



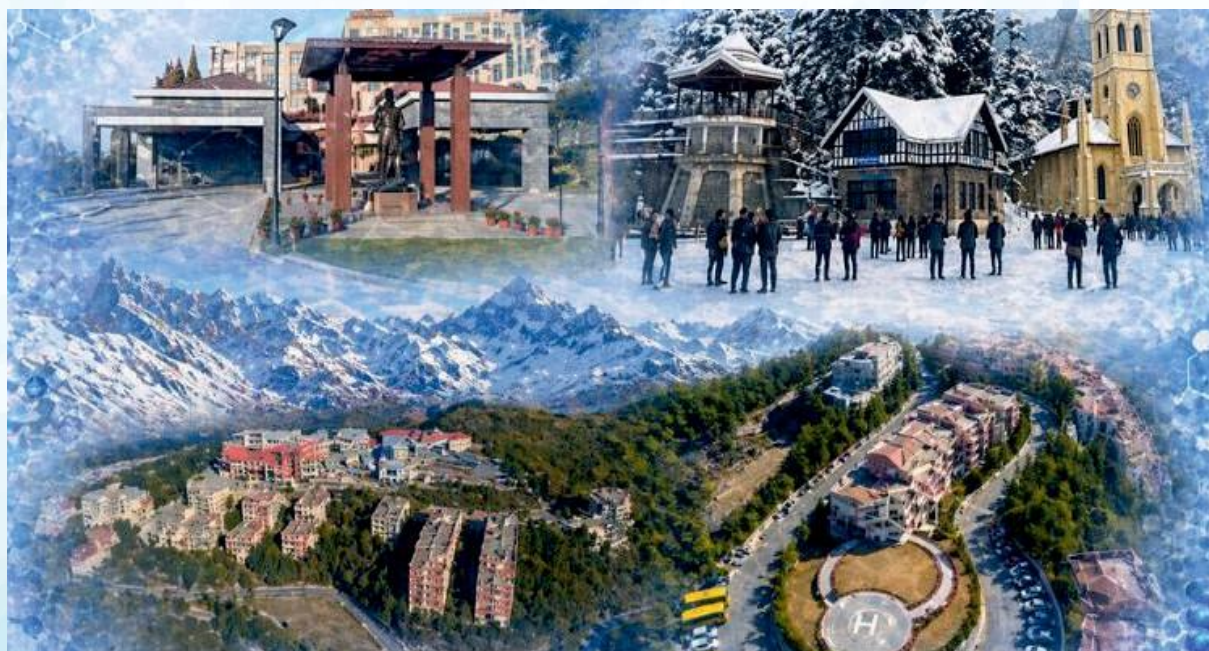
Proceedings of 3rd International Conference on Biotechnology and Bioinformatics

**Sustainable Healthcare, Agriculture, Environment and
Computational Biology**

ISBN: 978-93-5987-314-5

ICBAB - 2026

28 – 30 May 2026



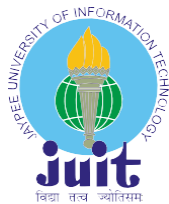
Chief Editor:
Dr. Saurabh Bansal

Editors:
Dr. Ashok K Nadda
Dr. Shikha Mittal

Organized by
Department of Biotechnology and Bioinformatics
Jaypee University of Information Technology
Waknaghat, Solan, Himachal Pradesh INDIA (173234)

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CSIR Sponsored 3rd International Conference on Biotechnology and Bioinformatics

(ICBAB-2026)

**“Sustainable Healthcare, Agriculture, Environment and
Computational Biology”**

28 – 30 May 2026

CHIEF EDITOR

Dr. Saurabh Bansal

EDITORS

Dr. Ashok K Nadda

Dr. Shikha Mittal

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**Department of Biotechnology and Bioinformatics
Jaypee University of Information Technology
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III: International Conference on **Biotechnology and Bioinformatics** (ICBAB 2026)

EDITORS: Dr. Saurabh Bansal, Dr. Ashok Kumar Nadda, Dr. Shikha Mittal

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About Jaypee University of Information Technology, Solan:

The JUIT was conceived by a joint vision of the Govt of Himachal Pradesh and the Founder Chairman of Jaypee Group, Shri Jai Prakash Gaur, in 2000. Land was provided on lease by the State Govt., and the university was established by Act No. 14 of 2002 vide Extraordinary Gazette Notification of the Govt. of Himachal Pradesh dated May 23, 2002. The University Grants Commission accorded its approval under Section 2(f) of the UGC Act vide their Letter No. F 9-10/2002(CPP-1) dated 09 Dec 2002. The JUIT is also a member of the Association of Indian Universities (AIU). The academic activities of JUIT commenced in July 2002 and are currently offering undergraduate B. Tech. degree programs in Bioinformatics, Biotechnology, Civil Engineering, Civil Engineering with Computer Application, Computer Science & Engineering, Electronics & Communication Engineering, Electronics & Computer Engineering and Information Technology, Mathematics and Computing. Besides B. Tech. programs, the university is presently offering M.Tech. in Biotechnology, Civil Engineering with specialization in Structural Engineering, Construction Management and Environmental Engineering, Computer Science and Engineering, Computer Science and Engineering with specialization in Information Security and Data Science, Electronics and Communication Engineering, Electronics and Communication Engineering with specialization in Internet of Things, Electronics and Computer Engineering. BBA and M.Sc. Programs are also offered in Biotechnology, and Microbiology. Ph.D. programs are offered in Biotechnology, Bioinformatics, Civil Engineering, Computer Science and Engineering, Electronics and Communication Engineering, Humanities and Social Sciences, Mathematics, Physics and Materials Science.

About Wahnaghat:

Wahnaghat is located in the Solan district of Himachal Pradesh. Wahnaghat is located midway between Shimla and Solan, around 25 km each, at an altitude of 1,700 m (5,600 ft) on average. Wahnaghat has a cool climate. Wahnaghat is easily accessible by road. It is 93 km (58 miles) from Chandigarh.

About the Conference:

The 3rd International Conference of Biotechnology and Bioinformatics (ICBAB-2026) aims to bring together leading academicians, industry experts, research scientists, and scholars to exchange and share their knowledge, experiences, and findings across diverse domains of biotechnology and bioinformatics. The goal of the conference is to provide a dynamic platform for updating and disseminating advancements in sustainable healthcare, agriculture, the environment, and computational biology. The event has also been designed to include interactive workshops, keynote lectures, and a discussion forum amongst selected academicians, industry delegates, researchers, and other resource personnel to foster collaboration, networking, and future partnerships. The theme of the conference is “Sustainable Healthcare, Agriculture, Environment, and Computational Biology”. However, ICBAB-2026 solicits original papers and contributions in all of the related areas.

FROM THE DESK OF THE CHIEF EXECUTIVE OFFICER

JUIT, WAKNAGHAT



Shri Manu Bhaskar Gaur
Chief Executive Officer

It is a matter of great pride and privilege to welcome you to the **3rd International Conference on Biotechnology and Bioinformatics (ICBAB-3) - 2026**, organized by the Department of Biotechnology and Bioinformatics at Jaypee University of Information Technology.

The theme of this year's conference, "*Sustainable Healthcare, Agriculture, Environment, and Computational Biology*," reflects the vital role of biotechnology and computational sciences in addressing global challenges and shaping a sustainable future. At a time when innovation and interdisciplinary research are transforming the world, ICBAB-3 serves as a significant platform for knowledge exchange, collaboration, and scientific advancement.

By bringing together leading researchers, academicians, industry experts, and young innovators from across the globe, the conference aims to inspire pioneering ideas and meaningful partnerships that can create lasting societal impact.

I sincerely appreciate the efforts of the organizing committee, contributors, and participants, and I gratefully acknowledge the support of Council of Scientific and Industrial Research (CSIR) in making this event possible.

I am confident that ICBAB-3 (2026) will foster insightful discussions, transformative research, and innovative solutions for the betterment of science and society. I wish all participants a productive and enriching conference experience.

Manu Bhaskar Gaur

FROM THE DESK OF THE VICE CHANCELLOR

JUIT, WAKNAGHAT



Prof. (Dr.) Rajendra Kumar Sharma
Vice Chancellor

It is my great pleasure to warmly welcome all contributors to the 3rd International Conference on Biotechnology and Bioinformatics (ICBAB-3), organized by the Department of Biotechnology and Bioinformatics, Jaypee University of Information Technology. We gratefully acknowledge the financial support of Council of Scientific and Industrial Research for this conference, scheduled from May 28–30, 2026.

ICBAB-3 aims to provide a vibrant platform for researchers, academicians, and professionals working in Biotechnology, Bioinformatics, Drug Discovery, Genomics, Microbiology, Toxicology, and related areas to exchange innovative ideas and research outcomes. The conference focuses on addressing key scientific challenges and fostering multidisciplinary collaboration for impactful advancements in these fields.

The enthusiastic response, with over 170 participant confirmations, reflects the significance of this conference within the scientific community. I extend my sincere appreciation to all participants, organizers, and supporters for their valuable contributions and efforts.

I wish the conference great success and hope it inspires meaningful discussions, collaborations, and breakthroughs in Biotechnology and Bioinformatics.

