analyses have traditionally served as the foundation of genetic research; however, these approaches generate population-averaged signals that obscure cell-to cell variability within complex tissues. Single-cell genomics has emerged as a powerful paradigm that enables high-resolution interrogation of genomic, transcriptomic, and epigenomic landscapes at the

level of individual cells, thereby redefining cellular identity, functional heterogeneity, and lineage dynamics. Technological advancements such as single-cell RNA sequencing (scRNA-seq), single-cell assay for transposase-accessible chromatin sequencing (scATAC-seq), and single-cell multi-omics platforms have facilitated the systematic dissection of cellular heterogeneity across developmental, physiological, and pathological contexts. These approaches have uncovered rare cell populations, transitional cellular states, and context
dependent regulatory programs that remain undetectable using bulk methodologies. In cancer research, single-cell genomics has provided critical insights into intratumoral heterogeneity, clonal evolution, and therapy-resistant subpopulations, offering a refined understanding of tumor progression and therapeutic failure. Despite its rapid expansion, several challenges limit the translational application of single-cell genomics. These include technical noise, dropout events, batch effects, and the computational complexity associated with high-dimensional datasets. Furthermore, integrating multimodal single-cell data and achieving robust temporal resolution for dynamic cellular processes remain active areas of investigation. The lack of standardized analytical pipelines and clinical validation further constrains its implementation in routine diagnostics. This poster highlights the conceptual framework, methodological advances, and biological implications of single-cell genomics, emphasizing its capacity to resolve cellular heterogeneity and elucidate disease mechanisms. By addressing current limitations and future directions, single-cell genomics holds significant potential to advance precision medicine, enabling cell-specific diagnostics and targeted therapeutic strategies.

Keywords: Single-cell genomics, cellular heterogeneity, RNA sequencing, single-cell ATAC sequencing, single-cell multi-omics, intratumoral heterogeneity, clonal evolution, precision medicine.

ICABB26-MOC-P40

Computational Analysis of Genetic Variants in PCO–Related Genes and Network-Based Evaluation of Nutraceutical Interventions

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Abstract

Polycystic Ovary Syndrome (PCOS) impacts countless women worldwide, leading to hormone imbalances, insulin resistance, ovarian cysts, irregular cycles, and fertility issues. Insulin signalling, steroid hormone synthesis, inflammation control, and oxidative stress balance are disrupted by changes in critical genes like INSR, IRS1/2, FTO, CYP11A1/17A1/19A1, LHCGR, FSHR, SHBG, and DENND1A.

In this research, bioinformatics, network mapping, and genetic analyses are used to identify these molecular drivers as well as evaluate natural nutraceuticals as multi-target treatments, including myo-inositol, D-chiro-inositol, curcumin, resveratrol, quercetin, omega-3 fatty acids, NAC, vitamin D, berberine and polyphenols. Gene expression data from GEO datasets revealed differences between PCOS patients and healthy controls. Through GO and KEGG enrichment, STRING-built protein interaction networks identified hub genes in insulin signalling, PI3K, AKT pathways, and inflammatory responses.

A number of genetic variants retrieved from ClinVar, dbSNP, gnomAD, and Ensembl are analysed using ANNOVAR, VEP, SIFT, PolyPhen-2, CADD scores, and structural review using AlphaFold or PDB models. Nutraceutical targets sourced from STITCH, DrugBank, and BindingDB are integrated into Cytoscape networks; molecular docking verified interactions such as inositol's ability to enhance INSR/PI3K-AKT activity and curcumin's ability to inhibit CYP17A1-driven androgen synthesis.

The unified variant-gene-pathway-nutraceutical networks demonstrate how these compounds target multiple sites to improve ovarian health and neutralize harmful genetic hubs, paving the way for personalized therapies. This computational framework strengthens systems biology approaches for effective, safer PCOS care.

Keywords: PCOS, gene variants, nutraceuticals, molecular docking, insulin pathways, bioinformatics, network analysis

ICABB26-MOC-P41

Transforming Cancer Therapy Through Artificial Intelligence-Driven Precision Oncology

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Abstract

Cancer manifests as a highly heterogeneous and dynamically evolving disease, exhibiting substantial inter- and intra-tumoral heterogeneity across genomic, transcriptomic, proteomic, and phenotypic dimensions. Conventional therapeutic modalities—such as surgery, chemotherapy, radiotherapy, targeted therapy, and immunotherapy—predominantly employ population-averaged strategies that inadequately address patient-specific tumor biology, resulting in inconsistent efficacy, acquired resistance, and dose-limiting toxicities. These shortcomings emphasize the critical demand for precision oncology paradigms that enable real-time, individualized therapeutic adaptations. Advancements in artificial intelligence (AI), notably machine learning (ML) and deep learning (DL), facilitate the robust integration of multidimensional cancer datasets from multi-omics profiling, radiomics, digital pathology, and longitudinal clinical records. AI models are progressively utilized in therapeutic decision support, encompassing biomarker-based patient stratification, prediction of drug sensitivity and toxicity profiles, and optimisation of treatment sequences. AI excels particularly in the rational design of combination therapies through simulation of drug-drug interactions, identification of synergistic combinations, forecasting of resistance pathways, and delineation of tumor evolutionary dynamics under therapeutic selective pressure. Multimodal AI architectures enhance interrogation of tumor-microenvironment interactions and immune landscape evolution, thereby fostering adaptive, personalized treatment regimens. Although obstacles persist in achieving model interpretability, ensuring data integrity, and attaining clinical generalizability, the convergence of explainable AI techniques, adaptive learning frameworks, and clinically validated decision-support systems heralds AI as a pivotal catalyst for precision oncology and enhanced patient outcomes**.**

Keywords: Tumor, Artificial Intelligence, Oncology, Personalised therapy

ICABB26-MOC-P42

Ai-driven *De Novo* Molecular Design for Acetylcholinesterase and Other CNS Drug Targets

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Abstract

Acetylcholinesterase (AChE) is a critical enzyme in cholinergic neurotransmission and a well-established therapeutic target for central nervous system (CNS) disorders such as Alzheimer s disease, Parkinson s disease, and myasthenia gravis. Despite the availability of AChE inhibitors, current drugs suffer from limitations including limited selectivity, peripheral side effects, and suboptimal pharmacokinetic profiles. The expanding chemical space and complex CNS constraints necessitate novel strategies for identifying optimized small-molecule inhibitors.

Recent advances in artificial intelligence and machine learning have enabled de novo molecular design, allowing the generation of chemically valid, target-specific compounds beyond traditional screening libraries. This review explores AI-driven frameworks-such as deep generative models, reinforcement learning, and graph-based neural networks-for the rational design of novel AChE inhibitors. These approaches integrate structural information, ligand target interaction data, and multi-objective optimization to simultaneously enhance binding affinity, blood brain barrier permeability, drug-likeness, and toxicity profiles.

Using AChE as a representative CNS target, this work highlights how AI-based pipelines can transition from target selection and molecular generation to in silico evaluation, including docking, ADMET prediction, and synthetic feasibility assessment. Furthermore, the review discusses the

broader applicability of these methodologies to other CNS drug targets, emphasizing their potential to accelerate lead discovery while reducing cost and experimental burden.
Overall, AI-driven de novo molecular design represents a transformative paradigm in CNS drug discovery, offering scalable and data-efficient solutions to long-standing challenges in neurotherapeutics development.
Keywords: Alzheimer's disease, CNS targets, Machine learning, de novo molecular design, toxicity

ICABB26-MOC-P43

AI/ML Applications in Drug Discovery and Biomarker Prediction

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Abstract
The rapid expansion of genomics and molecular datasets has promoted the use of artificial intelligence and machine learning methods for disease analysis and biomarker identification. Complex diseases such as breast and lung cancer involve multiple genes and molecular pathways, making single-gene approaches inadequate. Consequently, advanced machine learning models are increasingly used to analyse high-dimensional biological data and support precision medicine.
Recent studies have reviewed and compared several machine learning techniques for disease classification and biomarker prediction, including Support Vector Machines (SVM), Random Forest (RF), XGBoost, and Neural Networks. These models have been applied to genomic and molecular datasets to distinguish healthy samples from diseased conditions and to identify potential biomarkers.
Supervised learning approaches are commonly used due to the availability of labelled data. Random Forest is widely reported for its ability to manage high-dimensional features, reduce overfitting, and provide feature importance measures useful for biomarker prioritization. Support Vector Machines are also frequently employed because of their strong performance in high-dimensional spaces and well-defined decision boundaries.
Neural Networks are applied to model complex nonlinear gene interactions and often achieve high predictive accuracy, but their limited interpretability restricts biological insight.
XGBoost has gained significant attention as a gradient-boosted decision tree model due to its robustness to noisy data, built-in regularization, and capacity to model complex feature interactions. While it demonstrates strong predictive performance and effective feature importance estimation, XGBoost requires careful hyperparameter tuning, can be computationally demanding, and may produce biased importance scores in correlated datasets. These limitations highlight the need for complementary methods and biological validation in biomarker discovery.
KEYWORDS: Machine learning, Biomarker identification, Genomics, XGBoost, Cancer biomarkers, Big Data, Support vector machines

ICABB26-MOC-P44

Circulating DNA fragmentomics and cancer screening.

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Abstract
Cancer remains a leading cause of global mortality, with over ten million deaths reported annually. A major contributor to this burden is the limited effectiveness of existing screening strategies, which are largely restricted to a small subset of cancers and frequently fail to detect disease at early, asymptomatic stages. Imaging-based modalities and protein biomarkers often suffer from insufficient sensitivity, limited specificity, and poor scalability, particularly for population-wide or multi cancer screening. These limitations highlight the urgent need for minimally invasive, robust, and broadly applicable diagnostic approaches.
Liquid biopsy has emerged as a promising alternative, enabling the detection of tumor-derived molecular signals from peripheral blood. **Circulating tumor DNA (ctDNA)**, released during

apoptosis and necrosis of malignant cells, carries biologically informative fragmentation patterns that reflect tumor-specific chromatin organisation and epigenetic regulation. Fragmentomic features, including fragment size distributions, genomic positioning, end motifs, and nucleosome footprinting, have been shown to differ systematically between cancer-derived and non-malignant circulating DNA. Importantly, these features provide complementary information to sequence-based alterations and support accurate inference of tissue of origin.

Advances in high-throughput sequencing and computational analysis have facilitated the integration of machine learning techniques for fragmentomic profiling. Supervised learning models, including ensemble methods and deep neural networks, have demonstrated high sensitivity for cancer detection, including early-stage disease across multiple cancer types. In several studies, fragmentomics-based approaches have outperformed mutation- and methylation-centric assays in detecting stage I malignancies while maintaining clinically acceptable specificity.

In this review, we synthesise recent developments in circulating DNA fragmentomics and evaluate machine learning frameworks applied to early cancer screening. We further discuss analytical challenges, clinical translation considerations, and the potential of fragmentomics-driven liquid biopsy to address existing gaps in cancer screening. Collectively, these advances position ctDNA fragmentomics as a compelling biomarker platform for scalable, non-invasive multi-cancer early detection.

Keywords: Circulating tumor DNA, fragmentomics, liquid biopsy, early cancer screening, machine learning

ICABB26-MOC-P45

Computational Integration of Multi-Omics Data Using Deep Learning for Human Disease Analysis

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Abstract

The pathogenesis of complex human diseases does not arise from a single molecular alteration but from interactions across multiple biological layers, which was failed to explain by single omics analysis. Multiomics integration provides a system level view of disease mechanism underlying human health and diseases particularly in context of environmental exposures. However effective integration of multiomics remains challenging due to heterogeneity, high dimensionality , missing values and complex non linear interactions. While the utility of assessing multi-omics data is clear, the integration of all the single omic data poses significant computational challenges that range from the need for developing statistical methods that are appropriately adapted to multi-omics integration, to the need for providing comprehensive open source resources that provide validated relationships between omics types, biological pathways, and diseases.

Data from single omics is typically transformed so that they follow a Gaussian or "Normal" distribution, which is commonly used for statistical analyses. Importantly, as some analyses will not work on missing data, missing values can be imputed. One can analyze or model each omic modality separately and then integrate results (a posteriori integration) or one can integrate data for all omic modalities before any statistical or computational modeling. Large-scale public databases including GEO, ENCODE, KEGG, and Reactome further support integrative analyses by providing well-annotated multi-omics and disease-related datasets.

Integration of multiple omics data is invaluable for comprehensively understanding causal relationship between environmental exposure and environmental health. Furthermore, cohort based multi-omics studies are in activation worldwide and the approaches could strengthen comprehension on how environmental factors affects human health by alteration of molecular level of biological mechanisms.

The development of sophisticated AI and deep learning models is crucial for handling the high dimensionality and complexity of multi-omics data, improving prediction accuracy and interpretability, aiming to unfold the multi layer biological system and integrate it to combat key challenges and stepping into a futuristic biological world.

Keywords: Multiomics, deep leaning, Disease analysis, KEGG, health.

ICABB26-MOC-P46

Deciphering the role of MYC Gene Variants in Childhood Cerebral Adrenoleukodystrophy (ccALD) using Integrative Transcriptomic and Variant Analysis

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Abstract

Childhood cerebral adrenoleukodystrophy (ccALD) is a severe neurodegenerative disorder involving rapid demyelination and blood–brain barrier (BBB) breakdown. Although mutations in the ***ABCD1*** gene are known to cause the disease, downstream molecular mechanisms remain unclear. This study aimed to identify key regulatory genes and functional variants contributing to ccALD pathology using an integrative multi-omics approach. RNA sequencing (RNA-Seq) data from **brain microvascular endothelial cells (BMECs)** of ccALD patients and healthy controls were analyzed to identify differentially expressed genes. Gene network analysis was performed in **Cytoscape** to determine major hub genes. Variant calling followed the **GATK Best Practices pipeline**, including preprocessing, alignment, base quality recalibration, variant identification, and annotation using **GATK Funcotator.** Differential expression analysis revealed **1,039 upregulated** and **744 downregulated** genes in ccALD BMECs. Network analysis identified **MYC** as the top hub gene, indicating its central involvement in disease-associated molecular pathways. Variant analysis detected two mutations within the MYC gene: **rs2130098148 (C>A)** causing a **missense mutation**, and **rs2130107263 (A>T)** causing a **stop-gain mutation**. Both variants were associated with the **MAPK signaling pathway**, suggesting functional impairment of MYC. The integrative transcriptomic and variant analysis demonstrates dual disruption of **MYC** at both expression and genetic levels in ccALD. These findings support MYC as a potential modifier gene contributing to BBB dysfunction and neuroinflammation. This multi omics approach provides valuable insights into the molecular mechanisms underlying ccALD and identifies MYC as a promising therapeutic target.

Keywords: ccALD, MYC, RNA-Seq, variant analysis, MAPK, FOS

ICABB26-MOC-P47

Integrating Multi-Omics and Artificial Intelligence for Drug Discovery and Biomarker Prediction in Hematological Cancers

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Abstract

Hematological cancers like leukemia, lymphoma and multiple myeloma are one of the leading contributors to global cancer morbidity and mortality. The course of disease progression and therapeutic responses for such malignancies is due to complex and heterogenous molecular alterations. Despite several developments in molecular profiling, the biological complexity of these cancers is still not understood completely. Consequently, limiting biomarker discovery and drug development. In the past, single-omics approaches have provided some insight, but failed to give information about the multiple regulatory networks that control the disease initiation, progression and drug resistance. Modern developments in high throughput and omics methodologies allow the integration of genomic, epigenomic, transcriptomic, proteomic and metabolomics of blood malignancies. But the large size of such datasets requires improved methods. In recent times, Artificial intelligence (AI), particularly machine learning and deep learning methods have helped to recognize molecular patterns. AI-driven multi-omics frameworks allow the detection of disease subtype, prognostic biomarker identification, therapeutic target discovery and drug response prediction. Studies indicate that such integrated models have the ability to record interactions between the molecular pathways in a better way, thus improving accuracy. Network-based and graph based approaches have facilitated to build a stronger foundation for precision drug discovery and personalised therapeutic decision making. However, despite their

promise, challenges such as data heterogeneity, limited patient group sizes, lack of interoperability as well as poor standardization still exist, making clinical implementation difficult. Strategies like standardized multi-omics pipelines, explainable AI and large scale validation studies are expected to overcome these challenges in the future. This study highlights the need of the combination of multi-omics with AI for drug discovery and biomarker prediction in hematological cancers, marking a major step towards precision oncology.

Keywords: Hematological cancers, multi-omics integration, artificial intelligence, drug discovery, precision oncology**.**

ICABB26-MOC-P48

Molecular Docking and Dynamics Simulation of Phytochemicals as Potent Inhibitors of EGFR- Mutant Lung Cancer

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Abstract

Drug resistance to tyrosine kinase inhibitors (TKIs) is a major challenge in treating Epidermal Growth Factor Receptor (EGFR)-mutant lung cancer. This study explores the therapeutic potential of natural phytochemicals derived from medicinal plants as alternative inhibitors of mutant EGFR proteins. Using a structure-based drug design approach, we screened a library of bioactive compounds against the crystal structure of EGFR containing the T790M resistance mutation. Molecular docking studies were performed to evaluate binding affinities, identifying several high-potency phytochemicals that exhibit stronger binding energies than standard inhibitors like Gefitinib. To validate the stability of these ligand-protein complexes, we conducted 100 ns Molecular Dynamics (MD) simulations. The results analyzed Root Mean Square Deviation (RMSD) and Root Mean Square Fluctuation (RMSF), confirming that the identified phytochemicals maintain stable conformations within the active site of the mutant protein. This research highlights the efficacy of computational tools in repurposing traditional knowledge for modern oncology. The identified natural compounds offer a promising foundation for developing novel, low-toxicity adjuvant therapies for drug-resistant lung cancer, aligning with the principles of integrative health and AYUSH-based innovations.

Keywords: Molecular Docking, Phytochemicals, EGFR Mutation, Lung Cancer, MD Simulation, Drug Discovery, Natural Bioactive

ICABB26-MOC-P49

Decoding the Multi-Target Mechanism of *Curcuma longa* in Lung Cancer Treatment: An Integrated Network Pharmacology and Molecular Docking Approach

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Abstract

Traditional AYUSH systems have long utilized Curcuma longa (Turmeric) for its therapeutic properties, yet the complex molecular mechanisms underlying its efficacy in lung cancer remain partially understood. Unlike conventional "one-target, one-drug" paradigms, traditional formulations often act synergistically on multiple biological pathways. This study employs a systems biology and network pharmacology framework to map the interaction network between bioactive compounds of C. longa and lung cancer-associated targets.

We retrieved active phytochemicals from public databases and predicted their potential gene targets using SwissTargetPrediction. Simultaneously, lung cancer-related disease targets were collated from the GeneCards and OMIM databases. The intersection of these datasets revealed 42 common core targets. We constructed a Compound-Target-Pathway network using Cytoscape, which highlighted key hub genes, including TP53, AKT1, and EGFR. Gene Ontology (GO) and KEGG pathway enrichment analyses indicated that these bioactive primarily modulate the PI3K-Akt signaling pathway and

apoptosis regulation. To validate these network predictions, molecular docking was performed, demonstrating that the primary bioactive, Curcumin, exhibits high binding affinity (-8.9 kcal/mol) with the EGFR mutant protein, surpassing standard inhibitors. This study provides scientific validation for the holistic nature of AYUSH-based therapies, offering a robust, data-driven rationale for using *C. longa* derivatives as multi-target agents in integrative lung cancer management.

Keywords: Network Pharmacology, Lung Cancer, *Curcuma longa*, Systems Biology, Molecular Docking, AYUSH, Multi-Target Therapy

ICABB26-MOC-P50

In-Silico Identification and Validation of Prognostic Biomarkers for Early-Stage Non Small Cell Lung Cancer (NSCLC)

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Abstract

Non-small cell lung cancer (NSCLC) accounts for approximately 85% of lung cancer cases and remains the predominant cause of cancer mortality worldwide, with survival rates critically dependent upon early detection and prognostic stratification. Despite advances in molecular oncology, the paucity of robust, clinically actionable biomarkers for early-stage disease necessitates comprehensive genomic interrogation to identify novel prognostic determinants. This study integrates multi-dimensional bioinformatics approaches to elucidate differentially expressed genes (DEGs) underlying NSCLC progression and their prognostic significance. Leveraging high-throughput RNA-sequencing datasets from The Cancer Genome Atlas (TCGA) and Gene Expression Omnibus (GEO), we performed rigorous differential expression profiling, identifying 847 significantly dysregulated genes (adjusted $p < 0.05$, $|\log2FC| > 1.5$). Systems-level functional enrichment analyses revealed profound enrichment in cell cycle checkpoint regulation, p53-mediated apoptotic signalling, and DNA damage response pathways, implicating these molecular circuits in NSCLC pathogenesis. Protein-protein interaction network topology analysis identified 15 hub genes exhibiting centrality metrics indicative of driver roles in tumour evolution. Kaplan-Meier survival analyses stratified by gene expression quartiles demonstrated that elevated expression of candidate biomarkers correlated significantly with diminished overall survival (log-rank $p < 0.001$, HR = 2.34, 95% CI: 1.87–2.93), establishing their prognostic validity. This computational framework advances precision oncology by identifying biologically validated targets amenable to therapeutic intervention while providing a cost-effective paradigm for translational biomarker discovery. These findings harbor substantial clinical implications for risk stratification algorithms and personalized therapeutic decision-making in early-stage NSCLC management.

Keywords: Non-small cell lung cancer, computational genomics, prognostic biomarkers, differential gene expression, survival analysis, systems biology, precision oncology

ICABB26-MOC-P51

From Simplicity to Synergy: The Evolving Landscape of Prosthetic Technologies

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Abstract

The development of prosthetic limbs has progressed through distinct technological phases, transitioning from basic structural aids to intelligent, neuroresponsive systems. Conventional prostheses are broadly categorized as passive serving cosmetic or supportive roles without powered movement and active, which utilize body-driven or externally powered mechanisms to restore limited functionality. While such devices have historically addressed essential mobility needs, they often lack precision, adaptability, and user feedback. The introduction of advanced active systems, such as myoelectric prostheses, marked a significant leap forward by allowing users to control limb movement through electromyographic signals. Yet, these systems still rely on indirect inputs and provide minimal sensory

integration. The latest generation of prosthetic limbs leverages brain–machine interfaces (BMIs), enabling direct neural control and real-time bidirectional communication between the nervous system and the device. These neurocontrolled systems offer not only improved movement precision but also reintroduce sensory perception and user embodiment. This progression—from mechanical constructs to cognitively integrated systems underscores a multidisciplinary convergence of neuroscience, engineering, robotics, and AI, opening new possibilities in restoring autonomy and redefining human–machine interaction.

Keywords- Myoelectric Control, Neuroprosthetics, Brain–Machine Interface, Sensorimotor Integration, Neural Interfaces, Human–Machine Communication, Cognitive Embodiment.

ICABB26-MOC-P52

Single-Cell RNA-seq Identification of Drug-Resistant Subclones in EGFR-Mutant Lung Adenocarcinoma

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Abstract

Epidermal growth factor receptor (EGFR) mutant lung adenocarcinoma initially responds well to EGFR tyrosine kinase inhibitors (TKIs); however, the inevitable emergence of drug resistance remains a major clinical challenge. Conventional bulk sequencing approaches obscure intratumoral heterogeneity and fail to detect rare resistant subclones that drive disease progression. Understanding the cellular and transcriptional basis of resistance at high resolution is critical for improving therapeutic outcomes in EGFR-mutant lung cancer patients.

In this study, single-cell RNA sequencing (scRNA-seq) was employed to profile tumor samples from EGFR-mutant lung adenocarcinoma patients before and after TKI treatment. Unsupervised clustering and differential gene expression analyses were used to identify distinct tumor cell subpopulations. This approach revealed rare drug-resistant subclones characterized by unique transcriptional programs, including activation of epithelial-to-mesenchymal transition, altered metabolic pathways, and upregulation of survival and stress-response genes. Additionally, ligand–receptor interaction analysis highlighted altered communication between resistant tumor cells and the tumor microenvironment, suggesting a supportive niche for resistance development.

Overall, this single-cell–based analysis provides critical insights into the cellular heterogeneity underlying EGFR-TKI resistance. Identification of transcriptional signatures specific to resistant subclones offers potential biomarkers for early detection of therapeutic failure and reveals novel targets for combination treatment strategies. These findings demonstrate the power of single-cell transcriptomics in uncovering clinically relevant tumor evolution and advancing precision oncology in lung adenocarcinoma.

Keywords : Single-cell RNA sequencing; Lung adenocarcinoma; EGFR mutations; Drug resistance; Tumor heterogeneity

ICABB26-MOC-P53

Exploration of *Saccharomyces boulardii* as a biocontrol agent against *Fusarium oxysporum*

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Abstract

Fusarium oxysporum is a toxin-producing plant pathogen that causes vascular wilt. Earlier, bioactive compounds *Saccharomyces boulardii* showed significant inhibition of *Aspergillus flavus* in a culture assay at ration 20:1 (*Saccharomyces boulardii*: *Aspergillus flavus*). During co-culturing of *S. boulardii* with *A. flavus* (20:1), a total of 23 extracellular metabolites were identified. On analysis, bioactive compounds showed antimicrobial and antioxidant properties. In the current study, co-culture

analysis of *Saccharomyces boulardii* with *Fusarium oxysporum* on PDA at 30˚C was performed at various ratios (1:1, 5:1, 10:1, 15:1, 20:1, 25:1). A higher ratio of *S. boulardii* against *F. oxysporum* (25:1) showed prominent inhibition. Secondary metabolite extraction using chloroform of co-culture (*S. boulardii* : *F. oxysporum*, (25:1)) and both *Fusarium oxysporum* and *S. boulardii* alone was performed. Samples were further subjected for nLCMS analysis. Secondary metabolite data analysis may reveal the potential virulent factor or the potential of bioactive compound from *S. boulardii* as a control against plant fungal pathogen.

Keywords-*Fusarium oxysporum*; *Saccharomyces boulardii*; biocontrol; co-culture; probiotic yeast; gene expression analysis.

Session 3:
Multi-Omics Approaches and AI in Biotechnology
Oral Presentations

ICABB26-MOC-OP01

Bioprocess Parameters Optimization for DHA Production from *Schizochytrium sp*.

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Docosahexaenoic acid (DHA; C22:6 n-3) is a highly vital long-chain omega-3 fatty acid associated with cardiovascular health, the control of inflammation, neurodevelopment, and visual function. Concerns about sustainability and the rising demand for DHA derived from fish oil underscore the need to explore alternative sources. The unicellular algae *Schizochytrium* sp. have emerged as a potential source of interest, gaining scientific attention due to their ability to produce fatty acids rich in DHA under regulated abiotic culture conditions.

The current study investigates the impact of culture conditions on Schizochytrium sp. to optimize key bioprocess parameters, with the goal of maximizing DHA productivity. Carbon substrates, nitrogen sources (yeast extract), pH, aeration rate, salinity, and cultivation time were evaluated for their effects on biomass formation, lipid accumulation, and DHA yield using a systematic Design of Experiments (DoE) framework. Carbon-rich, readily metabolizable substrates significantly enhance lipid biosynthesis, according to preliminary cultivation studies, while pH modulation and controlled aeration increase metabolic flux through the PKS pathway. One crucial factor that affected the formation of unsaturated fatty acids and cell growth was the availability of oxygen. Lipid profiling analysis and growth kinetics were used to measure the amount of DHA produced under each ideal circumstance.

The study also suggests a productive downstream approach that combines solvent extraction, cell disruption, and purification processes to produce high-purity DHA appropriate for nutraceutical uses. All things considered, this study shows that microbial DHA productivity can be significantly increased by carefully adjusting the media composition and fermentation conditions. The results enable the production of DHA in an economical, scalable, and environmentally sustainable manner, aligning with the objectives of the global bioeconomy and the industrial demand for premium omega-3 fatty acids.

Keywords: Schizochytrium sp.; Docosahexaenoic acid (DHA); Bioprocess optimization; Heterotrophic fermentation; Polyunsaturated fatty acids (PUFAs)

ICABB26-MOC-OP02

AI-Assisted Discovery Platform for Rapid Identification of Repurposed Therapeutics Against ESKAPEE Pathogens

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Abstract:

Antimicrobial Resistance (AMR) is a pressing global health threat, propelled by drug misuse. The ESKAPEE pathogens (*E. faecium, S. aureus, K. pneumoniae, A. baumannii, P. aeruginosa, Enterobacter spp.*, and *E. coli*) are multidrug-resistant bacteria causing hospital-acquired infections and listed by WHO as priority pathogens. Among them, *A. baumannii*, *P. aeruginosa*, and *Enterobacteriaceae* are categorized as severe threats to public health. They evade resistance through mechanisms like beta-lactamase production, alteration of drug targets, and active efflux pumps, resulting in increased mortality and healthcare burden. Traditional *in vitro* and *in silico* workflows for antimicrobial discovery are time consuming, resource-intensive, and dependent on multidisciplinary expertise, underscoring the need for rapid, scalable alternatives. To address these limitations, we

targeted ESKAPEE pathogens with AI
powered approaches, predictive screening, and rational design for novel/repurposed antimicrobial agents that can significantly accelerate analysis of high-priority target identification and expeditious drug candidate evaluation. Our platform integrates a curated database of ESKAPEE targets into a predictive ML engine, deriving efficacy metrics from molecular structures (PDB, SMILES, SDF) with an AI-powered RAG (Retrieval Augmentation and Generation) interface that presents predictions with supporting evidence from with evidence from literature and experimental datasets. By fine-tuning the AI engine specifically on ESKAPEE-focused datasets and coupling it with a bespoke ML predictor, the platform significantly mitigates hallucination and enhances analytical reliability—addressing the limitations of earlier binary decision frameworks such as the Stokes model and RAG2MOL. This web-based platform enables real-time, high-throughput virtual screening of novel and repurposed antimicrobial candidates. Its integrated AI/ML engine rapidly prioritizes targets, predicts activity, and evaluates chemical scaffolds, accelerating the discovery of next-generation therapeutics against ESKAPEE pathogens and strengthening AMR surveillance.

Keywords: Antimicrobial Resistance, ESKAPEE Pathogens, Drug Discovery, AI /ML, Retrieval Augmentation and Generation (RAG), Therapeutic Screening

ICABB26-MOC-OP03

Multi-Omics Identification of VAV Proteins as Therapeutic Targets in Atherosclerosis: From Network Biology to Experimental Validation

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Abstract

Atherosclerosis, the leading cause of cardiovascular mortality, is a chronic inflammatory disease driven by dysregulated immune signalling and cytoskeletal remodelling. The VAV family of guanine nucleotide exchange factors (VAV1, VAV2, VAV3) integrates immunoreceptor, PI3K, and Rho-GTPase pathways, yet their isoform-specific contributions in human lesions remain poorly characterised. We conducted an integrative omics analysis combining literature synthesis (2010–2024), high confidence protein–protein interaction networks (STRING v12.0, confidence ≥0.70/0.90), and differential expression across four GEO cohorts: carotid atheroma vs. intact tissue (GSE43292), circulating immune subsets (GSE9820), plaque macrophages (GSE41571), and whole blood from CAD patients (GSE20681).

STRING networks positioned all VAV isoforms as central hubs linking immune adaptors (SYK, ZAP70, LCP2), PI3K subunits (PIK3R1/PIK3CA), and Rho GTPases (RAC1, CDC42, RHOA), with highly significant enrichment in T/B-cell receptor signalling, FcγR-mediated phagocytosis, and cytoskeletal regulation (FDR < 10^{-30}). Transcriptomic profiling revealed a striking lesion-centric dysregulation pattern: robust upregulation of VAV1 ($log_2FC = 0.72$, FDR = 2.7×10^{-6}) and VAV3 ($log_2FC = 1.03$, FDR = 3.0×10^{-6}) in carotid atheroma, macrophage-biased VAV3 elevation in circulating immune cells, modest trends in ruptured plaque macrophages, and near-null changes in whole blood — establishing a clear spatial hierarchy. Given VAV2's non-redundant role in CD36-mediated oxLDL uptake and foam-cell formation, we performed structure-based virtual screening of >13,000 FDA-approved/investigational compounds against its catalytic DH domain (AlphaFold model). Hits were refined by docking, ADME filtering, 100 ns MD simulations, MM-PBSA, and PCA. Experimental validation in PMA-differentiated THP-1 macrophages showed that lead repurposed

compound Talazoparib significantly suppressed oxLDL-induced foam-cell formation, achieving a 2.24-fold reduction in lipid accumulation (Oil Red O staining, $p < 0.0001$) at sub-cytotoxic concentrations (IC50 = 0.133 μM, MTT assay). This integrated systems biology approach establishes VAV proteins as central signalling hubs with lesion-specific dysregulation in human atherosclerosis and provides proof-of-concept that VAV2 is a druggable anti-atherogenic target amenable to rapid repurposing.

Keywords: VAV2; Drug repurposing; Molecular docking; Foam cells; Atherosclerosis

ICABB26-MOC-OP04

Exome-based investigation in Indian ulcerative colitis patients identifies previously unreported genes affecting epithelial barrier integrity, DNA repair, vesicle trafficking, and immune signalling

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Abstract

Despite extensive genome-wide association studies, a substantial portion of ulcerative colitis (UC) heritability remains unexplained, particularly in non-European populations. This study aimed to investigate the contribution of rare and common coding variants to UC predisposition in an Indian population. Whole-exome sequencing was performed in 160 UC patients and 379 ethnically matched controls. Gene-based burden tests were conducted using the CMC and SKAT-O methods to identify genes enriched for rare coding variants in UC. Exome-wide common variant association testing was performed using KGGSeq VarAssoc module. A total of 89 previously unreported genes ($P < 0.05$) showed a significant excess of rare variants in UC, consistently detected by both CMC and SKAT-O analyses. The top 22 genes ($P_{CMC} \leq 5X10^{-3}$ OR 2.2-10.91) included notable candidates involved in epithelial integrity, immune signalling, DNA repair, and vesicle trafficking. Exome-wide association analysis further identified 55 variants (in 46 previously unreported genes) surpassing the Bonferroni-corrected threshold ($P_{allelic} \leq 5.57X10^{-7}$), with 36 protective and 16 conferring risk. Most of these genes mapped to functional categories similar to those observed in the burden analysis. STRING network analysis revealed functional interactions between seven novel unreported genes and established inflammatory bowel disease associated genes. Notably, a significant number of novel genes were found to be differentially expressed in colonic and whole blood tissue-based expression studies of UC patients. This first exome-wide study from an Indian population expands the known genetic landscape of UC and highlights population-specific disease mechanisms, likely driven by unique gene-environment interactions. Identification of these previously unreported genes in other molecular datasets along with their functional significance provides strong preliminary evidence of their role in disease biology and generates testable hypotheses for functional validation. In addition, these results open avenues to explore population-specific pathways, identify potential therapeutic targets, and AI-ML based integrative analyses combining genetic/other molecular data and clinical information to stratify patients into distinct molecular subtypes.

Keywords: Ulcerative colitis; Rare variant; Gene burden; Exome sequencing, Exome wide association testing

ICABB26-MOC-OP05

From Interaction Networks to Intervention: Identifying Critical Genes and Targets in Sudden Cardiac Arrest

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Abstract

Sudden cardiac arrest (SCA) is a leading cause of global mortality, increasingly affecting younger individuals. In India, cardiovascular diseases account for approximately 28–30% of all deaths, and within the younger age group (18-44 years), of which 17% of cardiovascular deaths remain unexplained, highlighting a critical gap in diagnosis and underlying cause identification. In the current study, we identified top known causes of SCA and further compiled associated genes from multiple sources and generated a protein–protein interaction (PPI) network. Sub-network and functional enrichment analyses identified key hub genes which are critical for regulation of heart rate and muscle contraction. These hub genes will be useful in identifying molecular mechanisms of SCA and offers promising opportunities for developing early diagnostic biomarkers, personalized risk-stratification tools, and novel therapeutic drug targets.

Keywords: Arrythmias, Cardiomyopathies, Cardiovascular diseases, Hypertrophic cardiomyopathy, Sudden cardiac arrest

ICABB26-MOC-OP06

In Silico Interactions of Selected PPCPs With Biological Systems

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Abstract:

Personal care products (PCP), along with pharmaceuticals, belong to a wider group of pollutants known as pharmaceuticals and personal care products (PPCPs). Pharmaceuticals and personal care products (PPCPs) have emerged as a significant group of micropollutants in the environment, as they are widely used in daily life and frequently detected in aquatic systems worldwide. India's personal care sector is rapidly expanding, with shampoos, soaps, lotions, and cosmetics being widely consumed in both urban and rural areas. These everyday-use products are an important source of pharmaceuticals and personal care products (PPCPs) released into the environment. PPCPs such as, estradiol and clotrimazole have gained attention as significant environmental contaminants due to their persistence and bioactivity across ecosystems. To evaluate their possible toxicity and bioaccumulation it is important to understand how these PPCPs interact with proteins from algae, plants, and humans at the molecular level. The purpose of this work is to find interaction of these PPCPs with proteins from plants, algae, and humans using docking analysis. CB-Dock 2 platform was used to perform docking simulations. The interactions were predominantly stabilized through hydrophobic contacts and hydrogen bonding, with subtle variations influenced by differences in protein conformation and binding site characteristics. The results indicate that PPCPs can effectively interact with proteins across biological kingdoms, providing molecular-level evidence of their potential to interfere with essential biochemical pathways and

contribute to ecological and health-related risks.

Keywords: PPCPs, docking, estradiol, clotrimazole,CB-Dock2.

ICABB26-MOC-OP07

Carrier Screening and Molecular Profiling of β-thalassemia among Youths in Delhi NCR.

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ABSTRACT

β-thalassemia is an autosomal recessive disorder with a 25% chance of inheriting the affected gene when both parents are carriers. With a nationwide prevalence of 3-4%, it causes significant health challenges. The deficit in public education has perpetuated unawareness of the disorder among the majority of the population. This study focuses on screening and molecular profiling of β-thalassemia among youth in Delhi NCR to reduce its impact on the community. After obtaining informed consent and conducting a survey, 2 mL of peripheral blood was collected, a Complete Blood Count was performed, and HbA2 levels were measured for suspected cases. Sequencing and variant analysis were carried out for cases with elevated HbA2 levels. A total of 2,269 youths (38.9% male, 61.1% female) from 16 colleges were screened between 2023-2025, with 146 (6.4%) suspected carriers and 47 (2.1%) confirmed carriers. This study identifies IVS1:5(G>C) (42.5%) as the most common variant, followed by Cd 41/42(-TCTT) (14.9%), Cd26 (G>A) (10.6%), and nine other less frequent variants, emphasizing the importance of early screening and awareness to lower the prevalence of β-thalassemia in the population, while also compiling variant data to help build targeted diagnostic panels and improve precision in detecting the disorder.