Prof. R K Sharma

FROM THE DESK OF THE REGISTRAR

JUIT, WAKNAGHAT



Brigadier RK Sharma, SM (Retd.)
Registrar

I am delighted to extend a cordial welcome to all eminent delegates, researchers, academicians, scientists, and industry experts participating in the **3rd International Conference on Biotechnology and Bioinformatics (ICBAB-3) – 2026**, organized by the Department of Biotechnology and Bioinformatics at Jaypee University of Information Technology.

ICBAB-3 (2026) provides a valuable forum for intellectual exchange, research collaboration, and discussions on emerging innovations in biotechnology and bioinformatics. The conference theme, *“Sustainable Healthcare, Agriculture, Environment, and Computational Biology,”* underlines the significance of scientific advancement in addressing pressing global challenges and promoting sustainable development.

This gathering of experts from academia, research institutions, and industry will undoubtedly encourage knowledge sharing, interdisciplinary interaction, and innovative thinking. Such conferences play an essential role in strengthening academic and research excellence while fostering meaningful collaborations.

I convey my sincere appreciation to the organizing committee, keynote speakers, reviewers, and contributors for their commitment and hard work in organizing this prestigious event. I also acknowledge with gratitude the valuable support provided by CSIR.

I wish all participants a highly informative, productive, and memorable experience at ICBAB-3 (2026).

Brigadier RK Sharma, SM (Retd.)

FROM THE DESK OF DEAN (ACADEMICS)

JUIT, WAKNAGHAT



Prof. (Dr.) Shruti Jain
Dean (Academics)

It is with immense pride and great pleasure that I extend a warm welcome to all delegates, researchers, academicians, scientists, and industry professionals to the 3rd International Conference on Biotechnology and Bioinformatics (ICBAB-3) – 2026, being organized from May 28–30, 2026, in hybrid mode at the Jaypee University of Information Technology.

The theme of this year's conference, "*Sustainable Healthcare, Agriculture, Environment, and Computational Biology*," reflects the growing need for innovative biotechnological and bioinformatics approaches to address global challenges and promote sustainable development. ICBAB-3 2026 aims to provide an interdisciplinary platform for eminent researchers, academicians, students, and professionals from around the world to share their latest research findings, technological advancements, and emerging trends in biotechnology, bioinformatics, computational biology, and allied fields.

The conference is expected to foster meaningful scientific discussions, encourage collaborative research, and inspire innovative solutions that can contribute significantly to healthcare, agriculture, environmental sustainability, and computational sciences. I encourage all participants to actively engage in the technical sessions, exchange ideas, and build strong academic and professional collaborations.

I sincerely hope that ICBAB-3 2026 will serve as a catalyst for transformative research and leave a lasting impact on the global scientific community. I wish all participants a highly enriching, productive, and memorable conference experience.

Prof. (Dr.) Shruti Jain

FROM THE DESK OF DEAN (RESEARCH AND INTERNATIONALIZATION)

JUIT, WAKNAGHAT



Prof. (Dr.) Sudhir Kumar
Dean (Research and Internationalization)

It is my great pleasure to welcome all participants to the 3rd International Conference on Biotechnology and Bioinformatics (ICBAB-3) – 2026. I warmly invite you to engage in meaningful discussions and explore potential research collaborations during the conference.

This third edition of ICBAB reflects our commitment to constantly deliberate and collaborate in research and innovation in the fields of biotechnology, bioinformatics, and sustainable development. We are privileged to host distinguished keynote speakers, experts, and all participants in the serene environment of Wajnaghat.

I extend my sincere gratitude to our management, external organizations, and sponsors for their encouragement and support. Good luck to organizing committee for a productive conference.

A handwritten signature in blue ink on a light-colored background. The signature is stylized and appears to read 'Sudhir Kumar'.

Prof. Sudhir Kumar

FROM THE DESK OF DEAN OF STUDENTS WELFARE

JUIT, WAKNAGHAT



Prof. (Dr.) Rakesh Kumar Bajaj
Dean of Students Welfare

It is my great privilege to extend a warm welcome to all distinguished delegates, academicians, researchers, scientists, and industry professionals attending the **3rd International Conference on Biotechnology and Bioinformatics (ICBAB-3) – 2026**, organized by the Department of Biotechnology and Bioinformatics at Jaypee University of Information Technology.

The theme of the conference, “*Sustainable Healthcare, Agriculture, Environment, and Computational Biology*,” emphasizes the vital role of biotechnology and bioinformatics in developing innovative and sustainable solutions to contemporary global challenges. ICBAB-3 (2026) serves as an important platform for sharing advanced research, exchanging ideas, and strengthening academic and industrial collaborations.

I am certain that this conference will encourage meaningful interactions, stimulate innovative thinking, and foster interdisciplinary research among participants from diverse fields. Such scholarly events significantly contribute to the growth of scientific knowledge and research excellence.

I sincerely appreciate the efforts of the organizing committee, keynote speakers, reviewers, and contributors whose dedication has made this conference possible. I wish all participants a rewarding, insightful, and successful experience at ICBAB-3 (2026).

Prof. (Dr.) Rakesh Kumar Bajaj

FROM THE DESK OF DEAN (ACCREDITATION)

JUIT, WAKNAGHAT



**Prof. (Dr.) Sunil Kumar Khah
Dean (Accreditation)**

The Department of Biotechnology and Bioinformatics at Jaypee University of Information Technology takes immense pride in welcoming distinguished delegates, researchers, academicians, scientists, and industry professionals to the **3rd International Conference on Biotechnology and Bioinformatics (ICBAB-3) – 2026**.

As an institution dedicated to academic excellence and advanced research, JUIT is pleased to host this prestigious conference, which serves as a dynamic forum for intellectual exchange, innovative research, and interdisciplinary collaboration in the fields of biotechnology and bioinformatics.

The theme of the conference, “*Sustainable Healthcare, Agriculture, Environment, and Computational Biology*,” highlights the crucial role of integrating biological sciences with computational technologies to address contemporary global challenges and promote sustainable progress.

ICBAB-3 (2026) aims to bring together experts from academia, research organizations, and industry to discuss emerging trends, share scientific advancements, and strengthen collaborative partnerships for future innovations.

I extend my sincere greetings and best wishes to all participants for a stimulating, productive, and enriching conference experience. I am confident that the deliberations and interactions during the conference will lead to valuable insights and impactful contributions to the scientific community.

Prof. Sunil Kumar Khah

FROM THE DESK OF ASSOCIATE DEAN (INNOVATION)

JUIT, WAKNAGHAT



Prof. (Dr.) Tiratha Raj Singh
Associate Dean (Innovation)

It gives me immense pleasure to welcome all distinguished delegates, researchers, academicians, innovators, industry experts, and young scholars to the **3rd International Conference on Biotechnology and Bioinformatics (ICBAB-3) – 2026**, organized by the Department of Biotechnology and Bioinformatics at Jaypee University of Information Technology.

As Associate Dean, Innovation, I believe that innovation and interdisciplinary research are key to addressing global challenges in healthcare, agriculture, environment, and computational biology. The theme of ICBAB-3 (2026) reflects the growing importance of research-driven and technology-enabled solutions for sustainable development.

Being actively involved in research in bioinformatics and computational systems biology, I strongly believe that AI-driven and data-centric biological research will shape the future of precision healthcare and life sciences.

At JUIT, we remain committed to fostering innovation, entrepreneurship, and industry-academia collaboration. I am confident that this conference will provide an inspiring platform for knowledge exchange, meaningful collaborations, and impactful scientific discussions.

I congratulate the organizing committee and wish all participants a productive and memorable experience at ICBAB-3 (2026).

Prof. (Dr.) Tiratha Raj Singh

**FROM THE DESK OF HEAD OF DEPARTMENT
(DEPARTMENT OF BIOTECHNOLOGY & BIOINFORMATICS),**

JUIT, WAKNAGHAT



**Prof. (Dr.) Jata Shankar
Head, Department BT & BI**

I welcome participants and invited speakers to ICBAB -3, the third International Conference on Biotechnology and Bioinformatics at Jaypee University of Information Technology (JUIT), Solan, Himachal Pradesh.

Conferences bring in experts from academia and industry from various parts of the world to ponder upon the pressing needs in certain areas of research. With a good mix of young and experienced researchers in ICBAB-3, I am sure our conference will lead to fruitful learning outcomes.

With an aim of interdisciplinary research, we are trying to provide an amalgamation of versatile fields of Biotechnology and Bioinformatics in ICBAB-3. With the utmost hard work of coordinators, faculty, staff, and students of the department, the ICBAB-3 will be a successful event. We intend to see new research collaborations and innovative ways to challenge scientific problems to get sustainable and technology-driven solutions.

We are grateful to CSIR for their financial support. We also acknowledge the support of JUIT management.

Prof. (Dr.) Jata Shankar

**FROM THE DESK OF CONVENERS
(DEPARTMENT OF BIOTECHNOLOGY & BIOINFORMATICS),
JUIT, WAKNAGHAT**



Dr. Saurabh Bansal
Associate Professor (BT & BI)



Dr. Ashok Kumar Nadda
Associate Professor (BT & BI)



Dr. Shikha Mittal
Assistant Professor (BT & BI)

Distinguished Keynote Speakers, Esteemed Delegates, and Participants,

On behalf of the conveners of the **3rd International Conference on Biotechnology and Bioinformatics (ICBAB-2026)**, it is with immense delight and honor that we extend a warm welcome to each of you. Your presence here, representing diverse institutions from across India and around the globe, fills us with pride as we gather at the prestigious Jaypee University of Information Technology in the enchanting hills of Himachal Pradesh.