Keywords: Awareness, β-thalassemia, Carrier screening,, Molecular profiling, Variant.

ICABB26-MOC-OP08

Decoding India's Recurrent β-Thalassemia Variants: A Geo-Genomic Meta-Analytic Study

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Abstract

Thalassemia remains India's primary genetic health concern, characterised by significant regional, ethnic, and genetic diversity that shapes its variant profile. Of the over 80 known variants in India, a few recurrent ones account for the majority of cases. Despite numerous region-specific molecular studies, prevalence data remain fragmented, creating a gap in national-level evidence. This systematic review and meta-analysis aimed to determine the pooled prevalence, heterogeneity, and regional differences of eight common variants across India. Following PRISMA guidelines, data were extracted from databases such as PubMed, ScienceDirect, ResearchGate, Google Scholar, IMSEAR, Semantic Scholar, and Web of Science, from January 1, 2000, to August 31, 2025. Data screening was conducted using Rayyan Software, and a random-effects meta-analysis for pooled prevalence, along with regional

subgroup analysis, was performed in R Studio. The protocol was registered in PROSPERO (registration no: CRD420251005863). The analysis included 40 studies from 15 data sources, involving 65,032 individuals. The IVS1:5(G>C) variant (59% [95% CI 0.53-0.64]) was most common nationwide, with the highest frequency in the eastern region (73%). Other variants contributed 619 del (7% [95% CI: 0.04-0.12]), Cd15(G>A) (6% [95% CI: 0.05-0.08]), Cd41/42(-TCTT) (5% [95% CI: 0.04-0.06]), Cd8/9(+G) (4% [95% CI: 0.02-0.06]), IVS1:1(G>T) (4% [95% CI: 0.03-0.07]), Cd30(G>C) (4% [95% CI: 0.03-0.05]), and Cd26 (2% [95% CI: 0.01-0.10]) among all variants nationwide. 619 del, Cd41/42(-TCTT), Cd8/9(+G), and IVS1:1(G>T) were regionally restricted to the north and west, Cd15(G>A) to the south and west, and Cd26(G>A) to the east, while Cd30(G>C) showed consistent distribution across regions. Most studies exhibited significant heterogeneity (I^2), reflecting intraregional genetic variations. Using variant-specific pooled frequencies, this study highlights the genetic mosaicism of thalassemia in India, shaped by region-specific variants, limited gene flow, and the historical founder effect, emphasising the need for targeted, region-specific screening and preventive strategies.

Keywords: Mutation spectrum; meta-analysis; beta thalassemia mutations; variants.

ICABB26-MOC-OP09

Biohydrogen production from starchy agro-residues by Clostridium *beijerinckii* G117

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Abstract

The growing demand for renewable energy has increased interest in biological hydrogen production from agro industrial residues. This study examined rice, wheat, and oat brans as sustainable substrates for fermentative biohydrogen production. Proximate analysis and mild acid hydrolysis released substantial fermentable sugars, with wheat bran yielding the highest (33.46 g/L). Four *Clostridium* strains were evaluated, of which *C. beijerinckii* G117 exhibited the most versatile sugar utilization, efficiently fermenting glucose, maltose, xylose, and starch mixtures to produce up to 1450 mL/L hydrogen.Acid hydrolysates supported robust sugar fermentation (maximum 2900 mL/L H_2), but starch conversion was limited by phenolic inhibitors. Remarkably, direct fermentation of untreated brans stimulated amylase and xylanase production, enabled complete sugar assimilation, and yielded record volumetric hydrogen levels—up to 4100 mL/L from wheat bran. The process showed high efficiency, with molar yields of 0.93–1.08 mol/mol glucose equivalent and overall mass/electron recoveries exceeding 89% across all brans.These findings establish *C. beijerinckii* G117 as a promising biocatalyst for hydrogen generation from minimally processed agro-residues. The results highlight the feasibility of low-input, high-yield bioprocessing, contributing both to waste valorization and the advancement of clean, scalable biohydrogen energy solutions.

Keywords Starchy waste, Agro-residues, Consolidated bioprocessing, Biohydrogen, *Clostridium beijerinkii*, Biomass valorization, One-pot fermentation

ICABB26-MOC-OP10

In silico Characterization, Biochemical Assays and *in vitro* Analysis of Ayurvedic Plants against Diabetic Cardiomyopathy and Hypertrophy

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Abstract

Cardiovascular diseases (CVDs) are the foremost cause of mortality globally, necessitating the exploration of safer and multi-target therapeutics. This study integrates classical Ayurvedic wisdom with contemporary biomedical methodologies to identify and evaluate potential herbal candidates for myocardial infarction. Based on Ayurvedic doctrines emphasizing holistic restoration, five botanicals: *Terminalia arjuna*, *Camellia sinensis*, *Rosa indica*, *Coffea arabica*, and *Elaeocarpus ganitrus*; were investigated for their cardioprotective potential. A multidisciplinary approach encompassing literature mining, in silico network pharmacology, molecular docking, and experimental validation was employed to elucidate interactions between plant-derived phytochemicals and critical CVD-related proteins such as MMP9, MMP2, CRP, PLG, and VTN.

A 50-protein cardiovascular network was constructed using the STRING database and analyzed via Cytoscape to identify essential hub proteins. Docking analyses performed in PyRx and Biovia Discovery Studio revealed that several phytochemicals exhibited strong binding affinities, surpassing standard reference drugs like aspirin. ADMET and toxicity profiling confirmed their favorable pharmacokinetic and safety properties. Experimental investigations, including phytochemical screening, antioxidant assays (DPPH and ABTS), and cell viability assessments on H9c2 cardiomyocytes, demonstrated significant antioxidant capacity and cytoprotective effects under stress conditions.

Overall, the findings suggest that integrating Ayurvedic pharmacological insights with modern computational and experimental tools can accelerate the discovery of effective, safe, and holistic cardioprotective agents. This research underscores the relevance of traditional knowledge systems in guiding innovative therapeutic development for chronic and lifestyle-associated cardiovascular disorders.

Keywords: Ayurveda, MMP-9, MMP-2, PLG, CRP, VTN, Terminalia arjuna, Camellia sinensis, Rosa indica, Coffea arabica, and Elaeocarpus ganitrus

ICABB26-MOC-OP11

AI-Driven Drug Discovery: Accelerating Innovation through Machine Learning

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Abstract:

Artificial Intelligence & Machine Learing (AI-ML) is a core part of the modern drug discovery pipeline. ML is used to identify proteins responsible for unknown disease phenotypes by detecting possible associations between proteins and phenotypes resulting from their dysfunction, utilising reference data (via Graph Neural Networks, Random Forests, Bayesian networks, and multi-task deep neural networks). The possible proteins are traced back to parent genes using genomics and studied through proteomics in parallel to identify the cause of dysfunctionality, whether due to gene mutations or post-translational defects such as misfolding (using CNN-based effect predictors and transformer models

like ProtBERT and ESM). AI-ML models are again used to trace the entire biochemical pathway of the targeted protein to establish whether it is central or peripheral, upstream or downstream (using pathway-level Graph Neural Networks and network propagation models). As a principle, targeting central and upstream areas is preferred, as it leads to better disease regression and avoids pathway compensation. Once the target protein is finalised, target site data—such as geometry and ligands—are fed to AI models (using protein structure prediction models like AlphaFold and 3D convolutional neural networks), which perform virtual screening to generate an optimised list of hits with good binding affinity while removing toxic candidates (using deep docking models, GNN-based interaction predictors, and QSAR models). This saves a significant amount of time compared to HTS used in classical drug discovery. These hits then undergo laboratory testing through chemical assays. AI models use data from these tests to recommend lead optimisation to improve potency, ADME properties, and reduce toxicity (using reinforcement learning, genetic algorithms, variational autoencoders, and multi-objective optimisation models). Once optimised, leads enter preclinical trials on animal cell cultures and models. Preclinical data are used to determine safe human dosage ranges and common side effects (using ADMET prediction models and Bayesian neural networks). After passing preclinical testing, they enter clinical trials in three to four phases, after which the lead becomes a certified drug. Thus, AI-ML transforms traditional drug discovery into a faster, more efficient, and data-driven process with higher chances of therapeutic success.

Keywords: Artificial Intelligence and Machine Learning; Target Identification; Virtual Screening; Lead Optimisation; ADME Properties

ICABB26-MOC-OP12

Computational Discovery of Plant-Based Regulatory Networks in Lung Cancer

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Abstract

Lung cancer remains the leading cause of cancer mortality, highlighting the need for new therapies. Phytochemicals show anticancer potential via microRNA–transcription factor modulation, but knowledge is fragmented. This study used AI-assisted literature mining and network pharmacology to consolidate evidence and build a framework for targeted botanical interventions in lung cancer.

Systematic literature retrieval was performed using PubMed's AI-enhanced search algorithms, screening publications from 2015 to 2024 that documented phytochemical– microRNA–transcription factor interactions in lung cancer contexts. Approximately 50 bioactive compounds, including curcumin, resveratrol, epigallocatechin-3-gallate, and quercetin, were analyzed for their regulatory effects on lung cancer–associated microRNAs (miR-21, miR-34a, and the let-7 family) and transcription factors (NF-κB, AP-1, HIF-1α, β-catenin, and p53). Network construction and topological analyses were conducted using Cytoscape, while pathway enrichment analyses were performed using STRING and KEGG databases.

The systematic integration identified approximately 280 experimentally validated molecular interactions spanning mechanisms of proliferation, apoptosis, metastasis, and drug resistance. Centrality analyses revealed multi-targeting phytochemicals exhibiting synergistic regulatory potential. Critical knowledge deficits were identified in areas related to bioavailability optimization, lung-specific delivery mechanisms, and clinical translation paradigms. This computational framework provided mechanistic rationale for designing multi-component phytotherapeutic formulations targeting central regulatory nodes in lung cancer, thereby facilitating the transition from empirical to precision-guided

botanical medicine.

Keywords: Lung cancer, phytochemicals, microRNA networks, transcription factors, network pharmacology, precision oncology, botanical therapeutics

ICABB26-MOC-OP13

Integrated Bioinformatics and Experimental Validation of Shared Genetic Targets in AKI and Ovarian Cancer for Phytocompound-based Therapeutics

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Abstract

Ovarian cancer is the most lethal and common malignancy among women, patients with ovarian cancer are more subjected to Acute Kidney Injury due to two reasons disease and therapeutics. Tumour burden and metastasis can cause obstruction or direct invasion of the urinary tract, impairing renal function. Moreover, cytoreductive surgery combined with cisplatin-based chemotherapy, also put patients to risk of developing AKI. This study investigates the molecular links between (OC) and (AKI), conditions that share overlapping pathogenic mechanisms but remain poorly understood in their interconnectedness. The aim was to identify common differentially expressed genes (DEGs) and explore their potential as therapeutic targets, identify common pathways associated with both and evaluate the potential of phytocompound as dual action on AKI and OC via molecular docking and experimentally. The study design focuses on analysis of commonly expressed genes in both OC and AKI via GEO datasets and further find out the overlapping pathways and molecular mechanisms associated; the study design also studies the potential of phytocompound via molecular docking and in vitro experiments against both AKI and OC. The results identified twelve common genes between ovarian cancer and acute kidney injury (AKI), with five genes (MDM2, EZH2, CD44, CCL5, IL1B) shown to be druggable targets through molecular docking with a phytocompound. Pathway enrichment revealed shared involvement in signalling pathways regulating cell proliferation and repair. The phytocompound exhibited selective cytotoxicity against ovarian cancer cells (SKOV3) without affecting kidney cells (HEK) in vitro. These findings highlight potential dual-target therapeutic strategies for mitigating tumour progression alongside renal injury in ovarian cancer patients.

Keywords: Biological functions Differentially expressed genes, Docking, druggable targets, MTT, Pathway analysis.

ICABB26-MOC-OP14

Integrated Transcriptomic Profiling of Metabolic Alterations in Breast and Ovarian Cancer

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Abstract

Cancer progression is closely associated with extensive metabolic reprogramming that supports enhanced energy demand, biosynthesis, and survival of tumor cells. In this study, a metabolism-centric integrative bioinformatics approach was employed to identify key dysregulated metabolic pathways and

genes across breast and ovarian cancers. Initially, dysregulated metabolic pathways in cancer were curated and used to construct a protein–protein interaction (PPI) network. Network topological analysis was performed using CytoHubba, and the top 10 hub genes were shortlisted based on degree centrality, highlighting their potential regulatory importance within metabolic networks. Functional enrichment analysis using g:Profiler revealed significant enrichment of pathways related to mitochondrial function, oxidative phosphorylation, and energy metabolism, validating the biological relevance of the selected hub genes.

To further validate these findings, expression profiling of the shortlisted genes was conducted across six independent GEO datasets comprising tumor and normal samples, including four breast cancer datasets and two ovarian cancer datasets. Consistent dysregulation of the hub genes was observed across cancer types, with tumor samples showing distinct expression patterns compared to normal tissues. Co-expression analysis demonstrated strong correlation among the hub genes, while differential expression analysis confirmed their significant dysregulation in tumor conditions. Principal component analysis (PCA) further revealed clear separation between tumor and normal samples based on the expression of these genes, underscoring their collective contribution to cancer-associated metabolic alterations. Overall, this integrative analysis identifies key metabolic hub genes consistently dysregulated across breast and ovarian cancers, providing mechanistic insights into cancer metabolism and a strong foundation for downstream functional and therapeutic investigations.

Keywords: Cancer metabolism; Metabolic reprogramming; Hub genes; CytoHubba; g:Profiler; Breast cancer; Ovarian cancer; Differential gene expression; Co-expression analysis; Principal component analysis (PCA); Mitochondrial dysfunction; Oxidative phosphorylation

ICABB26-MOC-OP15

Metagenomic Insights into taxonomic composition and Functional Diversity of Microbial Communities Associated with Fermented Kalanamak Rice Broth

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Abstract

Metagenomic and predictive functional profiling were employed to characterize the taxonomic structure and functional diversity of microbial communities associated with fermented Kalanamak rice broth. Taxonomic analysis based on relative abundance revealed dominance of *Proteobacteria* (68%) and *Firmicutes* (26%), with minor contributions from other bacterial phyla. At the genus level, the microbial community was dominated by unclassified *Enterobacteriaceae* (24%), followed by *Paenibacillus* (14%), Pseudomonas (12%), *Clostridium* (10%), and *Azospirillum* (8%), indicating a metabolically diverse consortium of facultative anaerobic and fermentative bacteria. Predictive functional analysis using PICRUSt and KEGG pathway annotation demonstrated a strong enrichment of metabolism-related genes, accounting for 45% of total predicted functions, while environmental information processing (18%) and genetic information processing (15%) were also highly represented, reflecting active substrate transport, signal transduction, replication, and transcriptional processes during fermentation. Functional pathways associated with carbohydrate metabolism, energy metabolism, and secondary metabolite biosynthesis were prominent, supporting efficient starch utilization and organic acid production. Genes related to cellular processes (5%) and stress adaptation further suggest microbial resilience under fermentative conditions. Overall, integration of taxonomic and functional metagenomic data reveals a functionally versatile microbial ecosystem driving fermentation-mediated biochemical

transformations in Kalanamak rice broth, highlighting its potential as a nutritionally enriched and bioactive traditional fermented food.

Keywords: Kalanamak rice; metagenomics; microbial diversity; PICRUSt; KEGG pathways; functional profiling; fermented foods

ICABB26-MOC-OP16

IN VITRO AND IN SILICO EVALUATION OF NEUROPROTECTIVE PHYTOCOMPOUNDS AGAINST HYPOXIA-MIMETIC INJURY IN NEURONAL AND GLIAL MODELS OF TRAUMATIC BRAIN INJURY

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Abstract

Traumatic brain injury (TBI) is often associated with cerebral hypoxia and oxidative stress, leading to ongoing neuronal loss and glial activation. Current treatments offer limited neuroprotection, highlighting the need for new, multi-targeted agents. Naturally occurring phytochemicals with antioxidant and anti-inflammatory properties are promising candidates for TBI treatment. In this study, we examined the neuroprotective potential of selected phytochemicals in human neuronal and glial cell lines subjected to hypoxia-mimetic injury. Chemical hypoxia was induced to mimic post-traumatic hypoxic stress, followed by treatment with non-cytotoxic concentrations of phytocompounds, identified through preliminary viability screening, to evaluate their therapeutic neuroprotective effects. Simultaneously, an in-silico

approach was used to identify protein targets of the phytochemicals within TBI and hypoxia related pathways. Hub genes from transcriptomic datasets were integrated with pathway analysis to prioritize targets, followed by molecular docking to assess binding affinity and interaction profiles. Collectively, the integrated in vitro and in-silico findings provide mechanistic evidence that selected phytochemicals exert multi-target neuroprotective effects under hypoxia-mimetic conditions, supporting their potential development as adjunctive therapeutic strategies for TBI.

Keywords: Hub genes, Hypoxia, Neuroprotective, Oxidative stress, Phytocompounds

ICABB26-MOC-OP17

AI-Assisted Computation screening of Phytocompounds for Multi-Protein Targeting in Neurodegenerative Diseases

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Abstract

Neurodegenerative diseases (NDs), including Alzheimer's, Parkinson's, and Huntington's diseases, are progressive disorders characterized by neuronal degeneration, cognitive impairment, and motor dysfunction. With increasing global prevalence and no definitive cure, these diseases pose a significant healthcare burden. Protein misfolding and aggregation involving key targets such as Amyloid Precursor Protein (APP), Butyrylcholinesterase (BChE), and Microtubule-Associated

Protein Tau (MAPT) play a central role in ND pathogenesis, highlighting the need for effective multi-target therapeutic strategies. Conventional drug discovery approaches are often time-consuming and resource-intensive, necessitating the more efficient and integrative methodologies.
In this study, an AI-assisted computational screening was employed to identify phytocompounds with multi-protein targeting potential for the treatment of NDs. A curated library of neuroactive phytocompounds was subjected to artificial intelligence–guided virtual screening combined with ADMET profiling to evaluate drug-likeness, pharmacokinetic behavior, and safety. Compounds demonstrating favorable profiles were further analyzed using molecular docking to assess their binding affinity and interaction patterns with APP, BChE, and MAPT. The stability and dynamic behavior of the top-ranking protein–ligand complexes were subsequently evaluated through molecular dynamics (MD) simulations. Among these, Hesperidin demonstrated superior stability across multiple targets during MD simulations, indicating its potential therapeutic relevance. Further research focuses the experimental validation of the identified compounds to assess their efficacy in clinical application.
Keywords: Neurodegenerative diseases; Amyloid precursor protein (APP); Butyrylcholinesterase (BChE); Microtubule-Associated Protein Tau (MAPT); Molecular docking; Drug-likeness; ADMET; Molecular dynamics simulation.

ICABB26-MOC-OP18

Comparative gene interaction analysis of electron transfer pathway for efficient power generation in microbial fuel cell

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Abstract
Exo-electrogenic bacteria possess the unique ability to transfer electrons to external electrodes, making them vital for microbial fuel cell (MFC) operations. This study investigated the genetic mechanisms underlying exo-electrogenic properties in various bacteria, which have significant potential for applications in MFCs. The study focused on targeting the genes responsible for these capabilities and examining the evolutionary relationships among these bacteria. Phylogenetic analysis assists in connecting Protein-Protein Interaction (PPI) results with the exo-electrogenic properties of the bacteria. This research delves into the genetic foundations and phylogenetic connections of various exo-electrogenic bacteria. It was found that some genes *(pilT, omcA, mtrA, and mtrB*) displayed high connectivity, emphasizing their importance in facilitating extracellular electron transport. These genes were primarily found in species such as *Shewanella*, *Geobacter* are renowned for their effective exo-electrogenic abilities. Gene Ontology analysis revealed that organisms with these highly interconnected genes produced higher electrical outputs. A functional and gene expression analysis of these genes was also performed using in-silico methods. This study highlights the genetic determinants of bioelectrochemical performance, offering insights for enhancing bacterial strains to boost energy production in microbial fuel cells.
Keywords: Exo-electrogenic bacteria, microbial fuel cells, phylogenetic relationships, gene interaction

ICABB26-MOC-OP19

Explainable Artificial Intelligence-Based Identification of Tamoxifen Resistance Biomarkers in Breast Cancer

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Tamoxifen resistance remains a major impediment to effective endocrine therapy in estrogen receptor–positive breast cancer, underscoring the need for predictive and interpretable computational frameworks that can elucidate underlying molecular mechanisms. In this study, we developed an explainable machine-learning model to predict tamoxifen resistance and identify its key transcriptional drivers using transcriptomic profiles from tamoxifen-sensitive and tamoxifen-resistant MCF7 subclones that were systematically curated and analyzed. An extreme gradient boosting (XGBoost) classifier was trained to distinguish between resistant and sensitive phenotypes and was further assessed for its performance via five-fold cross-validation. The model achieved a remarkable mean accuracy of 0.95 and an f1_macro score of 0.94. Subsequently, to interpret the XGBoost model, explainable artificial intelligence (xAI) was implemented. Based on the integration of Shapley Additive exPlanation (SHAP) and log2 fold change values, the most prominent genes influencing tamoxifen resistance in breast cancer were identified. This approach enabled the identification of a refined panel of 20 genes that consistently exhibited high attribution scores, collectively accounting for the majority of the model's predictive power of tamoxifen resistance. Functional annotation of this 20-gene signature revealed that these genes can thus be used as a biomarker to assess tamoxifen resistance in cancer patients non-invasively, which would facilitate better personalized and precision therapies for such resistant cases. Furthermore, these genes can also be targeted with a small-molecule inhibitor to support tamoxifen-based treatment, where the resistance-inducing genes are suppressed, and consequently, tamoxifen can function more effectively. Importantly, the parsimonious nature of this gene set preserved predictive performance while enhancing interpretability and translational feasibility. The findings lay a foundation for subsequent experimental validation and multi-omics extension toward precision management of tamoxifen-resistant breast cancer.

Keywords: Tamoxifen resistance, Breast cancer, Explainable Artificial Intelligence, Transcriptomics, Biomarker

ICABB26-MOC-OP20

Rewriting the Epigenetic Clock: Mechanisms and Therapeutic Approaches to Age Reversal

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ABSTRACT

Aging is increasingly understood as a complex, multifactorial process driven not only by chronological time but also by dynamic changes at the epigenetic level. Recent evidence indicates that age-associated alterations in DNA methylation patterns, chromatin architecture, noncoding RNA networks, and histone modifications contribute to systemic decline, genomic instability, stem-cell exhaustion, and mitochondrial dysfunction - all hallmarks of organismal aging and age-related diseases. Importantly, such epigenetic drift is not strictly unidirectional, suggesting potential avenues for biological age reversal and healthspan

extension. Partial cellular reprogramming via Yamanaka factors or subsets thereof has shown promise in resetting epigenetic clocks and enhancing regenerative potential, while extrinsic manipulations have hinted at systemic rejuvenation effects without dedifferentiation. A pioneering small clinical trial reported that a combined regimen of growth hormone, dehydroepiandrosterone (DHEA), and metformin could partially reverse DNA methylation age and stimulate thymic renewal in humans, highlighting translational potential despite unresolved questions regarding long-term phenotypic benefits beyond epigenetic markers. Concurrently, a comprehensive review of epigenetic regulation underscores the intricate interplay between multiple layers of epigenetic information across tissues and the necessity for precision strategies to translate mechanistic insights into safe, personalized anti-aging interventions. Emerging approaches such as CRISPR-based epigenome editing, OSKM partial reprogramming, NAD^+/sirtuin boosters, histone deacetylase inhibitors, and lifestyle or microbiome-targeted therapies are critically evaluated for their ability to reset epigenetic age and restore tissue homeostasis. Integrating high-resolution multi-omics and advanced epigenetic clock technologies is proposed as a roadmap to refine these interventions, catalyzing the evolution of epigenetic rejuvenation from conceptual frameworks to clinical application.

Keywords: Epigenetic aging; DNA methylation; Epigenetic clock; Partial cellular reprogramming; Yamanaka factors; Age reversal; Thymic regeneration; Biological age; Chromatin remodeling; Epigenome editing; Anti-aging therapies; Rejuvenation.

ICABB26-MOC-OP21

Computational Screening of Herbal Extract Constituents for Interaction with Parkinson's Disease-Associated Mutant Proteins

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Abstract

Computational screening of herbal phytochemicals is an efficient and sustainable method for discovering new neuroprotective agents for Parkinson's disease (PD). This study applies in silico techniques to assess bioactive constituents of herbal medicines targeting PD-related proteins such as α-synuclein, LRRK2, PARK7, and parkin. Molecular docking techniques have been utilised to determine the binding affinities, interaction energies, and contact residues in the active and allosteric sites responsible for protein aggregation and misfolding. The phytochemicals that exhibited the strongest and most stable binding profiles were further studied in greater depth using molecular dynamics (MD) simulations to evaluate the stability of the protein-ligand complex, as well as the flexibility of the constituent and protein, and the presence of stabilizing hydrogen bonds and/or other interactions. Examining the ADME/T properties, along with investigating the permeability of the blood-brain barrier, provided a means of determining which compounds could possess an optimal level of both potential pharmacological benefit and toxicity, applicable for targeting the CNS. The attention placed on naturally occurring substances that can simultaneously combat oxidative stress and prevent protein aggregation is vital, as these mechanisms are part of the progression of Parkinson's disease. This form of computational modelling offers an excellent, moreover, inexpensive means for detecting other software-generated, plant-based proteins and PD-relevant inhibitors or modifiers. The probable candidates generated by this method should be subjected to further positive reinforcement from in vitro models as a means of determining their potential for neuroprotection and therapeutic applications.

Keywords: Parkinson's disease, α-synuclein, molecular docking, phytochemicals, ADMET

ICABB26-MOC-OP22

Predicting PCOS Risk Using Machine Learning: Development of an Integrated Digital Menstrual Health Platform

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Abstract

Polycystic ovary syndrome (PCOS) is one of the most common endocrine and metabolic disorders in women of reproductive age, with a recent global prevalence of 9.2% (95% CI: 6.8–12.5%). Prevalence varies by diagnostic criteria, ranging from 5.5% under NIH to 11.5% under Rotterdam definitions, indicating a substantial worldwide burden. PCOS is characterized by hyperandrogenism, ovulatory dysfunction, and metabolic disturbances, increasing long-term risks such as insulin resistance, obesity, type 2 diabetes, and cardiovascular disease. Because symptoms often present gradually, many women remain undiagnosed for years, emphasizing the clinical need for accessible digital tools. Period-tracking and PCOS-prediction platforms can help identify irregular cycles, monitor symptoms, and support earlier medical evaluation. Lifestyle and nutrition-based interventions form the cornerstone of PCOS management. The main objective of this project is to build an integrated, machine-learning-powered digital health platform that improves menstrual health management through evidence-based diet recommendations, predictive analytics and personalized insights. In this study, we have developed machine learning algorithms based on menstrual profiles, clinical symptoms, hormonal parameters and lifestyle characteristics so as to provide early detection. Methods including LR for baseline risk prediction, SVM to classify hyperandrogenism/oligomenorrhea profiles, MMPs (MLP) for nonlinear menstrual-cycle pattern recognition and XGB for high-accuracy prediction of PCOS across diverse health data types all showed great promise in early detection of risk in patients at-risk. These models can use variation in ovulation disturbances, menstrual cycle length, metabolic markers and self-reported symptoms to predict individualized PCOS-risk scores, as well as offer personalized nutrition-based advice based on the individuals' symptom pattern with the aim for early risk stratification and healthcare-seeking behavior. Low glycemic index diets, as well as Mediterranean and anti-inflammatory diets, ketogenic and high-fiber diets, omega-3–rich foods improve insulin sensitivity, hormonal profiles, and menstrual regularity.

Keywords: PCOS, Machine Learning, Nutrition Recommendation, Personalized diet, Health Management Platform

ICABB26-MOC-OP23

Structure-Based Ranking of EGFR Inhibitors to Overcome Mutation-Driven Resistance in Lung Cancer

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EGFR (Epidermal Growth Factor Receptor) is a receptor protein that is responsible for several cellular pathways, like the MAPK pathway for cell division and the PI3K–AKT–mTOR pathway for inhibiting cell apoptosis. On ligand binding, the EGFR molecules dimerize, forming an asymmetric pair. The activator forces the receiver to take its active configuration, enabling ATP binding between the N and C terminals of the intercellular tyrosine kinase domain, leading to the phosphorylation of tyrosine, setting the base for the cellular pathways to begin. However, internal factors such as transcription or replication errors, or external agents like pollution, radiation, and cigarette smoke, can cause mutations like the Exon 19 in-frame deletion and the L858R point mutation that replaces leucine with arginine at position 858, which stabilise the active configuration of the EGFR protein. As a result, cell division occurs uncontrollably, leading to tumour formation, a prevalent example of which is non-small cell lung cancer (NSCLC), a subset of lung cancer associated with EGFR mutations. Several classical drugs like Gefitinib and Erlotinib inhibit ATP binding through competitive inhibition but fail in the case of

the T790M point mutation that replaces threonine with methionine at position 790, and prevents their binding due to high steric hindrance and increased ATP affinity. Modern drugs like Afatinib and Dacomitinib are more potent but are limited by toxicity and reduced effectiveness against the T790M. Currently, only Osimertinib is effective for this mutation. Thus, mutated EGFR and NSCLC are constantly evolving, and there is a need to develop better and improved drugs that effectively inhibit ATP binding and remain active against various mutations. The purpose of this study is to compare several existing drugs used in NSCLC, namely Gefitinib, Erlotinib, Afatinib, Dacomitinib, and Osimertinib, based on their binding affinity at the ATP-binding site through molecular docking, potency, toxicity, and stability, paving the way to introduce lead optimization strategies to these drugs, helping in solving future mutations.

Keywords: EGFR, Non-Small Cell Lung Cancer (NSCLC), Tyrosine Kinase Inhibitors, ATP-Binding Site, Molecular Docking, Drug Resistance

ICABB26-MOC-OP24

IN SILICO SCREENING OF PHYTOCONSTITUENTS FROM ENGLISH VIOLET FLOWERS AGAINST COMMUNICABLE VIRAL TARGETS

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Abstract

Communicable viral infections remain a significant global health concern, highlighting the need for novel antiviral agents with improved safety and efficacy. English violet *(Viola odorata)* is a medicinal plant traditionally used for the management of respiratory ailments and infectious diseases, and is known to contain diverse bioactive phytoconstituents. In the present study, an integrated in silico approach was employed to evaluate the antiviral potential of phytoconstituents derived from English violet flowers against key communicable viral targets. Phytochemical compounds were retrieved from the IMPPAT and KANSpack databases and screened based on oral bioavailability and drug-likeness criteria. Potential molecular targets of the selected compounds were predicted using SwissTargetPrediction and STITCH, while virus-associated disease genes were collected from GeneCards and OMIM databases. A compound–disease–target interaction network was constructed and analyzed using Cytoscape to elucidate key molecular interactions. Functional enrichment analysis, including Gene Ontology and KEGG pathway analysis, was performed to identify the biological processes and signaling pathways involved. Molecular docking studies were conducted to assess the binding affinity of the phytoconstituents toward essential viral and host-related proteins associated with communicable viral infections. The phytoconstituents of English violet *(Viola odorata)* demonstrated strong binding with five key gene targets- AKTI, PPARG, CASP3, ESRI and SRC which are involved in immune regulation, inflammatory responses, and viral pathogenesis. Several phytoconstituents exhibited strong binding interactions with these targets, with one compound showing notably high antiviral potential.

Overall, this study suggests that English violet *(Viola odorata)* flower phytoconstituents may serve as promising candidates for the development of natural antiviral agents. However, further in vitro and in vivo studies are required to validate their therapeutic efficacy and safety.

Keywords*:* English violet; phytoconstituents; molecular docking; antiviral activity; communicable viral diseases

ICABB26-MOC-OP25

In Silico Characterization of Transcription Factor Implicated in Lung Cancer

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Abstract

Lung cancer is a leading cause of cancer-related deaths worldwide, primarily due to late-stage diagnosis, molecular heterogeneity, and insufficient prognostic biomarkers. Transcription factors have a crucial role in tumor formation, progression and resistance to therapies. TFs that have not been studied adequately on lung cancer are numerous. The paper provides an in-silico analysis to determine unexplored transcription factors (TFs) that may be implicated in the pathogenesis of lung cancer. A systematic curation of 13 TFs identified in databases and their analysis showed that TFs form complex regulatory interactions. The target gene network analysis revealed that the projected targets are enriched in cellular processes like cell death, differentiation, and proliferation indicating both shared and TF-specific roles in regulation. Motif analysis showed a high level of cis-regulatory element conservation, which implies high specificity of DNA-binding of some TFs such as ZNF266, TSH2 and TSH3. The analysis of the PPI network showed enriched interaction network (23 nodes, 57 edges, PPI enrichment p value < 1.0e-16**)** in which the core cluster of proteins was represented by mitotic regulation and cell-cycle control. PCGF2 is a sparsely connected group that mediates Polycomb-mediated epigenetic control, and has significant interconnections in cell-cycle control, in p53 pathways, and in cancer-related pathways. Profiling of genomic alteration in lung adenocarcinoma and squamous cell carcinoma pathways identified common alteration of PCGF2, which occurred through mutations and copy number increase, indicating that the protein could be involved in transcriptional and epigenetic dysregulations in lung cancer. This study characterises new transcription factors (TFs) whose functions in lung cancer are not initially known and proposes a systematic bioinformatics system to focus on the key regulatory drivers in the future to study the work and develop TF-based biomarkers and therapeutic targets.

Keywords: Lung cancer, Transcription factors, In silico analysis, PCGF2, Bioinformatics

ICABB26-MOC-OP26

Antileishmanial Potential of Mushroom-derived fractions: *In vitro* Evaluation and *In silico* Molecular Studies

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Abstract

Leishmaniasis is neglected tropical disease caused by *Leishmania* parasite which causing 65,000 deaths annually. The disease manifests in cutaneous, mucocutaneous and visceral forms representing a significant health burden in endemic regions. The parasite survives and proliferates within host macrophages in its amastigote form. Various synthetic drugs are utilized to combat this disease but there are several drawbacks like toxicity, drug resistance, high treatment costs, prolonged treatment duration and the emergence of drug-resistant strains. So, we aim to find better drug alternative from natural resources like medicinal mushrooms. Mushrooms are recognized as rich reservoirs which contains several bioactive including phenolics, polysaccharides, terpenoids, alkaloids and secondary metabolites with a potential of antiparasitic activity. In this study, mushroom was evaluated for *in vitro* antileishmanial activity against *Leishmania* promastigotes using the MTT assay. Primary screening was carried out using mushroom extracts prepared in solvents of increasing polarity namely n-hexane, ethyl acetate, and ethanol. Screening of three non-polar, mid polar and polar fractions from medicinal and edible mushroom revealed that ethyl acetate fraction had excellent activity against promastigote stage of *Leishmania donovani*. Miltefosine was used as the standard positive control in *in vitro* antileishmanial assays. The result revealed significant inhibitory activity which indicating may be contributed by the presence of bioactive compounds with antileishmanial potential. Growth inhibition

was also observed in a dose-dependent manner further, suggesting promising efficacy at promastigote level. The presents study warrants future investigation of bioactive fraction with respect to evaluation against amastigote form of the parasite. This study highlights mushrooms as a promising natural source of antileishmanial agents and integrates *in vitro* and *in silico* approaches to accelerates drug discovery against leishmaniasis.

Keywords: *Leishmania donovani*, Edible mushroom, Medicinal mushroom, Antileishmanial, *Leishmania*

ICABB26-MOC-OP27

Computational Dissection of Fenugreek Phytochemicals Reveals Convergent Targeting of Metabolic Inflammation and Cancer Signalling

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Abstract

Metabolic disorders and hormone-dependent cancers, including type 2 diabetes mellitus (T2DM), obesity, and breast cancer, are biologically interconnected through shared molecular pathways involving chronic inflammation, dysregulated glucose metabolism, and aberrant cell signaling. In our *in silico* study, an integrated computational framework combining network pharmacology, and molecular docking was employed to elucidate the multi-target pharmacological mechanisms of fenugreek (*Trigonella foenum-graecum* L.) across these interconnected disease states. Bioactive phytochemicals of fenugreek were screened using computational drug-likeness and ADMET parameters, followed by target prediction and network construction. Network analysis identified key inflammatory, metabolic, and oncogenic targets, including IFNG, IL1B, IL6, CXCL8, EGFR, TP53, and histone-related proteins H3C13 and H4C6, which are critically involved in insulin resistance, adipose tissue inflammation, and cancer progression. Pathway enrichment analysis revealed significant involvement of cytokine signaling, insulin resistance, PI3K/AKT, EGFR signaling, and chromatin regulation pathways. Molecular docking demonstrated strong binding affinities of selected fenugreek phytochemicals toward these targets, with interaction profiles comparable to or exceeding those of the standard antidiabetic drug metformin for metabolic and inflammatory targets. Overall, this study provides mechanistic insights into the multi-component, multi-target actions of fenugreek and highlights its potential as a source of bioactive molecules capable of modulating shared molecular networks underlying diabetes, obesity, and breast cancer.

Keywords: Fenugreek, Network pharmacology, Molecular docking, Diabetes, Obesity, Breast cancer, Multi-target mechanism.

ICABB26-MOC-OP28

Peptide inhibition of the mTORC1 signalling: A trend in Cancer Therapeutics

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Abstract

Cancer is the second most leading cause of death in the world and has been manifested by various hallmarks including uncontrolled cell proliferation, increased cell survival, abnormal angiogenesis, eluding of antitumor immunity and acquisition of metabolic processes unique to cancers. Interestingly, mTOR signalling is associated with all of these hallmarks, making it the most appropriate choice for target therapies against cancer. Inhibition of the target protein by peptides designed using the interfacial amino acids of its interacting partners is one of the approaches of targeted therapies. This approach has been engaged here to inhibit the association of the mTOR kinase and RHEB. A part of an amino acid sequence of mTOR kinase, present in the mTOR-RHEB interface, was utilized to design three different

native peptides, which were further modified by incorporating evolutionary changes occurring in amino acid sequences of mTOR as mutations. All the peptides were tested for their affinity with the RHEB, by performing protein-peptide docking on the HADDOCK 2.4 docking interface and by binding energy calculation on the FoldX5.0 interface. Also, their mutual interactions were analyzed using the ligplot^{+}tool. The peptides were named N1-3, M1-3 and C1-3 among which the peptide M2 and M3 showed comparable binding energies to the entire mTOR-RHEB complex. This was also supported by many Hydrogen bonds and other positive interactions. All these shreds of evidence support the potency of these peptides to interrupt the mTORC1 signalling which can be further established using *in vitro* models for cancer therapeutics.