This conference serves as a remarkable platform to connect researchers, academicians, and industry professionals worldwide. It fosters the exchange of knowledge, sharing of experiences, and cultivation of collaborative relationships. True to its vision, ICBAB-2026 offers invaluable opportunities for open discussions on critical issues and cutting-edge research, guided by our distinguished keynote speakers and esteemed academicians. Through such interactions, we collectively pave the way for innovative breakthroughs in Biotechnology and Bioinformatics.

We express our heartfelt gratitude to the Honorable Vice Chancellor, the esteemed Dean (Academics), Dean (Research & Internationalisation), Dean (Accreditation), Associate Dean (Innovation) and the respected Registrar of JUIT, whose unwavering support has been instrumental in organizing this event. We also extend sincere appreciation to **CSIR** for their invaluable financial support, which has significantly contributed to the success of this endeavor.

Our profound thanks go to the dynamic faculty and staff of the Department of Biotechnology and Bioinformatics, whose relentless efforts and dedication have shaped ICBAB-2026 into the outstanding conference it is today.

To all attendees and participants, we extend our warmest wishes for a pleasant and rewarding stay at JUIT. May this conference be an unforgettable experience—where ideas flourish, collaborations blossom, and new frontiers in science are discovered.

Thank you, and let ICBAB-2026 commence in the spirit of boundless knowledge and collective growth.

Technical Program

3rd International Conference on Biotechnology and Bioinformatics (ICBAB-2026)

JUIT, Wajnaghat

May 28-30, 2026

Conference Day-1 Thursday May 28, 2026	
Venue	Reception, Academic Area
8:30 - 9:30 AM	Registration
Venue	LT-3
Inaugural Session	
9:30 AM	Welcome of the Chief Guest
9:35 AM	Lamp Lightening and Saraswati Vandana
9:40 AM	Felicitation of the Chief Guest by Hon'ble Vice Chancellor
9:45 AM	Welcome Address by Dr. Saurabh Bansal, Convener
9:50 AM	Address by Prof. Jata Shankar, Program Chair & Head of Department BT & BI
10:00 AM	Address by Prof. (Dr.) Sudhir Kumar, Dean (R & I)
10:05 AM	Address by Prof. (Dr.) Shruti Jain, Dean (Academics)
10:10 AM	Address by Prof. (Dr.) Rajendra Kumar Sharma, Vice Chancellor
10:30 AM	Launch of Conference Proceedings
10:35 AM	Address by Chief Guest, Prof. P. L. Gautam
10:55 AM	Vote of Thanks and National Anthem
11:00 AM	High Tea (Porche Area)
Session-1 (DLC) Session Chair: Prof. (Dr.) Hemant Sood	
11:30 - 12:15 PM	Prof. (Dr.) Bishwajit Kundu Professor, Kusuma School of Biological Sciences, IIT Delhi, India Do Bacterial and Viral Infections Trigger Neurodegeneration?
12:15 - 1:00 PM	Dr. Yosi Shacham Diamand Professor, The Scojen Institute for Synthetic Biology, head, Reichman University, Israel Synthetic Biology-based Functional Sensors and their Implementation
1:00 - 2:00 PM	Lunch Annapurna
Session-2 (DLC) Session Chair: Prof. (Dr.) Rahul Srivastava	
2:00- 2:30 PM	Prof. (Dr.) Sudha Srivastava Professor, Department of Chemistry, Jaypee Institute of Information Technology Noida, India

	Bridging Diagnostics and Care: Lateral Flow & Electrochemical Biosensors in Action
2:30 – 3:00 PM	Prof. (Dr.) Aklank Jain Professor Department of Zoology, Central University of Punjab, Bhatinda, India Exploiting the LINC00324/miR-493-5p/MAPK Axis as a Novel Therapeutic Target in Esophageal Squamous Cell Carcinoma
Session-3 (DLC) Session Chair: Prof. (Dr.) Anil Kant	
3:00 – 3:30 PM	Dr. Meena K. Chaudhary Scientist C Center of Innovative and Applied Bioprocessing (CIAB), Mohali, India Biovalorization of Corn Protein Meal as a Sustainable Alternative Protein Source
3:30 – 4:00 PM	Prof. (Dr.) N. Tejo Prakash Professor, Thapar Institute of Engineering and Technology, Patiala, Punjab, India Harnessing Selenium-Enriched Cereals- A Comprehensive Investigation into Biofortification, Bioaccessibility, and Health Implications of Seleniferous Crops
4:00 - 4:30 PM	Tea Break (Orange Shed)
Session-4 Parallel Session	
4:10 - 5:45 PM	Poster Presentation-I (Academic Block) Track-1: Healthcare Biotechnology – HB-P-1 to HB-P-26 Track-2: Agriculture Biotechnology – AB-P-1 to AB-P-20
4:20 - 5:45 PM	Short Oral Presentation-I (CR3)
4:20 - 5:45 PM	Rapid Oral Presentation-I Track-1: Healthcare Biotechnology (TR1) – HB-ROP-1 to HB-ROP-17 Track-2: Agriculture Biotechnology (TR2) – AB-ROP-1 to AB-ROP-12 Track-3: Environment Biotechnology (TR3) – EB-ROP-1 to EB-ROP-11 Track 4: Computational Biology and Bioinformatics (TR4)- BI-ROP-1 to BI-ROP-12
7:30- 9:00 PM	Dinner Annapurna

Conference Day-2 Friday May 29, 2026	
Venue	DLC
Session-5 Session Chair: Dr. Garlapati Vijay Kumar and Dr. Rajesh Kumar Verma	
9:15 - 10:00 AM	Prof. (Dr.) Xue-Jun Li Professor, University of Illinois, Chicago, USA

	A Human Pluripotent Stem Cell Platform for Target Discovery in Hereditary Spastic Paraplegias
10:00 - 10:30 AM	Prof. (Dr.) M. Sudhakara Reddy Professor, Thapar Institute of Engineering and Technology, Patiala, India Bacteria as a resource material for healing the cracks and improvement of cementitious properties
10:30 – 11:00 AM	High Tea
Session-6 Session Chair: Prof. (Dr.) Gopal Singh Bisht	
11:00 – 11:30 AM	Dr. Indrani Ghosh Principal Technical Officer Innovation Protection Unit (IPU), CSIR, New Delhi Protecting Your Research – Pipettes to Patents
11:30 – 12:00 PM	Dr. Ram Karan Associate Professor, Department of Microbiology, University of Delhi South Campus, New Delhi Genetic Treasures of Extreme Habitats: Bioengineering Extremozymes and Protein Nanoparticles for Green and Sustainable Environmental Biotechnology
Session-7 Parallel Session	
12:00 - 1:00 PM	Poster Session -II (Academic Block) Track-3: Environment Biotechnology – EB-P-1 to EB-P-21 Track 4: Computational Biology and Bioinformatics- BI-P-1 to BI-P-20
12:00 - 1:00 PM	Rapid Oral Presentation- II Track 4: Computational Biology and Bioinformatics (TR4)- BI-ROP-13 to BI-ROP-20
01:00 - 2:00 PM	Lunch – Annapurna
Session-8 Session Chair: Prof. (Dr.) Tiratharaj Singh and Prof. (Dr.) Poonam Sharma	
02:00 – 2:45 PM	Dr. Yen Wah Tong Professor, National University of Singapore, Singapore Digestate to Dinner: Microalgae-Drive Single-Cell Protein for the Urban Economy
02:45– 3:30 PM	Dr. Anshu Bhardwaj Scientist F, CSIR-IMTECH Chandigarh Antimicrobial Resistance Knowledgebase towards understanding resistance mechanisms and targeted drug discovery for AMR
3:30– 4:00 PM	Tea Break (Orange Shed)

Session-9 Session Chair: Prof. (Dr.) Jata Shankar and Dr. Tyson	
4:00– 4:30 PM	Dr. Santosh K. Gupta Senior Scientist ICAR-Indian Institute of Millets Research, Hyderabad Robust Plant Transformation: A Foundation of Genome Editing in Chickpea, Rice bean. and Pearl Millet
4:30 – 5:00 PM	Dr. Ankit Srivastava Associate Professor (Research) Department of Biotechnology and Chemical Engineering, Manipal University, Jaipur Amplifying the Invisible: Detecting Parkinson’s Disease Through Seed Amplification Assays
5:00 – 5:20 PM	Dr. Khushbu Kushwaha Manager, Wiley Publishers Wiley’s Initiatives in India

Conference Day-3 Saturday May 30, 2026	
Venue	DLC
Session-10 Session Chair: Dr. Udaybanu M	
9:15 - 10:00 AM	Prof. (Dr.) Rajesh K. Sani Professor Departments of Chemical and Biological Engineering & Applied Biological Sciences-South Dakota School of Mines and Technology (SDSMT)-Rapid City, SD-USA
10:00 - 10:30 AM	Prof. (Dr.) Gunjan Goel Professor, Department of Microbiology, Central University of Haryana, Mahendergarh, Haryana, India Gut Health Modulation Through Probiotic Intervention
10:30 - 11:00 AM	Dr. Raju Shankarayan Associate Professor, Shri Mata Vaishno Devi University (SMVDU), Katra, Jammu & Kashmir, India Green Nanomaterials: Their Synthesis and Applications
11:00 – 11:30 AM	High Tea
Session-11 Session Chair: Dr. Jitendraa Vashistt	
11:30 – 12:15 PM	Dr. Sudesh Kumar Yadav Director, CSIR - Institute of Himalayan Bioresource Technology, Palampur, India From Peak to Pipelines: Transforming Himalayan Biodiversity into Bioinnovation

12:15 – 12:45 PM	Dr. Vishvanath Tiwari Associate Professor (Biochemistry) & Director (Research & Development), Central University of Rajasthan, Ajmer, India Reversing Carbapenem Resistance in <i>Acinetobacter baumannii</i> by Targeting the AdeABC Efflux Pump and MurB Protein
12:45-1:45 PM	Valedictory Function and certificate distribution (Participants, Best Paper Oral/Poster Presentation Awards)
1:45 - 2:45 PM	Lunch in Annapurna

Main Tracks:

Healthcare Biotechnology (Track-1)	Agricultural Biotechnology (Track-2)	Environmental Biotechnology (Track-3)	Computational Biology & Bioinformatics (Track-4)
• Molecular Diagnostics, Biomarkers and Personalized Medicine • Gene editing (CRISPR, base editing) and therapeutic applications • Vaccine Development & Immunotherapy • Regenerative Medicine & Stem Cell Technologies • Biotech Startups in Healthcare Innovation	• Genetically Modified Crops & Food Security • Plant-Microbe Interactions & Soil Health • Biopesticides, Biofertilizers and Sustainable Inputs • Climate-Resilient Agriculture and Precision Farming • AgriTech Startups & digital agriculture platforms	• Bioremediation and waste management • Bioenergy and biofuels for sustainable development • Microbial ecology and ecosystem restoration • Circular bioeconomy and green technologies • Policy, ethics, and sustainability frameworks	• AI & Machine Learning in Genomics and proteomics • Systems Biology & Network Modeling • Big Data Analytics in Biomedical and agricultural Research • Structural Bioinformatics & Drug Design • Cloud Platforms & Open-Source Tools and collaborative databases

Chief Guest

Prof. P. L. Gautam

Agricultural Scientist & Academic Administrator

**Chancellor, Dr. Rajendra Prasad Central Agricultural University,
Pusa, Bihar; Pro-Chancellor, Career Point University, Hamirpur**

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Gautam, Prof. (Dr.) Prem Lal (b. 12 December 1947, Bilaspur, Himachal Pradesh, India) is an Indian agricultural scientist and academic administrator specializing in genetics, plant breeding, and plant genetic resources. He graduated in agriculture from Himachal Agricultural College, Solan, and obtained his M.Sc. and Ph.D. in Genetics from the Indian Agricultural Research Institute (IARI), New Delhi.

Prof. Gautam served as Vice-Chancellor of G. B. Pant University of Agriculture and Technology, Pantnagar, as Director of the National Bureau of Plant Genetic Resources (NBPGR), ICAR, as Chairperson of the Protection of Plant Varieties and Farmers' Rights Authority (PPV&FRA), and as Chairman of the National Biodiversity Authority (NBA). He is currently Chancellor of Dr. Rajendra Prasad Central Agricultural University, Pusa, Bihar, and Pro-Chancellor of Career Point University, Hamirpur.

He has contributed to the development of improved varieties of bread wheat, soybean, ricebean, foxtail millet, buckwheat, and amaranth, and has played a key role in the augmentation and conservation of plant germplasm in the national gene bank. A fellow of the National Academy of Agricultural Sciences, National Academy of Biological Sciences, National Academy of Horticultural Sciences, and other learned societies, he has been honored with the Padma Shri, several national awards, and honorary doctorates for his contributions to agricultural science and institution building.

Guest of Honor

Dr. Sudesh Kumar Yadav

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Yadav, Dr. Sudesh Kumar (PhD) is a distinguished Indian scientist and academic administrator in the field of biotechnology, plant biotechnology, metabolic engineering, and Himalayan bioresource technologies. He holds a PhD in Biotechnology and has over two decades of research experience, with more than 200 research papers, 15–17 patents, and a high citation record (h-index ~55), placing him among the *top 2% scientists of the world* (Stanford-ranked list).

Dr. Yadav has served at premier CSIR laboratories and is currently Director of the CSIR-Institute of Himalayan Bioresource Technology (CSIR-IHBT), Palampur, Himachal Pradesh, a constituent laboratory of the Council of Scientific and Industrial Research (CSIR). In this role, he oversees research on Himalayan plant resources, bioprocessing, metabolic engineering, synthetic biology, and product development with a strong focus on technology transfer and industry collaboration.

He has guided several PhD, MSc, and project students and has been associated with national and international scientific panels, conferences, and collaborative projects as a keynote speaker and Guest of Honour. He is a member/fellow of several national and international scientific bodies and has received awards such as the CSIR Young Scientist Award and other recognitions for his work in biotechnology and bioresource development.

Keynote Speakers

Synthetic Biology-based Functional Sensors and their Implementation

Yosi Shacham-Diamand

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Abstract

First, we will review the topic of CMOS integrated biochips in general and with functional biosensing in particular. We discuss the background and engineering aspects as demonstrated in bacteria, yeast, and mammalian cells. We will describe the alternatives for plant-based sensors and the advantages of using synthetic biology for designing novel sensors for various applications. Next, we will present new strategies, based on a novel synthetic biology approach where we use gene expression to up/down-regulate the expression of other genes. We will present circuit modeling of such sensors, assuming both DNA and RNA regulations. We will discuss the issue of integrating such sensors with CMOS VLSI circuits. An example of the implementation of an electrochemical functional biosensing into hardware modeling language using Verilog A will also be presented. Next, we will discuss how to use synthetic biology, introducing new genetic circuits, improving signal-to-noise, allowing sensing of multiple excitations, and generating multiple outputs: optical or electrochemical. Finally, we will present a few examples using Tobacco plants, show recent results, and discuss the advantages and disadvantages of such an approach. Finally, we will describe our holistic system, integrating plant sensors, both synthetic biology-based and novel 4-point impedance sensors, with physics-based models and AI/ML big-data analysis, which was tested in a greenhouse and validated against gravimetry. An algorithm using a physics-based model reduces a large database to a small set of parameters, which are stored and transferred to the edge/cloud. The database is fused with external variables and fed into an AI/ML software library, where it is analyzed, yielding results superior to those of other published methods in the field of precision agriculture.

Keywords: Synthetic Biology, biosensors, VLSI & CMOS modelling

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Prof. Yosi Shacham-Diamand, Head of the Scojen Institute for Synthetic Biology at Reichmann University. His research is in the fields of Micro and Nanoelectronics science and technology, specifically on Synthetic Biology-based Biochips and functional biosensors, Nano-bio interfacing to electronics, and VLSI interconnects.

D.Sc. EE 1983, M.Sc. EE 1980, and B.Sc. EE (Summa-cum Laude) 1978, all in the Technion-Israel Institute of Technology, Haifa, Israel. 1983-post-doctorate at U.C. Berkeley, CA, USA. 1987- 1989 Senior lecturer, the Technion, Israel. 1989-1996 Assistant professor, Cornell University, Ithaca, NY, USA; 1997-2001 Associate professor; 2001-2021 a full professor at the School of EE, Tel-Aviv University. Since 2021, he has been a full professor at Reichman University.

He served in numerous academic and administrative positions at TAU, as well as a visiting professor in Japan, Italy, India, and Taiwan; As a consultant to numerous manufacturing and VC companies, and on the board of directors of a few public companies.

Currently, he is the acting CTO and chief scientist of the Israeli BioChip Corporation, IBCC Labs Ltd., providing design, manufacturing, and testing services in the field of microsystem technologies.

Dr. Rajesh K. Sani

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Sani, Dr. Rajesh K. (R. K. Sani) is a Distinguished Professor in the Karen M. Swindler Department of Chemical and Biological Engineering at the South Dakota School of Mines and Technology (South Dakota Mines), Rapid City, South Dakota, USA. He holds a PhD in Microbiology/Biotechnology (from the Institute of Microbial Technology/Panjab University, India) and has over two decades of research experience in extremophilic bioprocessing, bioenergy, biopolymers, gas-to-liquid fuels, genome editing, and space-relevant biology.

Dr. Sani leads a large research group at South Dakota Mines working on extremophiles from deep-mine environments (e.g., the Sanford Underground Research Facility / Homestake Gold Mine) for high-temperature bioprocessing of solid wastes, lignocellulosic feedstocks, and greenhouse-gas-derived substrates into biofuels and bioproducts. He has attracted over 65–70 million USD in competitive research funding from agencies such as NSF and state partners, authored more than 140 peer-reviewed articles, edited numerous books and book chapters, and holds several patents and invention disclosures.