Keywords: mTOR signalling, RHEB, Docking, mTORC1 complex, cancer.

ICABB26-MOC-OP29

Virtual Screening of phytocompounds from Peel of *Citrus limetta* to Combat Skin Cancer Targets: Molecular Docking and Molecular Dynamic Simulation Analysis

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ABSTRACT

Skin Cancer is the most common malignant disease worldwide. Scientists have been working to discover effective therapeutics and many of them are exploring phytocompounds. In this study five phytocompounds from *Citrus limetta* peel have been studied to dock with the major receptor targets: MEK1, CDK4 and IL1, involved in various pathways associated in Skin Cancer using molecular docking and ADMET analysis. Molecular docking was used to investigate important interactions between the phytocompounds and target proteins with reference to standard drug inhibitors available of respective target. The docked results revealed that among all the compounds selected, the 3 bioactive compounds, Ellagic acid, Hesperidin and Quercetin showed even better binding profile than the standard drugs available for their respective receptors. The molecular dynamics simulation of the complexes docked revealed the stability of the docked complexes at 100 ns simulation period . According to the findings of this study, the phytocompounds have anticancer activity and thus can be utilized as an alternative to commonly used synthesized drugs as therapeutic potential against Skin Cancer. Analysing the ADMET properties, predicted that all the compounds were found to be safe, non-toxic, and non-carcinogenic. Further the *In vitro* investigations are also required to confirm the potential of the phytocompounds against skin cancer cells.

Keywords: ADMET, Anticancer, Skin cancer, Molecular docking, Therapeutics

ICABB26-MOC-OP30

Integrative Machine Learning Analysis of TCGA-LUAD Data for Predictive Modelling of Lung Adenocarcinoma Subtypes

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Abstracts

The exponential growth of multi-omics data presents a unique opportunity to enhance cancer diagnostics through Artificial Intelligence (AI). This study leverages machine learning (ML) algorithms to analyze the The Cancer Genome Atlas Lung Adenocarcinoma (TCGA-LUAD) dataset, aiming to construct a robust predictive model for cancer subtyping and staging. We integrated genomic, transcriptomic, and clinical data to create a comprehensive feature set, addressing the high dimensionality of biological data through advanced feature selection techniques such as Recursive Feature Elimination (RFE). Several supervised learning models, including Random Forest, Support Vector Machines (SVM), and Gradient Boosting classifiers, were trained and validated. The Random Forest model achieved the highest classification accuracy, successfully identifying a signature of 15 key genesthat distinguish between early and late-stage adenocarcinoma with high sensitivity and specificity. Beyond classification, the model revealed non-linear

relationships between gene expression profiles and patient survival times. This AI-driven approach demonstrates the power of computational biology in decoding complex cancer heterogeneity. By automating the identification of critical genomic features, this framework paves the way for precision medicine tools that can assist clinicians in prognosis prediction and treatment planning based on individual genomic profiles.

Keywords: Machine Learning, TCGA, Lung Adenocarcinoma, Artificial Intelligence, Multi-Omics, Predictive Modeling, Precision Medicine

ICABB26-MOC-OP31

Artificial Intelligence Driven Pharmacovigilance for Probiotics: Advancing Safety Surveillance of Live Biotherapeutic Products

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Abstract

Probiotics live microorganisms administered to confer health benefits are increasingly used worldwide as consumer supplements and in clinical practice. Despite widespread adoption, safety profiles remain incompletely characterized. Case reports describe rare but serious adverse events, including bacteraemia, fungemia, and sepsis, particularly among immunocompromised or critically ill patients. Regulatory classification varies internationally, spanning foods, dietary supplements, live biotherapeutic products (LBPs), and biologics, complicating systematic safety oversight. To synthesize recent global evidence on probiotic-associated adverse events and evaluate how artificial intelligence (AI) machine learning (ML), deep learning, and natural language processing (NLP) can enhance pharmacovigilance across consumer and clinical settings, including opportunities, limitations, and regulatory implications. A focused literature synthesis used peer-reviewed studies, regulatory guidance, pharmacovigilance database analyses, and methodological research on AI-enabled adverse event detection published through 2025. Emphasis was placed on documented probiotic-related harms, AI-amenable data sources, and validated AI techniques for adverse event extraction, signal detection, and serious adverse event prediction. Evidence confirms clinically relevant risks, including opportunistic infections, immune modulation effects, and potential antimicrobial resistance concerns, disproportionately affecting vulnerable populations. AI-driven methods show promise: NLP enables extraction of adverse event data from unstructured text, while ML improves signal sensitivity and risk stratification over traditional disproportionality analyses. However, implementation is constrained by fragmented exposure data, inconsistent strain nomenclature, underreporting, limited training labels, and challenges in model transparency and regulatory acceptance. Emerging guidance emphasizes the need for explainable, auditable AI systems and harmonized post-market data standards. AI-enabled pharmacovigilance offers a scalable framework to detect and predict probiotic-related harms. Realizing this potential requires coordinated data standardization, validated datasets, explainable AI deployment, and regulatory alignment as global probiotic use expands.

Keywords: Probiotics; Pharmacovigilance; Adverse Events; Artificial Intelligence; Live Biotherapeutic Products

ICABB26-MOC-OP32

PHYTOCHEMICAL ANALYSIS AND EXPLORATION OF NOVEL BIOLOGICAL COMPOUNDS OF *MORCHELLA ESCULENTA* BY INSILICO STUDIES

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ABSTRACT

The main characteristic of Morchella esculenta, a medicinal plant with antioxidant and anti inflammatory properties, is its alkaloids component, which also has antimicrobial, anti-cancer, immune-regulating, and anti-diabetic properties. Commonly referred to as morel mushrooms, the plant thrives in soil that is high in organic matter and drains well.The most expensive edible fungus in the Morchellaceae family, *Morchella esculenta*, also known as Guchhi, is important for both nutrition and medicine. It is commonly found as a saprobic or mycorrhiza.The morel's main constituent is the mycelium. Individual fungal hyphae spread out below and grow in mass to Guchhi, a member of the Helvellaceae family, is sold to traders locally for Rs 10,000 per kilogram.There were two steps in the extract preparation process: first, the raw morels were cleaned thoroughly, and then they were boiled to extract the boiled extract. Second, liquid nitrogen was used to grind the dried morels into their extract. Quantification of the phytochemicals in the two samples i.e Aqueous Paste Of Gucchi (APG) and Chaps Solution Of Gucchi (CSG) indicates that in the Primary Metabolites the protein content is approximately 12.62 mg/ml in CSG and 20.17 mg/ml in APG the carbohydrate content is approximately 4.58 mg/ml in CSG and 5.28 mg/ml in APG. Additionally, in the Secondary Metabolite the CSG and APG contain 5.61 and 8.64 mg/ml phenols, 6.03 and 8.22 mg/ml alkaloids7.62 and 10.56 mg/ml of Flavonoids , and Gucchi Dissolved in Ethanol was 5.945mg/ml and Ethanol Gucchi Paste was 8.630 mg/ml antioxidants, respectively. This implies that the morel is a nutrient-rich resource that may be utilized to create a variety goods nutraceutical products. The present study evaluates the Phytochemical Analysis and Exploration of Novel biochemical Compounds by Insillico studies as the Protein biomarker compound found in the species of morels were compared with all the proteins of *Morchella Esculenta* by blast so their same domain and other functional regions of the protein could be located and further identification could be carried on.

Keywords : *Morchella esculenta* ; Aqueous Paste of Guchhi (APG) ; Chaps Solution Of Guchhi (CSG) ; Primary and Secondary Metabolites ; Phytochemical Analysis ; Insillico studies.

ICABB26-MOC-OP33

Molecular Interplay and Algorithmic Oversight Re-envisioning Pharmacovigilance through AI-Integrated Nutraceutical Surveillance

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Abstract

The traditional "one-size-fits-all" approach to dietary supplementation is increasingly challenged by emerging evidence of inter-individual metabolic variability. While the nutraceutical industry continues to expand, conventional consumption models fail to account for real-time physiological shifts, often leading to sub-optimal bioavailability or adverse nutrient-drug interactions. The convergence of deep learning and personalized biotechnology offers a transformative pathway toward precision health, yet a

unified framework for integrating real-time biometrics with molecular nutrient delivery remains largely theoretical.

To propose a high-level framework for "Adaptive Bio-Intervention" by evaluating the role of Artificial Intelligence (AI) and Digital Twin technology in optimizing nutraceutical efficacy, and to address the resulting ethical implications of biological data sovereignty. A comprehensive synthesis of high-level research published through 2025 was conducted, focusing on the integration of machine learning algorithms with multi-layered biological datasets. The study evaluated the technical feasibility of Biological Digital Twins—high-fidelity virtual replicas of metabolic landscapes and analyzed the utility of wearable sensor data, gut microbiome fluctuations in driving predictive models for nutrient demand. Findings indicate that AI-driven Digital Twins can accurately simulate metabolic responses, significantly reducing trial-and-error in supplementation. The application of Natural Language Processing (NLP) and predictive modeling enables the identification of subtle glycemic and inflammatory triggers, allowing for "Real-Time Optimization." Furthermore, advances in 3D-printing technology allow for the formulation of "smart poly-pills" that adjust dosages based on daily physiological flux. However, the study identifies critical hurdles regarding "Bio-Sovereignty," specifically the security of genomic data and the need for decentralized, user-controlled data architectures to prevent corporate exploitation of biological signatures.

AI-enabled nutraceutical frameworks offer a scalable and highly precise method for extending human healthspan. Realizing this potential requires a shift toward "Bio-Sovereignty" and the standardization of real-time biometric integration to ensure that personalized health technology remains secure, transparent, and accessible.

Keywords: Nutraceuticals; Artificial Intelligence; Digital Twins; Personalized Nutrition; Bio-Sovereignty; 3D-Printed Supplements

ICABB26-MOC-OP34

Repurposing Metabolic Drugs for Oral Cancer: An In-silico approach

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Abstract

Oral squamous cell carcinoma (OSCC) remains a major health concern characterized by dysregulated cell proliferation, invasion, and metastasis. Conventional therapeutic modalities, including surgery, chemotherapy, and radiation, often face significant limitations, such as suboptimal efficacy, high treatment costs, and adverse side effects. Drug repurposing—identifying new therapeutic indications for existing, approved drugs—has emerged as a promising strategy to mitigate these challenges. Among the various classes of drugs investigated for repurposing in cancer therapy, metabolic drugs have received particular interest due to their role in modulating the tumor microenvironment and cellular metabolism. FDA-approved drugs for metabolic disorders, such as type 2 diabetes, obesity, cardiovascular disease, hypertension, and others, are being explored for their potential anti-cancer effects. In this study, more than 1200 genes associated with OSCC progression were retrieved from KEGG, cBioPortal, and Reactome databases. These were analyzed through protein–protein interaction (PPI) network construction in *Cytoscape*, and topological analyses identified hub genes including EGFR, AKT1, TP53, and others. Candidate drug–gene interactions were mapped to highlight repurposable metabolic agents with therapeutic relevance. Molecular docking was conducted to evaluate the binding affinity between prioritized drugs and hub proteins, offering insights into their

mechanistic plausibility. Further validation will be pursued through molecular dynamics (MD) simulations to assess drug–target complex stability under physiologically relevant conditions. This integrative pipeline demonstrates the potential of combining systems biology with structural modeling to identify and prioritize repurposable metabolic drugs, ultimately contributing to the development of effective therapeutic strategies for oral cancer.

Keywords: Oral Cancer, Drug repurposing, Metabolic disorders, Networking, Molecular docking, MD Simulation

ICABB26-MOC-OP35

Genomics Blueprints of Vision: A Comparative History of Rhodopsin Evolution and Phototransduction

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Abstract

Light has the potential to be the most vital signal for living beings, as most life on Earth is ultimately powered by light energy. Many animals use light cues to regulate biological systems such as eyesight and the circadian clock. It is now well established that variation in the subtypes and spectral properties of the visual pigments that mediate color and dim- light vision is a prevalent mechanism for the molecular adaptation to diverse light environments. Opsins and their evolution through the lens of Comparative Genomics act as a bridge between molecular genetics and ecological adaptation. Opsins are a diverse family of G-protein coupled receptors (GPCRs) that serve as the fundamental molecular interface between light and biological signaling. Rhodopsin is the 7-helical G-coupled receptor transmembrane protein. It also contains 11-cis-retinal, bound to the opsin protein, primarily absorbs light and responsible for scotopic vision in dim light conditions. Comparison of rhodopsin gene was carried out at gene sequence level, coding region and protein level among the selected organisms from diverse groups including a set of model organisms like *Drosophila melanogaster, Danio rerio, Xenopus laevis, Rattus norvegicus, Gallus gallus, Macaca mulatta, Pan troglodyte and Homo sapiens.* The sequence alignment studies show percentage similarities across the genomes and derives different functional annotation exhibiting that rhodopsin plays different role in these genomes. Further the phylogenetic analysis show how they evolved over the time. The comparative genomic analysis of rhodopsin across diverse organisms effectively demonstrates how evolutionary pressures shape genetic architecture to meet specific environmental demands. Rhodopsin plays vital role in studying GPCRs vividly, mutations in rhodopsin leads to diseases like Retinitis Pigmentosa and Congenital Stationary Night Blindness which disrupts the normal vision and also affects the circadian rhythm, dysregulation causing sleeping disorders. It acts as the potential biomarkers for early detection of diseases like Alzheimer's and Parkinson's.

Keywords: Rhodopsin, G-coupled photoreceptor, vision, comparative genomics, evolution, Retinitis Pigmentosa

Session 4:
Next-Generation Nanobiotech and Nano-Enabled Theragnostics
Poster Presentations

ICABB26-NM-PO-01

From Green Tea to Targeted Therapy: Integrating Epigallocatechin Gallate (EGCG) into Modern Oncology

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Abstract

Millions of people worldwide drink green tea on a daily basis. Certain green tea polyphenol compounds have been found to have anticancer properties. The main catechin in green tea (Camellia sinensis), Epigallocatechin Gallate (EGCG), have an effect on a number of human diseases, based on a growing body of preclinical research. EGCG appears to be a potent antioxidant that protects healthy cells from oxidative damage. It also has antiangiogenic and anticancer properties and modulates the response of tumor cells to chemotherapy. Due to its low bioavailability, the significance of EGCG in cancer prevention is undoubtedly still debatable despite its efficacy and safety. Numerous research studies have demonstrated that nanotechnology-based techniques such as: encapsulation, liposomes, micelles, nanoparticles, and other formulations can be used to overcome low bioavailability.

This review's goal is to look at studies on EGCG in relation to cancer treatment and/or prevention. The anti-cancer, anti-oxidant, anti-inflammatory, anti-angiogenesis, and apoptotic properties of EGCG are the primary focus of this review. We also emphasized the potential of EGCG in various cancer types, focusing on clinical trial formulations that enhance our comprehension of the therapeutic management of cancer.

The literature for this paper was reviewed using Google Scholar and PubMed. The inclusion criteria cover papers published between 2010 and 2025. Publications written in English were considered. Approximately 200 papers, including research papers, systematic reviews, literature reviews, and comparative studies, were reviewed for this work and about 100 of these papers have been cited.

Studies conducted both in vitro and in vivo have shown that EGCG inhibits cell growth and increases the metabolic stress of cancer cells. These findings may support the long-standing therapeutic use of green tea in conventional therapies. EGCG has a chemopreventive impact by inhibiting the onset, promotion, and development of carcinogenesis. EGCG exhibits its effectiveness in managing cancer by modifying a number of cell signaling pathways, including those that control angiogenesis, apoptosis, proliferation, of various kinds of cancer cells.

Non-toxic natural compounds like EGCG may be helpful for treating human cancers and/or preventing the growth of tumors, either on their own or in conjunction with traditional treatments.

Keywords: Angiogenesis, Cancer, EGCG, Natural Compounds, Oxidative stress

ICABB26-NM-PO-02

Nanoparticle-Mediated Drug Delivery Across the Blood–Brain Barrier for Alzheimer's Therapy

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Abstract

Alzheimer's disease is a neurodegenerative disorder of the brain, which gets progressively worsens over time. It causes dementia and the degradation of other cognitive functions. Alzheimer's has no cure. Presently, Alzheimer's treatment is limited to managing symptoms and delaying the progression of the disease. This emphasizes the need for new therapeutic strategies. Medications do not have the desired

outcome due to their inability to cross the Blood-Brain Barrier (BBB), which limits their access to the central nervous system. To get around this obstacle, the nanotechnology-based delivery system is the new talked-of-therapeutic avenue. Nanoparticles (Polymeric nanoparticles, liposomes and solid lipid nanoparticles) may be produced for targeted drug delivery, enhanced drug solubility, and controlled release. The drug transport can be strongly promoted by the addition of ligands such as transferrin, lactoferrin, or apolipoprotein to the drugs. These bind to specific receptors and thus increase BBB permeability. The use of nanoformulations facilitates the delivery of anti-amyloid agents, antioxidants, and neuroprotective drugs, as per the studies. Besides, the drugs wrapped in nanoparticles are safe from the degrading enzymes in the body and the overall toxicity is lessened.

However, research on the immune reactions, safety in the long run, clearance routes, and the possibility of scaling these solutions for clinical use still leaves a question mark in front of the promising findings. More research on biocompatible, targeted, and BBB-selective nanocarriers may lead to the development of Alzheimer's disease precision therapy. This study could potentially slow the progression of the disease and enhance the quality of life of patients.

Keywords: Blood–Brain Barrier, Nanoparticles, Drug Delivery, Alzheimer's Disease, Targeted Therapy.

ICABB26-NM-PO-03

Organic Nanocarriers for Effective Breast Cancer Therapy: A Comprehensive Review

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Abstract

Breast cancer is one of the leading causes of cancer deaths among women, which shows the need for safer and more effective therapeutic strategies. Organic nanoparticles, including polymeric, lipid-based, and protein-based nanocarriers, have emerged as useful platform for targeted drug delivery and improved treatment results. These biocompatible nanocarriers can target tumors actively or passively, and reduce the systemic side effects of drugs. Recent progress shows they can help overcome drug resistance, codeliver multiple drugs, and change the tumor microenvironment. This review examines the studies on various types of organic nanoparticles used in breast cancer therapy. It covers their mode of action, performance focusing on drug encapsulation, release, cellular uptake, and anticancer effects. In conclusion, this review gives an overview of the current evidence supporting organic nanoparticles as promising tools for breast cancer treatment.