He has received multiple national and international awards, including the Waksman Outstanding Teaching Award (SIMB) for microbiology–biotechnology education and the Lifetime Achievement Award from the Society of Chemical and Synthetic Biology (SCSB), and in 2022 was honored as a Distinguished Professor at South Dakota Mines, the university’s highest faculty title. He is also the founder of a biotech start-up and director of the MASON Lab, which focuses on scalable, sustainable biotechnological solutions in bioplastics, bioenergy, methane regulation, and agriculture

Digestate to Dinner: Microalgae-Drive Single-Cell Protein for the Urban Economy

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Abstract

Urban food waste presents a persistent challenge and a missed opportunity for resource recovery. While anaerobic digestion (AD) can convert food waste into biogas and a nutrient-rich digestate, the land constraints of dense cities limit digestate use as a biofertilizer, creating a bottleneck to wider AD deployment. This plenary will present a circular, biotechnological pathway to address that gap: the upcycling of food-waste digestate into single-cell protein (SCP) via microalgal biotransformation.

We evaluated the feasibility of using digestate as a cultivation medium for microalgae, benchmarking growth performance under batch and semi-continuous operations to identify operational regimes that balance productivity and stability. To probe practical scalability, we advanced the process to a 100 L pilot and operated it over 10 weeks to assess long-term robustness. The talk will synthesise lessons from these trials, including media preparation and variability management, nutrient balancing, and process control considerations essential for reliable SCP production from heterogeneous waste streams.

Beyond the technical results, we will discuss integration pathways with urban AD infrastructure, potential nutritional and safety considerations for SCP applications, and the environmental and economic implications of coupling waste valorisation with low-carbon protein production. By reframing digestate as a feedstock for high-value biomass, this work outlines a resource recovery platform that can unlock broader adoption of AD in cities, advancing both decarbonisation and the circular bioeconomy.

Keywords: Anaerobic digestion, digestate valorisation, microalgae

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Professor Tong Yen Wah joined the Department of Chemical and Biomolecular Engineering at the National University of Singapore (NUS) in 2001 after graduating from the University of Toronto with a PhD in Chemical Engineering. His expertise is in biomaterials research for tissue engineering and in bioenergy from food wastes and biomass wastes, with over 300 publications and 22000 citations with a h-index of 86. His recent works in food waste management have been commercialized with distributed anaerobic digesters that can be effectively used in cities through a spin-off company from NUS. He is currently focusing on novel photobioreactor designs to grow cyanobacteria for biofuel production in a collaboration with Shanghai Jiaotong University.

A Human Pluripotent Stem Cell Platform for Target Discovery in Hereditary Spastic Paraplegias

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Abstract

Motor neurons, including upper (cortical) and lower motor neurons, are large projection neurons that control muscle movement. Their degeneration underlies several debilitating diseases, such as hereditary spastic paraplegia (HSP). HSP is a large group of rare genetic disorders characterized by the progressive degeneration of cortical motor neuron axons, leading to spasticity and weakness of the lower limbs. Currently, there remains no effective treatment to mitigate this axonal loss, a major cause of chronic neurodisability, partly due to limited human-relevant model systems. To address this gap, we generated human pluripotent stem cells (hPSCs) carrying patient-specific mutations and differentiated them into cortical projection neurons. Our data showed that the patient-specific neurons exhibited reduced axonal outgrowth, impaired axonal transport, and accumulated axonal swellings, recapitulating key disease phenotypes. Notably, targeting mitochondrial fission-fusion restores mitochondrial dynamics, rescuing axonal deficits in HSP neurons. Furthermore, these patient-specific hPSCs have been successfully differentiated into multiple neural subtypes, including astrocytes, providing platforms for investigating neuron-glia crosstalk and evaluating therapeutic strategies. Together, our work offers new insights into axonal degeneration and advances the development of targeted therapies for HSP.

Keywords: Human pluripotent stem cells, Hereditary spastic paraplegia, Motor neuron, Axon, Degeneration

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Dr. Xue-Jun Li received her PhD in Neurobiology and completed postdoctoral training in Stem Cell Research. She is a Full Professor in the Department of Biomedical Sciences at the University of Illinois College of Medicine Rockford and the Department of Biomedical Engineering at the University of Illinois Chicago. She has held the Michael A. Werckle

Endowed Professorship since 2018. Dr. Li's research focuses on specifying neuronal subtypes from human pluripotent stem cells and using these stem cell-derived neurons to study motor neuron and axonal degeneration. During her postdoctoral training in the Stem Cell Program at the University of Wisconsin-Madison, she studied neural specification from human stem cells and published a seminal report demonstrating the specification of spinal motor neurons from human pluripotent stem cells. This paradigm she developed has been widely used in motor neuron research. One focus of her current research is to model motor neuron diseases using human pluripotent stem cells and integrated platforms. By combining cellular, molecular, bioengineering, and in vivo animal model approaches, research in her lab aims to understand the pathogenic mechanisms of neurodegenerative diseases and to develop therapeutics for their treatment.

Do Bacterial and Viral Infections Trigger Neurodegeneration?

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Abstract

Evidence of cross-interaction between *E. coli* biofilm-forming protein CsgA, and host protein α -Syn has intrigued researchers. To decipher the mechanism of such interaction, we dissected the CsgA primary structure and revealed that it contains five amyloidogenic peptide stretches (R1–R5). We report that within these stretches, conserved six-residue motifs (Q-X-G-X-G-N) preferentially drive α -Syn fibrillization. We extended our study to common infectious viruses such as HIV, HSV, EBV, and SARS-CoV-2 using proteome-wide screening combined with aggregation-propensity prediction tools (PASTA 2.0, AggreScan, WaltZ, Tango, and FoldAmyloid). We identified viral peptide hotspots with strong co-aggregation potential toward α -Syn, prion and IAPP host proteins. Molecular dynamics simulations confirmed their self- and cross-associative properties. Biophysical analyses, including Thioflavin T (ThT) fluorescence kinetics and transmission electron microscopy (TEM), demonstrated accelerated fibrillization of the host proteins in the presence of both bacterial and viral peptides. Collectively, we highlight the dual contribution of bacterial and viral infection in modulating host protein misfolding and aggregation. Cellular uptake studies defined the mechanistic basis of infection-driven aggregation. Mapping these cross-aggregation networks identifies peptide hotspots as promising therapeutic targets for the development of small-molecule or peptide-based inhibitors as potential anti-neuropathic drugs.

Keywords: Viral peptides, Bacterial peptides, Cross-reactivity, Neurodegeneration, Prion, α -synuclein.

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Dr Bishwajit Kundu received his M.Sc. in Biotechnology from Madurai Kamaraj University and earned his PhD from IMTECH, Chandigarh, where he specialised in protein engineering with a focus on protein folding and aggregation. His doctoral research involved studies on alpha-crystallins, carbonic anhydrase, and thermostable xylanases. He subsequently pursued postdoctoral research at Case Western Reserve University, Cleveland, USA, in the Department of Physiology & Biophysics, working on the biophysical characterisation of human prion proteins. His contributions were recognised by the National Academy of Sciences, USA. Dr Kundu is a member of various prestigious academic bodies, such as the Association of Microbiologists of India (AMI), the Biophysical Society of India (BPS), the Protein Society of India (PSI), and the Society of Biological Chemists (SBC). He is the recipient of the FITT Trailblazer Award and the HIFAA Award. His current research interests include rational design of thermophilic enzymes, protein biophysics and thermodynamics, and aggregation and amyloid formation. His laboratory focuses on protein engineering and aggregation studies related to neurodegenerative, pathogenic, and viral diseases, as well as identifying therapeutic targets in multidrug-resistant pathogens.

Antimicrobial Resistance Knowledgebase towards understanding resistance mechanisms and targeted drug discovery for AMR

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Abstract

In response to this growing crisis of AMR, WHO in 2024 released an updated list of Bacterial Priority Pathogens (BPP). The availability of large-scale whole-genome and omics data provides a unique opportunity to develop integrated platforms for understanding the emergence of AMR mechanisms and prioritizing potential therapeutic targets. Towards this, we developed Antimicrobial Resistance Knowledgebase (ARKbase) as an integrated, curated, value-added knowledge-base for AMR, with a focus on WHO Bacterial Priority Pathogens. ARKbase has three core modules - Database Module, Insight Module and Comparative Genomics Module. The Database Module has curated reference genomes and pan genomes along with antimicrobial sensitivity profiles. The Insight Module offers deep annotations for curated genomes towards antimicrobial resistance genes (ARGs), virulence factors (VF), structure annotation (ST), host-pathogen interactions (HPI), biosynthetic gene clusters (BGCs), protein-protein interactions (PPI), drug targets (DT), drug target interactions (DTI), machine learning (ML) models, curated transcriptomic datasets for antibiotic exposure, etc. The strains included in ARKbase are quality checked and curated as per CLSI standards for antimicrobial sensitivity profiles and EUCAST guidelines for genome sequence datasets. The third core module on Comparative Genomics offers a simple interface for comparing ARGs, virulence factors and drug targets among different priority pathogens. ARKbase is the first comprehensive knowledgebase focusing on WHO priority pathogens and AWaRe classification, enabling a combined evidence approach towards a holistic understanding of AMR. ARKbase is freely available at <https://datascience.imtech.res.in/anshu/arkbase>. Since AMR is a socio-technical issue, the talk will also briefly discuss the outreach (serious video games and other resources) and community-led engagement efforts towards addressing AMR.