Keywords: Breast cancer, Lipid, Organic Nanoparticles, Polymeric, Protein

ICABB26-NM-PO-04

Transition Metal Nanostructures for Next-Generation Electrochemical Biosensing

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Abstract

Electrochemical biosensors have become an essential part of modern analytical systems because of their rapid, low-cost, and highly sensitive detection of biologically important molecules. The performance of these sensors depends significantly on the materials used at the electrode interface, where electron transfer and catalytic reactions take place. In recent years, nanostructures derived from transition metals such as oxides and sulphides of manganese, iron, cobalt, nickel, and vanadium, have

attracted considerable attention due to their rich redox chemistry, high surface activity, and ability to promote fast charge movement. These characteristics make them suitable for detecting a wide variety of analytes without relying on biological enzymes, a feature that can improve sensor stability and reduce fabrication cost.This review summarises current progress on the use of transition-metal nanomaterials in electrochemical biosensing, with a strong emphasis on the fundamental processes that enable signal generation. A range of nanostructure designs, such as nanosheets, nanowires, clusters, and hierarchical flower-like assemblies, are discussed to illustrate how controlling morphology influences electron-transfer pathways, catalytic efficiency, and overall sensing performance. Special attention is given to non-enzymatic detection of glucose, dopamine, hydrogen peroxide, and other medically relevant molecules, where transition-metal nanomaterials often outperform traditional enzyme-based systems. Hybrid structures that combine transition-metal nanomaterials with conductive carbon platforms (such as graphene or carbon nanotubes) or with polymeric matrices are also explored, as these composites frequently provide improved mechanical stability, enhanced conductivity, and better compatibility with biological samples. By bridging materials chemistry, catalysis, and biomedical diagnostics, this work provides an integrated perspective on how transition-metal nanomaterials are enabling advances in point of-care sensing and real-time bioanalysis. The challenges associated with selectivity, long-term stability, and toxicity are also outlined, offering future directions for research and device development.
Keywords: Transition-metal nanomaterials, electrochemical sensing, non-enzymatic biosensors, nanostructures, biomedical diagnostics, hybrid composites

ICABB26-NM-PO-05

Smart Stimuli Responsive Nanocarriers for Precision Drug Delivery in the Tumour Microenvironment

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Abstract

Nanoengineered drug delivery systems that respond to the internal conditions of tumours are changing the face of cancer diagnosis and treatment. While conventional chemotherapy eliminates cancer cells, its non-selective distribution results in low drug accumulation at the tumour site and some patient may suffer from side effects. Advances in nanotechnology have led to the development of stimuli responsive nanocarriers that are designed to take advantage of the distinctive biology of the tumour microenvironment like acidic pH, high glutathione levels, abnormal enzyme activity, excess reactive oxygen species, and low oxygen or hypoxic regions. Platforms including polymeric micelles, mesoporous silica nanoparticles, and modified metallic nanosystems enable spatially controlled therapy by releasing drugs selectively in response to defined tumour biological conditions. Carriers that are sensitive to pH can rapidly unload therapeutics inside endosomes and acidic cancer tissue, helping drugs build up where they are most needed. Redox responsive systems, often constructed with disulfide or similar linkers, use the strongly reducing environment of cancer cells to trigger precise delivery into the cytoplasm. At the same time, enzyme-activated designs targeting matrix metalloproteinases allow protective coatings to detach at the right moment, improving penetration into dense solid tumours. These multi-stimuli approaches illustrate that a single nanocarrier can adapt to different regions of a tumour rather than relying on one rigid mechanism. The emerging nanocarrier strategies enable more efficient treatments characterized by minimal dosing, accelerated response, and compatibility with point of care theragnostic. Challenges such as scalable reproducibility, integrity of RNA and drug payloads, and validated biocompatibility are evaluated to map feasible progression to clinical use. Overall, stimuli responsive nanocarriers represent a patient focused approach to cancer therapy, where technology collaborates with tumour biology instead of placing additional burden on the body, opening pathways for safer and more personalized disease modulation.

Keywords: Stimuli responsive nanocarriers; Tumour microenvironment; Targeted drug delivery; pH responsive micelles; Redox triggered release

ICABB26-NM-PO-06

Biomedical Application of Metal and Metal-Oxide Nanoparticles: A Compiled Review

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Abstract

Metals and their oxides belong to the class of inorganic nanoparticles that play an important role in the biomedical industry. Their distinct qualities, such as small size, high surface area, and variety of shapes, enable them to achieve a range of properties, including electrical, magnetic, physiochemical, and catalytic ones. Copper, silver, and zinc oxide nanoparticles exhibit strong antibacterial properties. Gold and cerium oxide nanoparticles aid in wound healing in the field of tissue regeneration. The biological system interacts with metal-based nanoparticles in ways that facilitate targeted drug delivery, treatment of cancer, neurodegenerative disorders, and the prevention of infectious diseases. The aim of this review is to present a common synthesis method and the physiological characteristics of metal-based nanoparticles to explore deeply into their biomedical applications.

Google Scholar and PubMed were used to review the literature for this paper. Papers published between 2007 to 2025 in English has been considered. Editorial, conference, seminar, and event summaries are among the exclusion criteria. About 200 papers were examined out of which 116 have been cited. Metal-based nanoparticles overcome the time commitment and limit therapeutic effects of conventional techniques. Gold and silver nanoparticles are utilized in oncology to identify tumor biomarkers. Iron oxide nanoparticles are used in MRI-based techniques to identify tumors, track the spread of metastases, and evaluate the real-time response to treatment. Using zinc oxide or titanium dioxide in fluorescence-based biosensors for rapid pathogen detection enables direct diagnostics for infectious diseases. Metal-based nanoparticles have enormous potential for the next generation of biomedical technologies as they have a multifunctional nature and high efficiency.

The review offers an in-depth evaluation of new developments and highlights important research domains, offering significant perspectives for the reasonable development of trustworthy and effective metal-based nanotherapeutics.

Keywords: Metal-based nanoparticles; Neurodegenerative disorders; Drug delivery; Tissue engineering; Infectious diseases; Cancer.

ICABB26-NM-PO-07

Essential Oil Derived Iron Nanoparticles: A Sustainable Approach for Arsenic Remediation

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Abstract

Arsenic is among one of the most toxic heavy metal pollutants in aquatic environments, posing serious risks to both ecosystems and human health due to its persistence, high mobility, and carcinogenic effects. Conventional treatment approaches often prove inadequate, being either costly, inefficient, or prone to generating secondary waste, which makes the search for sustainable alternatives essential. Nanotechnology, particularly through the use of metal nanoparticles, offers a promising pathway for developing cost

effective and eco-friendly remediation strategies. In this study, iron nanoparticles (FeNPs) were synthesized using tea tree oil as a natural reducing and stabilizing agent, presenting a green alternative to traditional chemical synthesis routes. The FeNPs were comprehensively characterized using nanoparticle tracking analysis (NTA), differential scanning calorimetry (DSC), Zeta- potential, Fourier-transform infrared spectroscopy (FTIR), X-ray diffraction (XRD), field emission scanning

electron microscopy (FESEM), and UV–Visible spectroscopy. These analyses confirmed their nanoscale size distribution, crystalline nature, thermal stability, functional group interactions, and distinct optical features, validating the success of the synthesis. Batch photocatalytic studies demonstrated promising efficiency in the degradation of arsenic, underscoring the potential of green nanoparticles FeNPs as stable and effective photocatalysts. Overall, this work highlights a sustainable synthesis route and establishes tea tree oil mediated FeNPs as strong candidates for advanced environmental remediation technologies.

Keywords: Arsenic, Iron nanoparticles, Tea tree oil, green synthesis, Photocatalysis, Environmental remediation

ICABB26-NM-PO-08

Functional Graphene Analogues: Bridging Nanoscience and Biomedicine ***Neakanshika Chadha[1], Aman Sahu[2], Akansha Aggrwal[3*]***

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Abstract

Owing to the outstanding mechanical strength, large surface area, electrical conductivity, and tunable chemical functionality, Graphene and its derivatives are highly appealing nanomaterials for biomedical applications. Thus, the blending of graphene derivatives in the form of hydrogels and aerogels has resulted in the creation of innovative hybrid materials that possess novel physicochemical and biological characteristics. Particularly, Reduced Graphene oxide (rGO) hydrogels exhibit good biocompatibility, tunable porosity, and improved mechanical stability and hence are relevant to drug delivery, tissue engineering, wound healing, and biosensing. In the same manner, rGO aerogels, with light-weight, highly porous three-dimensional structures, have a very good application in cell scaffolding, antibacterial systems, and neural tissue regeneration where conductivity and mechanical pliability are essential. In this context, surface modification and composite building routes further improve dispersion, biocompatibility, and responsiveness to physiological stimuli for these materials. This review outlines recent advances in the design, synthesis, and biomedical deployment of graphene-derived hydrogels and aerogels, with main emphasis on the multifunctional applications in next-generation regenerative and therapeutic technologies. Also, this study presents the current trend and limitations on large-scale production of graphene based aerogel for technological applications, especially in biomedical devices and their utilization from laboratory to industrial level. Additionally, this comprehensive review sums up the designing of graphene scaffolds at bulk level with future technological advancement for next-generation biomedicines which is required for societal upliftment.

Keywords: Graphene based aerogels, hydrogels, gel technology, next generation biomedicines, biomedical devices.

ICABB26-NM-PO-09

Fabrication and characterization of cellulose-chitosan composites and their applications in food packaging industry

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Abstract

According to the United Nations Environment Programme, global plastic waste generation exceeds 400 million tonnes annually, highlighting the urgent need for sustainable and biodegradable alternatives to conventional packaging materials. Bacterial cellulose (BC), extracellularly produced by *Komagataeibacter* species, is a pure form of cellulose with a dense nanofibrillar structure and good mechanical strength. Chitosan (CS), derived from chitin, is biodegradable, non-toxic, and known for its antimicrobial properties. Combining BC with chitosan can improve the functional performance of

cellulose-based materials and broaden their application potential in food packaging industry. The aim of this research work is to fabricate bacterial cellulose–chitosan (BC–CS) composite films and study their properties for possible use in food packaging. The objectives include revival of *Komagataeibacter saccharivorans* BC-C1, optimization of culture conditions for BC production, purification and characterization of the obtained bacterial cellulose, and fabrication of BC–CS composite films. In the present study, the BC-C1 strain was successfully revived and cultured in Hestrin–Schramm medium, leading to the formation of a thin, translucent film indicative of early cellulose production. Further work will involve confirmation and characterization of BC using fourier transform infrared spectroscopy, x-ray diffraction, differential scanning calorimetry and scanning electron microscopy. techniques, followed by solvent-casting-based composite fabrication and evaluation of antimicrobial activity.

Keywords: Bacterial cellulose, Chitosan, Biodegradable composites, Food packaging, Antimicrobial films, Sustainable materials

ICABB26-NM-PO-10

Nano-Enabled Tools for Fast Disease Detection in Low-Resource Areas

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Abstract

Nanotechnology is transforming modern diagnostics by making disease detection faster, more sensitive, and more accessible, especially in regions where healthcare resources are limited. Because nanomaterials possess unique optical, magnetic, and surface properties, they can enhance biomarker detection, improve imaging clarity, and be easily integrated into compact point-of-care (POC) devices. Recent research shows that gold nanoparticles, magnetic nanomaterials, quantum dots, and carbon-based nanostructures can create affordable and highly sensitive assays for infectious diseases, cancer markers, and digestive system disorders. These nano-enabled diagnostic tools often require only small sample volumes, deliver rapid results, and can be paired with microfluidic chips or smartphone-based readers, making them suitable for field use where laboratory support is minimal. However, challenges such as nanoparticle stability, batch-to-batch consistency, and the need for wider clinical validation remain. This poster highlights the latest progress in nanotechnology-driven diagnostics and emphasizes how these innovations can support early disease detection and improve healthcare accessibility in underserved communities.

Keywords: Biosensing, Healthcare accessibility, Microfluidics, Nanotechnology, POC diagnostics

ICABB26-NM-PO-11

Simulation and Design Optimization of Electrochemical Biosensor for Enhanced Sensitivity

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Abstract

Electrochemical biosensors have attracted considerable interest for real-time, portable, and point-of-care diagnostic applications. This work focuses on the simulation-driven design and optimization of an electrochemical biosensor, aimed at achieving enhanced sensitivity through modifications of the choice of device material and electrode geometry.

The proposed sensor consists of three electrodes: working, counter, and reference. Numerical simulations were conducted using COMSOL Multiphysics, a commercial finite element analysis (FEA) platform, to investigate cyclic voltammetry (CV) responses and analyte concentration profiles. Key

design parameters, including electrode shape, dimensions, surface area, gap between the electrodes, substrate material, and choice of electrode material, were varied to evaluate their influence on current response and sensing uniformity. Multiphysics simulations of the electrochemistry and AC/DC modules were used to analyze electrochemical reaction behavior and electric field distribution. The suggested model uses the current module and electrochemical processes that happen at the electrodes and within the electrolyte solution, with redox reactions taking place at the interface between the metal and the solution. Voltammetric scan rate across multiple electrode configurations was swept for the evaluation of the total current response generated at the working area of electrodes with different dimensions.

The results show that optimized combinations of electrode geometry and spacing significantly enhance current response, improve analyte diffusion characteristics, and promote more uniform electrochemical sensing, underscoring the effectiveness of simulation-based optimization before device fabrication.

Keywords: Electrochemical simulation, COMSOL Multiphysics, electrode design optimization, point-of-care device

ICABB26-NM-PO-12

Sustainable Nanotechnology: Characteristics and Application of Green Nanoparticles for Cr(VI) Removal

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Abstract

The primary causes of rising environmental pollution levels are population expansion and industrialization. Researchers are now particularly concerned about water contamination brought on by direct emissions of industrial waste matter from a variety of industries, including textile, food, dye, and paint, which contain a significant amount of suspended organic and inorganic chemicals. Because of its limited biodegradability and chemical stability, chromium is one of the most prevalent heavy metals. Compared to trivalent chromium (Cr(III)), hexavalent chromium (Cr(VI)) is 100 times more hazardous and has a high water solubility. Therefore, Cr(VI) can pollute drinking water and enter aquatic environments like subterranean water. Numerous techniques, including chemical precipitation, ion exchange, reduction, membrane separation, and reverse osmosis, have been employed to remove Cr(VI) from industrial effluent. However, a number of disadvantages have hindered the majority of these techniques, including the formation of hazardous sludge, costly equipment, high maintenance costs, substantial energy consumption, and insufficient metal removal. A review of the literature indicates that the adsorption method appears to be a practical and reasonable option for eliminating chromium from aqueous solutions. Green nanotechnology, a recently developed extension of nanotechnology, is the focus of research interest in order to get beyond these restrictions. Green nanotechnology offers a cost-effective and environmentally beneficial way to create new nanostructures with plant extracts. A revolutionary technique with several uses in food production, medicine, and agriculture is plant-mediated nanoparticle (NP) synthesis. The synthesis of NPs from plants is gaining popularity due to the physicochemical properties of NPs. This environmentally friendly way of synthesizing nanoparticles has the extra advantage of prolonging their lifespan, which gets around the drawbacks of conventional chemical and physical NP production techniques.

Key words: Nanoparticles, Green Synthesis, Heavy Metals, Chromium, Pollution

ICABB26-NM-PO-13

Recent Advances in Disease Diagnosis using Optical Sensing Techniques, Surface Plasmon Resonance

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Abstract

The quest to improve quality of life by rapid, early diagnosis of various lifestyle and genetic disorders has opened the way for integrating different sciences for developing novel disease diagnostics. Traditional methods for diagnosing diseases are ineffective at achieving low limits of quantification, making it difficult to detect conditions early. This underscores the need for innovation and breakthroughs in diagnostic tools. Surface Plasmon Resonance (SPR) is one such novel approach that has expanded its horizons for the detection of a catalogue of biomarkers and for the early detection of diseases. The SPR technique largely depends on the total internal reflection of wave fronts and changes in refractive index on complex formation of the analyte with the biosensing element. Recent studies have shown advances in the exploration of various binding materials and biosensing elements for biomarker detection. Surface Plasmon Resonance (SPR) biosensors use a thin layer of noble metal, usually gold, on a glass prism to detect substances. They work by applying Self-Assembled Monolayers (SAMs), which anchor biorecognition elements, such as enzymes, antibodies, or DNA. These elements then bind to specific targets in a sample. SPR technology is crucial in drug discovery, early disease detection, and food safety, providing real-time, sensitive results without the need for labels. The versatility of SPR biosensors makes them essential tools in various fields, ensuring rapid and accurate detection of analytes while maintaining the integrity of biological samples. The review will highlight recent advancements in SPR technology in the healthcare sector.

Keywords: Optical sensing, Optics, Surface Plasmon Resonance (SPR), Disease diagnosis, Clinical diagnostics.

ICABB26-NM-PO-14

Portable Electrochemical Detection of p-Tau217 and Aβ Biomarker Ratios for Early Alzheimer's Screening

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Abstract

Alzheimer's disease is a chronic neurodegenerative disorder that progressively damages brain cells and leads to memory loss. Pathologically, it is linked to misfolding and aggregation of amyloid-β (Aβ42 & Aβ40) peptides and tau protein (p-tau217,p-tau181,p-tau213) in the brain. This project aims to develop a sustainable, gold nanoparticle based electrochemical biosensor designed for early stage detection to reduce its long term adverse effects.

The sensor will target p-tau217, along with Aβ40 and Aβ42, and computes the Aβ42/Aβ40 ratio, a clinically validated indicator of early Alzheimer's pathology. This approach directly addresses the major limitations of current technologies such as Simoa, Roche Elecsys and Fujirebio Lumipulse which remain laboratory bound, extremely expensive (instrument>$100,000), and dependent on cold chain storage, restricting their accessibility for routine use.

The concept uses disposable screen-printed carbon electrodes (SPCEs) modified with gold nanoparticles (AuNPs) synthesised through a simple green-chemistry method using Camellia sinensis (black tea) extract, which increases the electrode's surface area and conductivity to enhance sensitivity. To recognise key Alzheimer's biomarkers, molecularly imprinted polymers (MIPs) will be formed on the electrode using L-arginine (helps improve specificity) and small synthetic fragments of p tau217, Aβ42, and Aβ40.

In early Alzheimer's, plasma p-tau217 increases from roughly 1–3 pg/mL to 6–20 pg/mL, while the Aβ42/Aβ40 ratio drops from about 0.12 to ~0.06; these shifts should yield measurable electrochemical changes. Based on comparable AuNP–MIP platforms, projected limits of detection are 0.5–1 pg/mL for p-tau217 and 5–10 pg/mL for Aβ peptides, potentially enabling biomarker detection a decade or more before symptoms and supporting accessible, decentralised, and antibody-free screening for early Alzheimer's disease.

Keywords: Alzheimer, electrochemical detection, portable

ICABB26-NM-PO-15

Biogenic Synthesis And Characterization Of Bimetallic Nanoparticles For Multifunctional Applications

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Abstract

Nanotechnology has become an integral part of modern scientific research due to the unique physicochemical properties of nanoparticles and their broad applications in medicine, environment and industry. However, conventional chemical synthesis methods often involve toxic chemicals, high energy requirements and environmental hazards, which limit their large-scale and biomedical applicability. Green nanoparticles are biologically synthesised nanomaterials produced using plants, microbes, algae and natural polymers that act as environmentally benign reducing and stabilising agents, offering a safer alternative to chemical and physical synthesis routes. They reduce toxic by-products, require lower energy input and enhance biocompatibility, making them highly relevant for sustainable nanotechnology. Among these, bimetallic nanoparticles have garnered considerable interest due to their superior synergistic properties compared to monometallic counterparts. Silver–iron (Ag–Fe) bimetallic nanoparticles, in particular, exhibit enhanced antimicrobial, catalytic and biomedical activities, making them promising candidates for multifunctional applications. To overcome these limitations, green synthesis has emerged as a sustainable and eco-friendly alternative. In green synthesis, plant metabolites, microbial enzymes, algal biomolecules and biopolymers simultaneously reduce Ag(I) to Ag(0) and cap the nanoparticle surface, while factors such as pH, temperature, precursor concentration and extract composition determine size, shape and stability. The combination of silver and iron at the nanoscale results in improved stability, reactivity, and functional performance, which is highly desirable for advanced technological applications. The present review aims to study Ag–Fe bimetallic nanoparticles wherein the plant-based or biological extracts are used as natural reducing and capping agents. Such green approaches utilise phytochemicals present in plant materials to facilitate metal ion reduction and nanoparticle stabilisation, minimising toxicity and environmental impact. Hence, aligns with the principles of green chemistry by reducing waste generation and avoiding hazardous by-products. Overall, bimetallic Ag-Fe nanoparticles represent a promising, sustainable platform with broad biomedical, environmental and industrial potential.