Keywords: Antimicrobial resistance; ARKbase; Drug discovery; AMR mechanism

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Anshu Bhardwaj has more than 17 years of experience in applications of data science in genomics and drug discovery. She did her Ph.D. from CSIR-CCMB in the domain of precision medicine. Her lab (AB-Data Science Lab) is dedicated to unraveling the intricacies of complex phenotypes, with a keen focus on infectious and mitochondrial diseases. Over the years, her team has developed new algorithms and platforms towards discovering novel targets and inhibitors utilizing network and AI/ML-based approaches. She served as an Associate Scientific Advisor to Science Translational Medicine and is on the Editorial Board of PLoS Global Public Health, Journal of Genetics, and Advisor to F1000 Research Galaxy Gateway. She has several publications, honors and awards to her credit - She was selected as one of the four Young Innovators in India by United National Development Program (UNDP), selected for the prestigious International Visitor Leadership Program by US State Department, awarded Newton-Bhabha Fund from the British Council and the Royal Society of Chemistry, UK and long-term Group Leader Fellowship by INSERM, France and more recently the Trinity Youth Challenge award by Cambridge, UK. She conceived, designed and implemented crowdsourcing as a tool to tackle challenging scientific problems, which is considered a futuristic approach to drive big data scientific projects and has trained over 500 students. She also utilizes innovative education technologies like video games to raise awareness on pressing health issues. More recently, her lab has developed a unique scientific video game for awareness on AMR, which is endorsed by the WHO in India.

Invited Speakers

Gut Health Modulation Through Probiotic Intervention

Gunjan Goel

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Abstract

The gut microbiota has been recognised as a central regulator of host health, particularly through its interaction with the central nervous system via the microbiota-gut-brain bidirectional axis. Within this regulation, the metabolites from gut microbiota act as a key signaling molecule capable of influencing neural, endocrine, and immune pathways. Neurons communicate through chemical messengers known as neurotransmitters, including γ -aminobutyric acid (GABA), serotonin, histamine, and catecholamines such as dopamine, adrenaline, and norepinephrine. Among the various dietary intervention to maintain gut homeostasis, probiotics and prebiotics are of the two of the most promising interventions for restoring gut microbiome. Fermented foods through probiotic lactic strains, can modulate this axis by secretion of neuroactive compounds and their precursors. Lactic acid bacteria (LAB) are especially promising candidates for GABA production owing to their well-recognized role in fermented foods and human gut. Moreover, the strains are classified as Generally Recognized as Safe (GRAS). Probiotic microorganisms, particularly lactic acid bacteria and bifidobacteria, have emerged as promising therapeutic agents capable of restoring microbial balance and improving gut health. The studies suggests that GABA-producing probiotics contribute to improved intestinal barrier integrity, reduction of gut inflammation, and modulation of neurotransmitter signaling associated with neurological disorders. Furthermore, these probiotics may restore gut microbial balance and enhance the production of beneficial metabolites, highlighting their therapeutic potential as psychobiotics for maintaining both gut and mental health. Our studies recognized different strains of LAB from fermented foods with an ability to produce GABA which was confirmed through qualitative and quantitative assays. The strains also exhibited probiotic activities using in vitro gastro-intestinal conditions and possess additional functional activities. The GABA containing supernatant from these probiotic strains increased cell viability in tested in stress-challenged Human Neuroblastoma SH-SY5Y cell lines. Our studies shows that the fermented foods are major reservoir of GABA-producing probiotics which can be further explored in animal models targeting gut-brain axis.

Keywords: Gut health, probiotic, GABA, Fermented Foods

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Dr. Gunjan Goel is working as a Professor in the Department of Microbiology, Central University of Haryana, Mahendergarh, India. Dr. Gunjan Goel has been working in the area of Food Microbiology and Gut microbial Ecology. He has already completed four different projects sponsored by DBT, DST, ANRF, Haryana DST, Haryana State Higher Education Council, where he has worked on different aspects of Food Microbiology. Dr. Goel has vast experience in the field of microbiology and probiotics with a strong focus on gut health, functional foods, and microbial biotechnology. His research interests include the isolation and characterization of probiotic microorganisms from traditional fermented foods, the evaluation of gluten-degrading and GABA-producing bacteria, and the development of novel probiotic interventions for gut health. His work also explores innovative applications of probiotics and postbiotics in food systems, nutraceuticals, and therapeutic formulations aimed at improving human health and well-being.

Protecting Your Research – Pipettes to Patents

Indrani Ghosh

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Abstract

Biotechnology research drives transformative advances in sustainable healthcare, agriculture, environment, and computational biology. Protecting these innovations through Intellectual Property (IP) rights is essential to ensure that scientific inventions are recognized, safeguarded, and translated into real-world impact. Effective IP protection not only prevents unauthorized use and biopiracy but also enhances opportunities for publication, funding, collaboration, technology transfer, and commercialization. For researchers, understanding patents and other forms of IP is increasingly important in converting laboratory inventions into valuable societal and economic outcomes. In a rapidly evolving innovation landscape, protecting biotech research empowers researchers to secure ownership of their ideas, attract industry partnerships, and contribute meaningfully to national and global innovation ecosystems.

Keywords: Research, Innovation, Patent

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Dr. Indrani Ghosh has played a pivotal role in shaping and advancing innovation ecosystem in India. Her contributions have been instrumental in driving several breakthrough innovations within the Council of Scientific & Industrial Research (CSIR), a premier R&D organization renowned for its cutting-edge knowledge base and expansive national network of laboratories, outreach centres, and innovation hubs. With over two decades of distinguished experience in Intellectual Property (IP) and Technology Management, she is a strong advocate of India's intellectual property movement. She combines deep scientific expertise with robust IP and commercialisation acumen. She holds a PhD in Biotechnology and is a Registered Patent Agent as well as a qualified Registered Technology Transfer Professional (RTTP). Her techno-legal proficiency is enriched by international exposure, having worked with globally reputed institutions such as the World Intellectual Property Organization (WIPO), Geneva; the Austrian Patent Office, Vienna; and the Indian Institute of Management (IIM), Ahmedabad. She was also selected for the prestigious Advanced Biotechnology and Pharmaceutical Patent Program conducted by the United States Patent and Trademark Office's Global Intellectual Property Academy in Washington, DC - an acknowledgment of her expertise in high-impact patent domains. Beyond her professional roles, she actively contributes to the IP and innovation landscape as a member of various committees, fostering collaboration and knowledge exchange among industry, academia, research institutions, and other key stakeholders. Her work continues to bridge the gap between scientific innovation and commercialization, strengthening innovation-led growth.

Biovalorization of Corn Protein Meal as a Sustainable Alternative Protein Source

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Abstract

Corn Protein Meal (CPM), a major byproduct of the corn wet milling industry, holds significant potential as a plant-based protein source for food and feed applications. However, its utilization is limited by an imbalanced amino acid profile (notably deficient in lysine and tryptophan), poor solubility and digestibility, and a strong off-odour that reduces palatability. This study evaluated various processing strategies including fermentation, chemical treatment, and enzymatic modification, to enhance the nutritional and sensory attributes of CPM. Among these, fermentation using mushroom mycelia significantly increased the crude protein content by approximately 20%. Sensory evaluation using a 10-point hedonic scale indicated that fermentation was most effective in mitigating the off-odour and improving palatability, with a rating of 8, followed by the chemical method (rating: 7). Although enzymatic treatment was ineffective in enhancing sensory properties, it helped maintain a balanced amino acid profile. These findings highlight mushroom mycelial fermentation as a promising strategy to overcome the key limitations of CPM. Improving its nutritional, functional, and sensory qualities. The valorization of CPM as sustainable protein supplement as value added product, aligning with the goals of a circular bioeconomy.

Keywords: Corn Protein Meal, Fermentation, Enzyme, De-odouring, Plant protein

Dr. Meena Krishania Choudhary

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Dr. Meena Krishania Choudhary is distinguishing Scientist at the National Agri-Food and Biomanufacturing (Formerly CIAB), Mohali. She did her B.Tech. in Biotechnology Engineering (2007), M.Tech. in Chemical Engineering (2009), and Ph.D. from IIT Delhi (2013). She briefly served as an Assistant Professor at Amity University before joining CIAB in 2014. Her research focuses on sustainable bioprocessing, valorization of agri-residues, industrial biotechnology and biomanufacturing. She has filed over 8 patents (four granted), transferred 3 technologies to industry, published 50+ papers, and authored 3 books. A recipient of several awards and grants, she is an active member of national and international societies and continues to innovate in biomass valorization and biomanufacturing technologies.

Genetic Treasures of Extreme Habitats: Bioengineering Extremozymes and Protein Nanoparticles for Green and Sustainable Environmental Biotechnology

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Abstract

Extreme environments, hypersaline lakes, polar ice, deep-sea brine pools, and alkaline soda lakes harbor microorganisms whose enzymes ("extremozymes") and macromolecular nanostructures retain catalytic function under conditions that inactivate conventional biocatalysts. Such polyextremozymes are emerging as green, energy-efficient alternatives to fossil-based industrial chemistry and support applications ranging from CO₂ sequestration to bioremediation of metal-laden wastewaters, aligning directly with the goals of the circular bioeconomy. Our objective was to mine, characterize, and bioengineer robust enzymes and microbial nanoparticles from globally distributed extreme ecosystems for environmental applications, including carbon capture, bioremediation, and waste-to-value conversion. Sediments and brines were collected from Deep Lake, Antarctica (−18 to +11.5 °C; 21–28% salinity), Red Sea brine pools (Atlantis II, Discovery, Kebrit; 23–68 °C; 26–33% salinity; elevated heavy-metal load), and eight Indian hypersaline and alkaline habitats. Culture-based isolation was integrated with single-amplified-genome (SAG) sequencing and Illumina NovaSeq X Plus metagenomics. Selected biocatalysts, a cold-active β-galactosidase, γ-carbonic anhydrase, Mn²⁺/Zn²⁺ alcohol dehydrogenase, proteases, esterases, and lipases, were heterologously expressed in *Haloferax volcanii*, structurally resolved by X-ray crystallography (2.1–2.5 Å), and rationally bioengineered for activity, stability, and substrate scope. Engineered enzymes remained active at salinities up to 25% (w/v), pH 5–10, temperatures from −10 to 80 °C, and in 20% organic solvents. A re-engineered γ-carbonic anhydrase showed a 17-fold activity gain, enabling biomimetic CO₂ sequestration into CaCO₃, while halophilic alcohol dehydrogenase supported cofactor regeneration for fine-chemical synthesis. Halophilic gas vesicle nanoparticles (GVNPs) were functionalized as multivalent

display and delivery platforms. GVNPs functioned as oxygen supply, biosensing, and antigen-display nanoplateforms. Together, these results establish extreme-habitat microbiomes as a renewable genetic reservoir for green biocatalysts and nanostructures driving bioremediation, carbon capture, and the circular bioeconomy.

Keywords: Extremophiles, extremozymes; carbonic anhydrase; circular bioeconomy; gas vesicle nanoparticles

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Dr. Ram Karan is an Associate Professor in the Department of Microbiology at the University of Delhi South Campus, India. He earned his Ph.D. from IIT Delhi and trained as an American Society for Microbiology International Fellow at the University of Maryland and the NIH, USA — the sole awardee from 48 Asian countries that year. He subsequently served as a Senior Research Scientist at KAUST, Saudi Arabia, for nearly a decade.

Dr. Karan has authored 60+ publications in journals including the Nature group, PNAS, and ACS, holds three international patents, and has secured over US \$5 million in funding from NASA, NIH, NSF, the Gates Foundation, ICMR, and KAUST. His research bioengineers extremophilic enzymes and gas vesicle nanoparticles for sustainable biotechnology and the search for life beyond Earth.

Robust Plant Transformation: A Foundation of Genome Editing in Chickpea, Rice bean. and Pearl Millet

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Abstract:

Efficient plant transformation systems are fundamental to the successful application of CRISPR/Cas9-based genome editing, particularly in recalcitrant legume and millet crops with limited genetic variability. Chickpea (*Cicer arietinum*), a nutritionally important protein-rich legume, presents significant challenges for in vitro regeneration and stable transformation. In this study, we report the development of an efficient and reproducible transformation platform that enhances genome editing efficiency in chickpea. Using this system, targeted mutagenesis of the phytoene desaturase gene (*CaPDS*) resulted in a 42% phenotypic mutation efficiency. Additionally, functional validation of key genes, including CaCKX3 and the R2R3-MYB transcription factor CaMYB39, demonstrated distinct phenotypic alterations in plant architecture and seed traits. Efforts are ongoing to extend this platform for functional characterization of over 100 candidate genes, although challenges remain in identifying edited alleles in segregating seeds. To further validate CRISPR/Cas9 efficiency in underexplored pulse crops, we established, for the first time, a genome editing system in ricebean (*Vigna umbellata*) by targeting the *VuPDS* gene. The use of a codon-optimized Cas9 driven by a double-enhanced CaMV35S promoter, along with sgRNA under the AtU6 promoter, resulted in albino mutant plants, confirming successful editing. This work establishes a robust pipeline for genome editing in ricebean and opens avenues for improving agronomic and nutritional traits. In pearl millet (*Pennisetum glaucum*), a climate-resilient cereal critical for food security in arid regions, rapid lipid degradation mediated by lipase enzymes limits flour shelf life. To address this, CRISPR/Cas9-mediated editing of seed-specific lipase genes (PgLIP1, PgLIP2, and PgLIP3) was performed. Molecular validation confirmed stable T-DNA integration, and Sanger sequencing revealed targeted indels across all three lipase genes in *To* plants. Overall, this study demonstrates the development of efficient genome editing platforms across multiple legume and millet crops and highlights their potential for functional genomics and targeted crop improvement, particularly for traits related to yield, nutrition, and postharvest quality.

Keywords: Pearl millet, Lipase, CRISPR/Cas9, Shelf life, Genome editing, PCR.

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Bridging Diagnostics and Care: Lateral Flow & Electrochemical Biosensors in Action

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Abstract

Diagnostic technologies are undergoing a transformative shift from centralized laboratory testing toward rapid, decentralized, and patient-centric healthcare solutions. Conventional diagnostic methods, while highly sensitive, often require sophisticated instrumentation, trained personnel, long turn-around times, and well-equipped laboratory infrastructure, limiting their accessibility in resource-constrained settings. This talk, titled “*Bridging Diagnostics and Care: Lateral Flow & Electrochemical Biosensors in Action*,” will discuss the evolution of disease diagnostics from conventional laboratory-based assays to portable point-of-care biosensing platforms designed for rapid and affordable healthcare delivery. The presentation will provide an overview of key parameters governing biosensor performance, including the selection of nanomaterials, immobilization strategies, electrode surface engineering, and biomolecule loading capacity. Particular emphasis will be placed on the rational design and selection rules of nanomaterials based on their functional groups, morphology, conductivity, and polydispersity. These factors critically influence biomolecule retention on sensor surfaces, preservation of biomolecular activity, minimization of structural alterations, and enhancement of analytical characteristics such as sensitivity, selectivity, linear range, and dynamic range. Strategies for reducing non-specific interactions and improving assay reproducibility for real-world clinical samples will also be discussed. The talk will further highlight the development of electrochemical biosensors for thyroid disorder and infertility diagnosis, demonstrating the utility of nanomaterial-enabled sensing platforms for quantitative hormone analysis with high sensitivity and rapid turnaround times. In parallel, lateral flow biosensors developed for acute myeloid leukemia (AML) mutation detection and tuberculosis diagnosis will be presented as examples of low-cost, user-friendly technologies suitable for decentralized healthcare and low-resource settings. Finally, we address critical translational challenges involved in converting laboratory-scale biosensor research into commercially viable diagnostic products, including device integration, manufacturability, regulatory considerations, clinical validation, and scalability for industrial and market adoption.

Keywords: Electrochemical biosensors; lateral flow biosensors, point-of-care device

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Prof. Sudha Srivastava is an Interdisciplinary translational researcher with 20+ years of experience in R&D. Strong education professional, passionate about teaching and curriculum development for higher education.

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With several industry collaborations and funded/Consultancy projects from ICMR, DST, AICTE, Kanpur Fertilizers and Chemicals Ltd (KFCL) and Ecozyme AB, Dr. Srivastava continues to advance translational nanotechnology research for healthcare and sustainable development.

Reversing Carbapenem Resistance in *Acinetobacter baumannii* by Targeting the AdeABC Efflux Pump and MurB Protein.

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Abstract

Acinetobacter baumannii is a major opportunistic pathogen responsible for pneumonia, respiratory tract infections, and urinary tract infections, particularly in hospitalized patients. The emergence of carbapenem-resistant *A. baumannii* (CRAB) has created a serious therapeutic challenge worldwide. Quantitative proteomic analysis and gene knockout studies confirmed that AdeABC contributes to carbapenem resistance, biofilm formation, motility, and host cell adherence and invasion. Structure-based virtual screening, and experimental validation identified naringin dihydrochalcone (NDC) as a potent inhibitor of the AdeB transporter. NDC-capped silver nanoparticles (NDC-AgNPs) were developed and exhibited multiple mechanisms of action, including efflux inhibition, disruption of membrane potential, and induction of reactive oxygen and nitrogen species. Similarly, in silico studies identified MurB as a potential target of the AMP Bactenecin. MurB was cloned, overexpressed, and purified, and binding was confirmed by BLI, fluorescence, UV-Vis, and CD spectroscopy, which demonstrated strong interaction and structural destabilization of the protein. Bactenecin inhibited cell wall synthesis, reduced peptidoglycan content, disrupted biofilm formation, and induced oxidative stress and membrane damage. Collectively, these findings demonstrate that targeting of the AdeABC efflux pump and the MurB cell wall biosynthesis enzyme represents a promising strategy to reverse carbapenem resistance in *Acinetobacter baumannii*.

Keywords: *Acinetobacter baumannii*, antimicrobial resistance, antimicrobial peptides, carbapenem resistance.

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He currently serves as Director (Research & Development), Chairman, IBSC and GIAN Coordinator at Central University of Rajasthan. His research focuses on antimicrobial resistance, host-pathogen interactions, and the development of novel therapeutics against ESKAPE pathogens, with particular emphasis on carbapenem-resistant *Acinetobacter baumannii*.

Dr. Tiwari has published around 100 research articles in leading international journals with more than 5,000 citations. He has been recognized by Indian National Science Academy (INSA Young Scientist), Indian Academy of Sciences (Associate Fellow), National Academy of Sciences, India, and Indian Council of Medical Research etc.