Keywords: Green synthesis, bimetallic nanoparticles, silver–iron nanoparticles (Ag–Fe NPs), phytochemicals, nanotechnology

ICABB26-NM-PO-16

Optogenetics and Chemogenetics in Parkinson's Disease Neuromodulation

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Abstract

Chemogenetics and optogenetics, today, have emerged as preferable options over traditional approaches for investigating and therapeutically modulating dysfunctional basal ganglia circuits in Parkinson's disease (PD). These technologies allow for cell-type-specific and spatiotemporally refined modulations of neuronal activity, which are improvements over deep-brain stimulation and pharmacotherapy, as they lack spatial and molecular resolution. In optogenetic PD models, opsins (light-sensitive channels

or pumps) such as halo- or channelrhodopsin are incorporated into target neurons using viral delivery mechanisms. Further, neuronal activity is manipulated by delivering light of particular wavelengths to the targeted brain region via implanted optical fibers or LEDs. Chemogenetics, particularly, is useful to study circuit plasticity, behaviour, and treatment responses over longer time periods. This approach also uses viral vectors to target brain regions, generating designer receptors, such as DREADDs, which are activated only by synthetic ligands. This method allows for reversible and long-lasting modulation of neural circuits. Collectively, these technologies have helped reduce akinesia, rigidity, and dyskinesia in animal models, investigate non-motor symptoms of PD, and determine how best to integrate neuromodulation with other invasive and noninvasive PD strategies. Many improvements in PD related neuromodulation, such as in viral vector delivery systems, opsin safety, and receptor designs, are being developed to bring these models towards clinical translation. The present review showcases optogenetics and chemogenetics, becoming the basis of circuit-centric advanced therapeutic models and elucidating the mechanisms underlying the pathophysiology of PD.

Keywords: Parkinson's disease, optogenetics, chemogenetics, deep brain stimulation, DREADDs

ICABB26-NM-PO-17

Herbal nanoformulations in neurodegenerative disorders: Current progress and translational potential for Parkinson's disease

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Abstract

Conventional therapies for neurodegenerative disorders such as Parkinson's disease (PD) generally falter due to poor bioavailability, phytochemical instability, and blood-brain barrier (BBB), resulting in inadequate delivery to the CNS. To address these herbal nanoformulations have emerged as targeted nanomedicines, using liposomes, polymeric, and metallic nanoparticles to encapsulate plant-derived bioactives for precise PD delivery. These biocompatible systems travels the blood-brain barrier and enable sustained brain release, enhancing the pharmacokinetic predictability and controlled dosing, thus allowing surface functionalization for receptor-mediated targeting of dopaminergic neurons. Emerging preclinical and early clinical evidence of key herbal agents like curcumin, resveratrol, quercetin, *Ginkgo biloba* ginsenosides, and *Nigella sativa* thymoquinone targeting PD hallmarks via Nrf2/ARE activation, PI3K/Akt modulation, and MAO-B inhibition, suggests their potential to enhance neuroprotection while minimizing off-target effects. Studies in 6-OHDA-induced PD models show curcumin-PLGA nanoparticles and green-synthesized silver nanoparticles restore dopaminergic function, curb ROS/inflammation, boost mitochondrial ATP, and enhance motor performance while limiting apoptosis, positioning herbal nanoformulations as promising adjuncts or alternatives in PD therapeutics. This review highlights herbal nanoformulation in neurodegeneration, focusing on PD translational potential through amplified brain uptake and multifunctionality, while addressing challenges in extract standardization, scalable synthesis, biocompatibility, and safety for clinical use thus representing phytotherapy nanotechnology fusion.

Keywords: Parkinson's disease, herbal nanoformulation, neurodegeneration, phytochemicals, oxidative stress, blood–brain barrier, nanocarrier, targeted delivery, neuroprotection, translational medicine.

ICABB26-NM-PO-18

Analysing Exosome-based Therapeutic Delivery for Parkinson's Disease: A Next-generation Nanomedicine Approach

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Abstract

Parkinson's disease (PD) is a neurodegenerative disorder characterized by progressive neuronal loss, oxidative stress, mitochondrial dysfunction, and abnormal protein aggregation. Despite the presence of pharmacological treatments, their ability to halt disease progression is limited due to inadequate drug

bioavailability and inaccessibility to the central nervous system (CNS). Exosome-based nanomedicines have recently been recognized for their ability to target specific diseases, in this case, Parkinson's disease. Exosomes are naturally occurring extracellular vesicles secreted by the cells for signalling that can efficiently cross the blood-brain barrier (BBB) and are biocompatible carriers of therapeutically important molecules. Various agents can be engineered to be added to exosomes for therapeutic applications to address critical mechanisms, such as oxidative stress, inflammation in the nervous system, mitochondrial dysfunction, and neuron aggregation. These therapeutic agents include neuroprotective agents, small interfering RNAs, microRNAs, and herbal compounds. Recent studies have proved that exosomes, both derived from stem cells and macrophages, have the ability to deliver neuroprotective agents to damaged neurons which improve the functioning of the mitochondria in these cells which lessen the rate of cell apoptosis. This review examines the current advancements in exosome-based nanotherapeutics for Parkinson's disease, highlighting their potential to revolutionize nanomedicine-driven neuroprotection. Additionally, it also discusses critical challenges in exosome isolation, large scale production, cargo stability, and safety profiling, which must be considered to translate this approach into viable clinical applications.

Keywords: Parkinson's disease, exosomes, nanomedicine, targeted delivery, blood–brain barrier, neuroprotection, alpha-synuclein, stem cell exosomes, oxidative stress, translational nanotechnology.

ICABB26-NM-PO-19

Nanobiofertilizers: Healing the Soil Sustainably

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Abstract

Nanobiofertilizers represents an innovative fusion of nanotechnology and plant growth-promoting rhizobacteria (PGPR) or beneficial fungi through engineered nanomaterials. It enhances nutrient use efficiency and simultaneously remediate contaminated soils. This technology offer a scientific strategy for sustainable agriculture. Evidences indicate that this technology can improve crop productivity, restore soil health, and mitigate heavy metal and organic pollutant stress effectively.

Intensive application of chemical fertilizers and pesticides has led to nutrient imbalances, loss of microbial diversity and accumulation of persistent pollutants reducing soil fertility. Conventional fertilizers exhibit low nutrient use efficiency and runoff and leaching of these chemicals worsens eutrophication and other issues. Thus there is urgent need for innovative methods that support high agronomic efficiency causing minimal environmental damages.

Nanobiofertilizers are formulations in which PGPR are associated with nanoscale carriers to enable targeted and controlled release of nutrients in the rhizosphere. Engineered nanoparticles (e.g., nano oxides or nano-encapsulated nutrients) associated with microbs improve nitrogen fixation, phosphate solubilization, siderophore production and phytohormones production in plants.

Studies report that nano-fertilizers can maintain agricultural yields with reduced application compared to conventional fertilizers. Nano-biofertilizers also stimulate soil enzyme activities such as urease and phosphatases. They also promote beneficial microbial diversity and organic matter turnover hence improving long-term soil fertility. This causes improvements in soil structure, aggregation and porosity, contributing to better water retention and resilience under drought and salinity stress. Nano-microbe partenership also accelerate degradation of pesticides and other organic pollutants and immobilize or transform toxic pollutants into less bioavailable forms reducing toxicity in soil systems. Metal and metal-oxide nanoparticles (e.g., nano-zero-valent iron, Fe- and Ti oxides) help to adsorb and immobilize cadmium, lead, zinc and other heavy metals. Associated PGPR reduce plant uptake and enhance detoxification through chelation, redox transformation and antioxidant defense.

Present review suggests that nano-biofertilizers can increase yields, improve nutrient-use efficiency and reduce dependence on synthetic fertilizers, hence helps in lowering nutrient leaching and soil degradation. Nanobiofertiliers also enhance plant tolerance to abiotic stresses (salinity, drought, and heavy metals), supporting sustainable soil health and consistant agricultural production

under changing climatic conditions. Still more research on field-scale validation, risk assessment and regulatory frameworks is required to fully realize the potential of this emerging technology in restoring degraded soils and securing food systems.

Keywords: Nanobiofertiliser, Plan growth promoting rhizobacteria (PGPR), Soil remediation, Sustainable agriculture

ICABB26-NM-PO-20

Advancement in Nano Medicine for Cancer Therapy

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Abstract

Cancer remains a significant global health challenge, representing one of the leading causes of mortality and morbidity worldwide, with millions newly diagnosed each year despite ongoing advances in medical science. Conventional cancer therapies like chemotherapy, radiotherapy, hormone therapy etc frequently encounter limitations including non-specific targeting, adverse effects and suboptimal efficacy. Therefore, exploring and developing more efficient methods to enhance cancer therapy is an urgently important problem that must be solved. With the development of nanotechnology, nanomedicine has shown a good application prospect in improving cancer therapy. Nanoparticles enable the precise delivery of therapeutic agents or genetic material to tumor sites via passive or active targeting mechanisms, thereby enhancing therapeutic efficacy and minimising harm to healthy tissues. Nanoparticles further exploit tumor microenvironment features—such as leaky vasculature, elevated interstitial pressure, and acidic extracellular pH to facilitate selective extravasation and payload release precisely at disease sites. Nanomedicine strategies also demonstrate remarkable potential in overcoming multidrug resistance by modulating efflux pathways, enhancing intracellular drug retention and facilitating co-delivery of chemotherapeutic agents with resistance-modulating compounds. Beyond mere tumor localization, nanocarrier systems promote deeper tissue penetration and superior cellular uptake, thereby elevating intracellular drug concentrations. Sophisticated approaches further enable targeting of specific subcellular organelles, thereby refining treatment precision and potency. Nanocarrier-mediated combination therapies integrate multiple modalities into a unified platform, yielding synergistic effects and superior clinical outcomes. Taken together, these capabilities position nanomedicine as a transformative paradigm in oncology, with the potential to bridge the gap between preclinical innovation and tangible clinical benefit.

Keywords: tumor, cancer therapy, nanomedicine, nanocarrier

ICABB26-NM-PO-21

TrigemPatch: TENS Device For Trigeminal Neuralgia

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Abstract

Older adults experiencing chronic nerve discomfort (trigeminal or post-herpetic) have difficulty carrying out their daily tasks. Significant surgical intervention or the use of highly concentrated pain-relieving medications, can have many risks, as well as inadequate funding for such treatments. Hence, we need to examine other options that are safe, inexpensive, and will consequently alleviate the burden of this condition on older adults. The TrigemPatch is a small, easy to use, wearable relief product, which can provide pain-free living to older adults who experience chronic nerve pain.

TrigemPatch being, skin-friendly as well as lightweight can be worn directly over the site of your nerve pain. The patch emits a constant low voltage pulse of electromagnetic energy to sooth your overactive nerves and stops pain signals before they reach your brain; hence, the patch should be effective for people of all ages. To complement this effect, and improve overall effectiveness, this patch allows

several types of natural anti-inflammatory herbs, which work to alleviate nerve irritation through a conductive gel that is applied to your skin.
In addition to providing a pain-relieving effect and reducing nerve irritation, the TrigemPatch contains built-in sensors that monitor your body's response to pain and automatically adjust shock stimulation levels, as needed, or when you experience increased pain levels.
Keywords: Trigeminal neuralgia , TENS Technology, Flexible Sensors, Volunteer Feedback , Arduino-based Prototype, Curcumin (Turmeric)

ICABB26-NM-PO-22

Bimetallic Nanocomposites for Advanced Water Purification: Synergistic Mechanisms, Comparative Performance, and Environmental Applications

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Abstract
Bimetallic nanocomposites are a new and improved system for treating water due to the synergistic interaction between two metals, which enhances reactivity, catalytic efficiency, and contaminant removal compared to conventional and monometallic systems. In this study, we compare different combinations of bimetallics, including Fe-Cu, Fe-Ni, Fe-Pd, Zn-Cu and Ag-Fe and appraise them as suitable for water purification to remove heavy metals, organic contaminants, nutrients, algal toxins and microbial contaminants. The advantages of the bimetallic treatment over the traditional ones, such as coagulation-flocculation, chlorination and single stage filtration, are is the fact that the bimetallic treatment has faster reaction kinetics, is more efficient at scavenging trace elements at lower levels, produces less secondary sludge and multifunctional mechanism of operation in one treatment step. A direct comparison between the bimetallic and monometallic systems reveals that the bimetallic systems have a better electron transfer, together with a higher catalytic activity and selectivity against contaminants due to the presence of galvanic coupling and surface synergy effects, which are not observed in the single-metal treatment. By working together, the adsorption-reduction and electron-transfer processes allow the efficient removal of heavy metals by Fe-Cu bimetallic nanocomposites, and indirectly reduce the risk of algal toxins by eliminating drivers of eutrophication. Cu-Ni systems are used to provide benchmarks of adsorption-based scale-up, though Fe-Ni and Fe-Pd are also used to directly degrade toxins by reductive catalysis and Fe-Ag composites are used to degrade toxins under light by photocatalysis. In addition to streams, the bimetallic types of treatment can be used in lakes, reservoirs, industrial effluents and drinking water sources, which points to the possibility of these types of treatment being scalable and high-performance alternatives to contemporary water purification.
Keywords: Bimetallic nanocomposites, Water purification, Synergistic effects, Heavy metal removal, Advanced water treatment

ICABB26-NM-PO-23

Microbiome-Safe Calcium Carbonate Nanocarriers Enhance Drought Tolerance in Iraqi Wheat

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Abstract

Especially in dry parts of the Middle East like Iraq, food security is seriously threatened by rising problems of climate volatility and severe water shortage.Under abiotic stress, calcium (Ca) is a necessary macronutrient that is vital for controlling signal transduction pathways and preserving cell wall integrity.Low solubility and variable bioavailability, however, restrict the traditional uses of bulk Calcium sources.This research looks at how well Calcium Carbonate nanoparticles (CaCO3 NPs) coated with the amphiphilic triblock copolymer Pluronic F68 (F68) can help the Iraqi wheat variety Triticum aestivum L. cv. Ibaa 99 receive more of its nutrients.To guarantee microbiome safety, the concurrent interaction of this nanocarrier system with a local helpful rhizobacterium, Pseudomonas sp. (isolate PK-1), was tested.The University of Karbala's laboratory facilities were the sole location for the study'sStable F68-CaCO3 composites were shown by physicochemical analysis to have been successfully produced.Biological studies showed that F68-CaCO3 NPs moved to shoot tissues and stuck to root surfaces, especially in leaf trichomes.Soil application of F68-CaCO3 NPs under drought stress circumstances boosted shoot dry weight by 13.6% ($p < 0.01$) and sustained greater Relative Water Content (84.7%) than controls.Along with these advances, proline buildup decreased, indicating that improved Calcium bioavailability and membrane stabilisation helped to reduce osmotic stress.Importantly, unlike the osmolyte glycine betaine (GB), the F68-CaCO3 system showed no toxicity to Pseudomonas sp. PK-1 and was not digested by the bacteria.Under the experimental settings of this research, this supports the hypothesis that F68-CaCO3 is a microbiome-friendly nanocarrier platform.These results indicate that biocompatible Calcium-based nanocarriers provide a sustainable and effective way to provide vital nutrients to Iraqi crops while also keeping the functional integrity of the helpful root microbiome.

Keywords: Nanotechnology, Wheat (Ibaa 99), Drought Stress, Calcium Carbonate Nanoparticles, Pseudomonas sp., Pluronic F68, Nanotoxicology, Microbiome-Safe.

Session 4:
Next-Generation Nanobiotech and Nano-Enabled Theragnostics
Oral Presentations

ICABB26-NM-OP-01

Effect of pH on Fungal Mediated Synthesis of Nickel Nanoparticles for Degradation of Azo dyes

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Abstract

Dyes are the coloured substances that are applied on different substrates such as textiles, leather and paper products, etc. Azo dyes released from the industries are toxic and recalcitrant wastewater pollutants therefore it is necessary to degrade these pollutants from water. Researchers have developed several physiochemical processes in the last few decades for partial and complete degradation of these dyes. Among these processes, the photocatalytic process is an effective method for degradation of dye, as it is physically and chemically stable. There are various photocatalysts that have been employed for the treatment of wastewater especially for degradation of azo dye. But these photocatalysts are generated through chemical or electrochemical methods. In the present study, the nickel nanoparticles (NiNPs), were generated through the biological process and exhibited for the catalytic degradation of azo dye. The NiNPs were synthesized by using the cell-free approach i.e. extract of fungal strain Rhizopus sp. (SG-01) from nickel nitrate, which significantly degrades the azo dye (methyl orange). The effect of pH on the synthesis of NiNPs was observed by varying the pH conditions from acidic to alkaline of cell-free extract of fungal strain. The maximum reduction of nickel nitrate was observed at pH 12.6 as Alkaline conditions favoured rapid reduction and higher nucleation rates, yielding smaller, more uniform nanoparticles, while acidic media produced larger, irregular aggregates due to limited reduction efficiency and weaker stabilization by fungal biomolecules. The amount of catalyst was optimized by varying concentration of NiNPs (4mg/ml, 8mg/ml, 12mg/ml, 16mg/ml and 20mg/ml) for 5ml of 10 ppm methyl orange (MO) dye separately. The concentration and time dependent study demonstrates that the biogenic NiNPs could effectively degrade the methyl orange dye up to 73.05% with minimum concentration (16mg/ml) of NiNPs within 24 h of reaction. Thus, the use of biogenic nickel nanoparticles for dye degradation as outlined in the present study can provide an alternative and economical method for the synthesis of NiNPs as well as degradation of azo dyes present in wastewater and is helpful to efficiently remediate textile effluent.

Keyword: Azo dyes; Wastewater treatment; Biogenic; Nickel nanoparticles; Degradation

ICABB26-NM-OP-02

POTENTIAL OF TRANSDERMAL DRUG DELIVERY SYSTEMS FOR TUBERCULOSIS TREATMENT IN INDIA

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Abstract

India reports an estimated 2.7-3.0 million tuberculosis cases each year, accounting for nearly one-quarter of the global TB burden. However, treatment outcomes are often affected by the long duration of therapy, high pill burden, and systemic side effects associated with conventional oral and injectable anti-tubercular drugs. First-line agents such as isoniazid and rifampicin show variable bioavailability, extensive first-pass hepatic metabolism, and fluctuating plasma drug levels, which can contribute to hepatotoxicity and treatment discontinuation during the standard 6-month regimen. Although the DOTS strategy is effective, programmatic data indicate loss-to-follow-up rates of approximately 5-15%, largely due to the need for repeated visits to healthcare facilities that interfere with patients' work, income, and daily responsibilities. In this context, transdermal drug delivery systems (TDDS) have gained attention as a potential alternative approach for TB treatment. Recent advances in transferosome-based carriers, polymeric nanoparticles, lipid vesicles, and microneedle-assisted patches have demonstrated the feasibility of delivering key anti-TB drugs through the skin in a sustained and

controlled manner, while bypassing hepatic first-pass metabolism. Transdermal platforms offer non-invasive, self-administered drug delivery with the potential to reduce dosing frequency and improve pharmacokinetic consistency. While clinical translation is still limited, available evidence highlights the promise of transdermal drug delivery as a patient-friendly strategy to support improved TB treatment outcomes in high-burden settings such as India.

Keywords: Tuberculosis, Transdermal drug delivery, Drug patches, Transdermal patches, Anti-TB drugs, Non invasive therapy

ICABB26-NM-OP-03

Nanotherapeutics for Lung Cancer

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Abstract

Lung cancer, known as one of the deadliest cancers with the highest mortality rate worldwide, is due to tumor heterogeneity, drug resistance, and systemic limitations of conventional therapies. Chemotherapeutic drugs for lung cancer have several limitations, including severe off-target toxicity, lack of tumor selectivity, and multidrug resistance,and so there are urgent therapeutic interventions. Nanotechnology has emerged as a transformative approach that offers the potential to revolutionize the treatments available for lung cancer by providing a targeted drug delivery system, enhanced bioavailability, and reduced side effects. This review comprehensively discusses the latest Advancements in the nanocarrier systems, including Exosomes, Niosomes, Liposomes, Polymeric nanoparticles, Solid lipid nanoparticles, and Dendrimers etc. Each of these nanocarriers offers unique structural and functional properties that can be utilized to enhance tumor targeting, bioavailability, efficacy, and controlled drug release, among other benefits. Liposomes and Niosomes help in enhancing encapsulation stability and efficiency. Polymeric nanoparticles facilitate tunable surface modifications and controlled release kinetics. Exosomes are the endogenous vesicles secreted by the cancer cells. This review establishes nanomedicine as a promising next-generation lung cancer therapy that is capable of addressing all existing challenges.

Keywords: Liposomes, Niosomes, Polymeric nanoparticles, Solid lipid nanoparticles, Exosomes, Dendrimers

ICABB26-NM-OP-04

Next Generation RNA Biosensing for CNS Disorders Using CRISPR-Cas13 and Gold Nanostructures

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Abstract

Central nervous system (CNS) disorders such as Alzheimer's disease, Huntington's disease, and amyotrophic lateral sclerosis are closely linked to abnormal RNA expression and toxic gene products. However, detecting these molecular changes at an early stage remains difficult because many disease biomarkers are present at extremely low levels. To overcome this limitation, CRISPR Cas13 RNA detection paired with gold nanostructures improves sensitivity while allowing accurate quantification of central nervous system biomarkers. CRISPR Cas13 is widely used for RNA diagnostics because of its unique ability to cleave nearby RNA molecules after recognizing a specific target sequence. This is

used to detect important targets such as CAG expanded huntingtin transcripts, mutant SOD1 RNA, and disease associated microRNAs including miR-21. Once activated, Cas13 triggers cleavage of reporter RNAs that control the behavior of gold nanoparticles (AuNPs). Owing to their strong plasmonic and electrical properties, even subtle molecular changes in AuNPs can be converted into measurable signals. To achieve accurate quantification, the released AuNPs are analyzed using solid-state nanopore sensing, where each nanoparticle produces a distinct electrical signature as it passes through the pore. This approach allows detection at femtomolar concentrations without the need for extensive target amplification with high specificity through the use of programmable guide RNAs. In contrast to conventional PCR based methods, that require complex laboratory equipment, this platform supports portable and point-of-care-friendly formats and provides reliable quantitative readouts. Overall, the integration of CRISPR Cas13 with gold nanostructures create a powerful diagnostic framework for CNS disorders. BBy combiningthe high specificity of programmable RNA targeting with the sensitivity of nanoscale materials and electronic readouts, this helps in identification of neurological biomarkers. This approach enables earlier detection, better tracking of disease progression, and personalized management of neurodegenerative diseases.

Keywords: Central nervous system disorders; CRISPR-Cas13; RNA diagnostics; Gold nanoparticles; Nanobiosensors

ICABB26-NM-OP-05

Tiny Particles, Big Impact: A Nano-Redesign of Bedaquiline for DR-TB

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Abstract

MDR-TB is one of the greatest global health concerns, with poor outcomes in terms of unsuccessful treatments and mortality often linked to poor adherence due to very prolonged drug regimens, among other factors. One of the major reasons for non-compliance in tuberculosis therapy is gastrointestinal irritation due to current anti-tubercular medications. Bedaquiline has recently revolutionized the treatment of MDR-TB by offering a more effective therapeutic option; however, its use is limited due to side effects such as nausea, abdominal pain, and hepatotoxicity, which may also result in non-compliance with this potentially life-saving therapy. This review examines the current landscape of oral nanoparticle delivery systems for bedaquiline, aiming to improve tolerability without affecting efficacy. Various studies have utilized PLGA to formulate the drug using biodegradable poly (lactic-co-glycolic acid) nanoparticles that could protect the drug from the harsh acid environment of the stomach. Nanoparticles were designed for targeted release within the small intestine under conditions of enhanced polymer erosion. The literature highlights that various computational models have been employed to investigate drug entrapment, nanoparticle stability, and drug release dynamics under conditions mimicking the gastrointestinal tract. Accordingly, a consensus across recent literature suggests a significant reduction in gastric delivery, and studies have demonstrated that PLGA-based formulations can extend bedaquiline release for up to 48-50 hours within the intestinal environment. Physiologically based pharmacokinetic modelling further predicts flatter plasma drug concentrations, with reduced fluctuations commonly linked with conventional oral formulation. Such stabilization of drug concentrations may decrease the probability of concentration-dependent side effects while maintaining the antibacterial effect. Nanoparticle encapsulation, by reducing direct contact of bedaquiline with the stomach lining, nanoparticle encapsulation is universally acknowledged as a strategy to enhance patient tolerance by minimizing gastrointestinal irritation. In fact, this may lead to improved treatment continuation and outcome in MDR-TB, pending confirmation through in vivo and clinical studies.

Keywords: Multidrug-resistant tuberculosis, Bedaquiline, PLGA nanoparticles, Sustained release, Gastro-protective formulation.

ICABB26-NM-OP-07

Advances in Theranostics for Biofilm-Associated Multidrug-Resistant Fungal UTIs: Innovations, Challenges, and Future Directions

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Abstract
Urinary tract infections (UTI) are one of the most prevalent infections in the world. It affects about 150 million humans every year. Even though these infections are usually seen as bacterial, the increasing number of fungal UTIs predominantly occurs due to Candida Albicans and "Super Fungi" such as Candida Auris which gives key worldwide health crises. These pathogens are most probably multi drug resistance (MDR) , they create a strong structure called biofilm on the surface of human tissue like urinary catheters. Biofilm operates as a safeguarding layer which keeps fungi protected from the host' immune system and also improves antifungal resistance up to 2000 times as compared to free floating cells. This leads to long term recurrent infections and increasing death rates among people with low immunity.
To address these challenges, theranostics has emerged as a novel approach. This strategy integrates rapid, point-of-care diagnostics with targeted therapies within a singular nanoplatform. It surpasses conventional, arduous culture methods by employing real-time detection via nano-biosensors, exemplified by SERS-based nanochips. Furthermore, it selectively targets specific constituents of the fungal cell wall including lipopolysaccharides and β-glucans. Major advancements include drug delivery systems that leverage nanotechnology, that use metals such as silver and gold, carbon-based materials like carbon dots and nanotubes, and Metal-Organic Frameworks (MOFs). These materials function as "smart" carriers, capable of sustained drug release, penetration of dense biofilms, and the provision of combined antimicrobial effects through photothermal hyperthermia and reactive oxygen species (ROS) generation.
Moreover, newly invented intelligent antimicrobial gadgets, including catheters coated to intercept biofilms and vaccine development offering ways to avoid infections before they even start. When these smart devices are coupled with natural plant based remedies like cranberry and garlic extracts which helps us in preventing microbe's adhesion. The therapies lead to the improvement in the efficiency of treatments and also lowering the dangerous side effects. Even though having complications in the clinical implementations and compatibility, these combined brings an innovating and remarkable step forward in proactive diagnosis and treatment of Multi Drug Resistant fungal UTI.
Keywords: Biofilms, UTI's, Plant based treatment, Theranostics, Nanotechnology

ICABB26-NM-OP-08

Cellular Viability and Uptake Studies of Berberine and Hesperidin Lipid Hybrid Nanoparticles in a Depression-Related Neuronal Cell Model

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Abstract
Depression is a complex neuropsychiatric disorder associated with neuronal dysfunction, oxidative stress, and altered cellular viability. Natural bioactive compounds have attracted considerable attention for their potential neuroprotective effects in depression-related cellular models. In the present study, the in vitro cellular effects of berberine lipid hybrid nanoparticles and hesperidin lipid hybrid nanoparticles were evaluated using Neuro-2a neuronal cells. Cell viability was assessed by the MTT assay, while cellular uptake studies were performed to examine intracellular internalisation. The MTT assay demonstrated high cell viability following treatment, with berberine exhibiting 95% cell viability and hesperidin showing 90.11%, indicating good cellular compatibility and neuroprotective potential in Neuro-2a cells. Cellular uptake was evaluated using confocal laser scanning microscopy, where rhodamine labelled nanoparticles exhibited red fluorescence, confirming intracellular internalisation,

while DAPI staining produced blue fluorescence, indicating the cell nuclei. The co-localisation of red fluorescence within the DAPI-stained cells confirmed efficient uptake of both nanoparticle formulations by Neuro-2a cells, supporting their intracellular activity. Overall, the findings suggest that berberine and hesperidin encapsulated nanoparticles elicit favourable cellular responses in depression-associated in vitro models and warrant further investigation for depression-related therapeutic applications.

Keywords: Depression, Lipid hybrid nanoparticles, Neuro-2a cells, Cellular uptake, Confocal microscopy, Neuroprotection.

ICABB26-NM-OP-09

Air Pollution Mediated Neuroinflammation and Its Therapeutic Intervention By Nanoparticles Based on Drug Delivery System.

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Abstract

Air pollution exposure causes systemic inflammation and oxidative stress; it can also migrate fine particulates (<2.5 μm) from the lungs to the brain via both the circulatory and olfactory systems. Thus, there is an important need to integrate nanotechnology with delivery methods that are specific to an inflammatory response to create nanoparticles that can block pro-inflammatory mediators, reduce oxidative stress, and establish the transmission and signaling pathways in the CNS. Therapeutic delivery systems engineered with the capability to treat neuroinflammation may provide a solution to one of the most critical factors facing cognitive decline and neurodegenerative disease(s) attributed to environmental pollutants.

Nanotechnology has provided a developing platform that will allow the engineering of multi-functional therapeutic systems with cellular and molecular mechanisms of action. The rationale behind this study is to investigate drug delivery systems using nanoparticles. The use of nanoparticles for drug delivery, particularly at the brain-lung axis level, shows how the immune and inflammatory regulatory pathways interact in both directions between the brain and lungs. Changes to the sizes and surface charges of nanoparticles, as well as the use of ligands during the functionalization process, are ways to improve their therapeutic effect. These changes will enhance the bioactivation of medications and enable them to target inflammatory regions in the lungs and central nervous system.

Future studies should pay more attention to enhancing the safety of nanoparticles, investigating the long-term distribution of nanoparticles in living organisms, and testing the efficacy in preclinical models of neuroinflammatory diseases derived from air pollution. This conceptual framework aims to guide researchers in designing next-generation nano therapeutics capable of mitigating the rising neurological burden associated with environmental pollutants.

Keywords: Nanotechnology, Brain–lung axis, Air pollution, Oxidative stress, Blood–brain barrier (BBB), CNS protection, Environmental neurotoxicology, Central nervous system

ICABB26-NM-OP-10

Bioengineered Nanocarriers for Targeted Drug Delivery Across the Blood–Brain Barrier

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Abstract

The blood–brain barrier (BBB) is a critical physiological safeguard that tightly regulates molecular exchange between the bloodstream and the central nervous system (CNS), thereby limiting the entry of most therapeutic agents into brain tissue. While essential for maintaining neural integrity, this selective permeability significantly restricts the effectiveness of conventional drug delivery approaches for neurological disorders.

Bioengineered nanocarriers have emerged as advanced delivery systems capable of addressing BBB-associated transport challenges. These nanoscale platforms are developed using biodegradable and biocompatible materials such as polymers, lipids, proteins, and biomimetic hybrids, enabling controlled

drug encapsulation and release. Surface functionalization with targeting ligands, peptides, or antibody fragments allows nanocarriers to exploit endogenous BBB transport mechanisms, including receptor-mediated and adsorptive transcytosis, thereby enhancing brain uptake.
Compared to conventional formulations, nanocarrier-based systems exhibit improved pharmacokinetic behavior, enhanced drug stability, and reduced off-target toxicity. Their modular architecture supports the delivery of diverse therapeutic cargos, including small molecules, nucleic acids, and biologics, making them suitable for treating complex CNS conditions such as neurodegenerative diseases, brain tumors, and neuroinflammatory disorders. Recent advances in stimuli-responsive nanocarriers further enable spatially and temporally controlled drug release within the brain microenvironment.
Despite their significant potential, challenges related to long-term biosafety, large-scale manufacturing, and regulatory translation remain key obstacles to clinical implementation. Addressing these issues through interdisciplinary research and rational nanocarrier design will be critical for advancing BBB-targeted drug delivery. Overall, bioengineered nanocarriers represent a promising and strategically important approach for improving therapeutic outcomes in CNS disease treatment.
Keywords: Bioengineered Nanocarriers, Blood–Brain Barrier (BBB) Targeting, Nanomedicine for Neurological Disorder, Receptor-Mediated Transcytosis, Targeted CNS Drug Delivery.

ICABB26-NM-OP-11

Development and Evaluation of Plant Extract-Loaded Liposomes as a Therapeutic Strategy for Acute Respiratory Distress Syndrome

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Abstract
Acute Respiratory Distress Syndrome (ARDS) is a severe inflammatory lung condition characterised by excessive oxidative stress, cytokine release, and impaired alveolar capillary integrity, leading to high morbidity and mortality. Although plant-derived phytochemicals possess potent antioxidant and anti-inflammatory properties, their therapeutic application is often restricted by poor stability and limited bioavailability. In this study ethanolic extract of the plant was encapsulated into liposomes to enhance its delivery and therapeutic efficacy against ARDS. the liposomal formulation was prepared using the ethanol-injection method and characterized for particle size, zeta potential, encapsulation efficiency and morphological properties. In vitro antioxidant assays were evaluated using standard assays. The extract-loaded liposomes exhibited nanoscale particle size, high encapsulation efficiency, and improved physicochemical stability compared to the free extract. These findings suggest that liposomal encapsulation enhances the therapeutic potential of plant ethanolic extract. Overall, this liposomal phytotherapeutic approach represents a promising nanotechnology-based strategy for managing ARDS.
Keywords: ARDS, liposomes, characterization, ethanolic extract, antioxidant

ICABB26-NM-OP-12

Green Synthesis of Platinum Nanoparticles Using Plant Leaf Extracts: A Comparative Study and Potential Applications

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Abstract
Green synthesis of metal nanoparticles has gained much attention as a sustainable alternative to conventional chemical and physical methods because it relies on eco-friendly, biologically derived reducing and stabilizing agents. In this study, platinum nanoparticles were synthesized using a green,

plant-based synthesis approach in which leaf extracts from *Azadirachta indica, Mangifera indica, Syzygium cumini, Hibiscus rosa-sinensis,* and Musa *spp.* were used as the reducing and stabilizing agents. Platinum salt was used as the metal precursor, while two different concentration combinations of each extract were tested to assess their effect on nanoparticle synthesis. During continuous monitoring, nanoparticle formation was predominantly observed in systems incorporating extracts of *Azadirachta indica, Mangifera indica,* and *Syzygium cumini*. Alterations in nanoparticle formation among the different plant extracts indicate that phytochemical composition and extract concentration play important roles in the reduction and stabilization of platinum ions.

The findings confirm that a wide range of plant leaf-derived extracts can be successfully used for the green synthesis of platinum nanoparticles and build a comparative framework for selecting biologically efficient sources. The synthesized nanoparticles demonstrate relevance across a wide range of applications because of the remarkable physicochemical and catalytic properties of platinum at nanoscale. These applications encompass catalysis and electrocatalysis in fuel cell systems, biomedical uses including anticancer and antioxidant studies, biosensor development through signal amplification, antimicrobial approaches aimed at bacterial inhibition, environmental remediation via pollutant degradation, and electronic applications involving sensors and nanoelectrodes. Collectively, the results indicate that plant-mediated synthesis represents an eco-friendly, versatile, and scalable approach for the production of platinum nanoparticles with broad interdisciplinary applications.

Keywords: Green synthesis, Platinum nanoparticles, Plant leaf extracts, Phytochemical-mediated reduction, Sustainable nanotechnology

ICABB26-NM-OP-13

Design and Simulation of a Label-Free MoS_2 BioFET for Femtomolar Detection of Lung Cancer Biomarkers

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Abstract

Early diagnosis of lung cancer is critical for improving patient survival rates, yet current diagnostic methods often lack the sensitivity required for detecting low abundance biomarkers. This paper presents the design and Technology Computer Aided Design (TCAD) simulation of a highly sensitive Biofield-Effect Transistor (BioFET) utilizing a monolayer Molybdenum Disulfide (MoS_2) channel. The 2D MoS_2 material is selected for its exceptional electrostatic control and high carrier mobility, which are advantageous for label-free biosensing.

The device is engineered to detect specific lung cancer biomarkers, such as Cytokeratin 19 fragment (CYFRA 21-1), by functionalizing the channel surface with specific antibodies. Our simulation results analyze changes in channel conductance and threshold voltage upon biomarker binding. The study optimizes device parameters, including channel length, oxide thickness, and doping concentration, to maximize the signal-to-noise ratio. The results demonstrate that the proposed MoS_2 BioFET achieves a detection limit in the femtomolar range, significantly outperforming traditional silicon-based sensors. This research validates the potential of 2D material-based FETs as rapid, point-of-care diagnostic tools, offering a scalable solution for non-invasive lung cancer screening through electronic readout systems.

Keywords: BioFET, MoS_2, Biosensor, Lung Cancer, TCAD Simulation, Nanotechnology, Label-Free Detection

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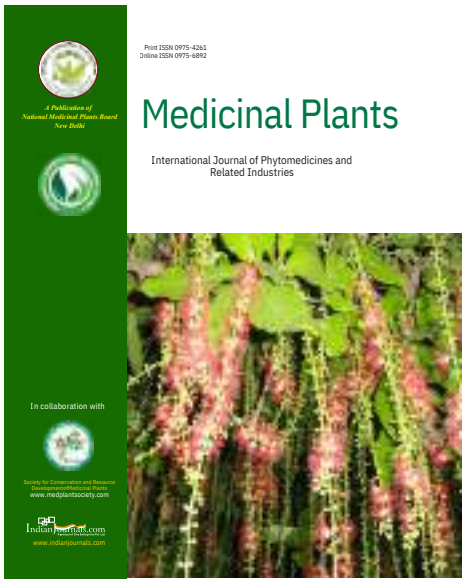

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Indexed in Google Scholar, CAS, ASI.

BIO Web of Conferences

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