Green Nanomaterials: Their Synthesis and Applications

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Abstract

Green nanomaterials refer to nanoscale materials or nanoparticles that are produced using environmentally friendly and sustainable methods and exhibit properties or applications that have a positive impact on the environment. These materials are designed to minimize the negative environmental and health effects associated with traditional nanomaterials and materials production processes. The key features and aspects of green nanomaterials includes Sustainable Production, Biodegradability and Low Toxicity. The production processes for green nanomaterials often prioritize energy efficiency and low carbon emissions, contributing to a reduced environmental footprint. They are designed to use fewer raw materials and generate less waste, promoting resource efficiency. Green nanomaterials find applications in various fields, including environmental remediation, clean energy, healthcare, and sustainable packaging. For example, they can be used in water purification, solar cells, drug delivery systems, and biodegradable packaging materials. The green nanomaterials applications include their use as Nanocellulose, Green Synthesized Nanoparticles, Carbon Nanotubes (CNTs), Nanoparticles for Water Treatment, Green Quantum Dots. Nanostructured materials made from renewable resources like wood or agricultural waste can be used in construction materials, insulation, and even as catalysts in chemical processes. Green nanomaterials can be used to encapsulate and deliver drugs with greater precision, reducing side effects. This is particularly beneficial in cancer therapy and other medical applications. In the field of Agriculture, Nanomaterials like nanoparticles and nanofertilizers can improve crop yields and reduce the use of chemical fertilizers. They can also be used for targeted pesticide delivery. They are applicable for energy generation as Green nanomaterials, can enhance the efficiency of solar cells and fuel cells, making renewable energy sources more accessible and sustainable. Apart from that, Biodegradable nanopolymers can be used in drug delivery systems and tissue engineering. They gradually break down in the body, reducing long-term environmental impact. The green synthesized nanomaterials can be used for production of Nanocatalysts which can improve the efficiency of chemical reactions, reducing energy consumption and waste in industrial processes. They can be used as nanocomposites for light weight materials, such as those based on bioplastics, which are used in automotive and aerospace industries to reduce weight and improve fuel efficiency. These all nanomaterials can be synthesized using various methods which includes biological Methods using microorganisms and plant extracts, chemical reduction using green reagents and solvents, electrochemical synthesis, sun-light assisted synthesis or microwave assisted synthesis. The choice of

method depends on the specific nanomaterial one wants to synthesize and the desired properties of the material. Green nanomaterial synthesis techniques aim to minimize the use of hazardous chemicals, energy, and waste generation. Researchers are continually working to develop and improve green nanomaterials as to make nanotechnology more sustainable and environmental friendly.

Keywords: Nanoparticles, Sustainable Production, Biodegradability

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Dr. Raju Shankarayan is a distinguished academic and researcher currently serving as an Associate Professor in the School of Biotechnology at Shri Mata Vaishno Devi University (SMVDU), Katra. With over a decade of experience at SMVDU since joining in 2012, Dr. Shankarayan has established himself as a specialist in Biochemical Engineering and Biotechnology.

His academic foundation is rooted in excellence, holding a Ph.D. from IIT Delhi, an M.Tech from Anna University, and a B.Pharm from B.R.A. Bihar University. His research interests are diverse, spanning green nanomaterials, drug delivery systems, and bioenergy. He has authored numerous high-impact papers in SCI-E indexed journals like *Springer* and *3-Biotech*, and has successfully guided doctoral research in medicinal plant bioactivity.

Beyond research, Dr. Shankarayan is a committed lifelong learner, consistently upgrading his skills through MOOCs from Stanford and Manchester University, and participating in numerous UGC-approved National Education Policy (NEP) orientation programs. As a life member of the Environment and Social Development Association (ESDA), he actively contributes to environmental advocacy. His leadership is further evidenced by his frequent roles as a Session Chair at international conferences and his dedication to mentoring B.Tech. and M.Sc. students in cutting-edge biotechnological applications.

Harnessing Selenium-Enriched Cereals- A Comprehensive Investigation Into Biofortification, Bioaccessibility, And Health Implications Of Seleniferous Crops

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Abstract

Selenium (Se) is an essential micronutrient that supports antioxidant defense, immune function, and cellular regulation through its role in selenoproteins. Both deficiency and excess of selenium pose health risks, with low levels linked to disorders such as Keshan and Kashin-Beck diseases, and high intake leading to selenosis. One effective strategy to address global selenium deficiency is the natural biofortification of crops, particularly cereals like wheat, maize, and rice grown in seleniferous soils. These crops can accumulate selenium in bioavailable organic forms, mainly selenomethionine (SeMet), making them valuable dietary sources. Studies investigating selenium content and bioavailability employed advanced analytical techniques such as neutron activation analysis, inductively coupled plasma mass spectrometry, and high-performance liquid chromatography coupled with molecular spectrometry. These methods enabled precise quantification, speciation, and assessment of selenium bioaccessibility in grains and food products. In vitro digestion models simulating gastrointestinal conditions revealed that selenium becomes more bioaccessible during intestinal digestion compared to gastric digestion, particularly from protein fractions such as albumins, globulins, glutelins, and prolamins. Selenium concentrations in grains ranged from 20 to 185 µg/g depending on crop type and soil conditions, with SeMet constituting over 75% of total selenium. Minor species like methylselenocysteine contributed additional bioactivity. Functional studies showed that selenium-rich diets enhanced antioxidant responses by upregulating enzymes like glutathione peroxidase (GPx-1) and reducing pro-inflammatory gene expression. Processing effects were also evaluated, with baked products such as roti retaining significant selenium levels, although some variation in other trace elements was observed. Overall, selenium-enriched cereals offer substantial nutritional and therapeutic benefits, especially in deficient populations. However, in regions with high natural selenium levels, excessive consumption may increase toxicity risks. These findings highlight the importance of balancing selenium intake and optimizing processing and dietary strategies to maximize health benefits while minimizing potential adverse effects.

Keywords: Selenoproteins, Bioaccessibility, Methylselenocysteine

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Bacteria as a resource material for healing the cracks and improvement of cementitious properties

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Abstract

Microbially induced carbonate precipitation (MICP) is a novel and eco-friendly technique to enhance the consolidation properties of building materials. In this study, the MICCP was carried out by heterotrophic bacteria to heal the cracks and improve the structural properties of cementitious and stone material. Ureolytic bacteria were isolated from marble dust and their efficiency in calcium carbonate precipitation was studied. Seven isolates of ureolytic bacteria were isolated and identified as *Bacillus cereus* MD1, *Bacillus paranthracis* MD2, *Bacillus paranthracis* MD3, *Bacillus paramycoides* MD4, *Bacillus paramycoides* MD5, *Bacillus paramycoides* MD6 and *Bacillus paramycoides* MD7 based on their 16S rRNA sequence analysis. The biomaterial was developed by immobilizing *B. paramycoides* MD6 spores in metakaolin (MK). The immobilized bacteria in MK was used as carrier material in concrete to improve the cementitious and self-healing properties. The nutrient broth (NB) and corn steep liquor (CSL) were used as nutrient media for self-healing. The biomaterial NB-4 and CSL-4 showed significant improvement in concrete compressive and flexural strength at 7 and 28 days. The sorptivity coefficients of NB-4 and CSL-4 were 0.006 and 0.002 at 7 and 28 days, respectively, which were comparatively lower than the control. The self-healing capability of biomaterial was investigated for approximately 0.5 mm crack in 400 × 100 × 100 mm prismatic specimens. The crack was completely healed with 99.14% and 98.2% crack healing efficiency in CSL-4 and NB-4 biomaterial-incorporated specimens, respectively. During the crack healing period, the ultrasonic pulse velocity (UPV) was observed to improve and get closer to the reference specimens, proving the complete healing of the crack. At the end of testing, the precipitated mineral was assessed by FESEM-EDS and XRD. This study also demonstrates that *B. paramycoides* effectively precipitated CaCO₃ on marble, increasing its mass and surface quality. Acid rain exposure caused deterioration, including weight loss and surface damage, was successfully restored by bacterial treatment. These results showed that bacteria play an important role in material restoration and improvement.

Keywords: Ureolytic bacteria, FESEM-EDS, XRD

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Amplifying the Invisible: Detecting Parkinson's Disease Through Seed Amplification Assays

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Abstract

Pathological alpha-synuclein aggregates (α SynD) are central to the progression of synucleinopathies such as Parkinson's disease (PD) and dementia with Lewy bodies (DLB), where they propagate through prion-like mechanisms. Seed amplification assays (SAAs), particularly real-time quaking-induced conversion (RT-QuIC), have emerged as highly sensitive platforms for detecting α SynD seeding activity in clinically relevant biospecimens. However, the quantitative limitations of conventional SAAs restrict their broader utility in disease staging, prognosis, and therapeutic monitoring. In this study, optimized end-point dilution (ED) RT-QuIC strategies were evaluated to improve assay sensitivity, reproducibility, and quantitative precision. Key experimental variables including dilution factor, replicate number, and statistical analysis approaches were systematically assessed. The use of 2-fold serial dilutions with increased replicate reactions significantly reduced assay variability and enabled detection of subtle differences in α SynD seed concentrations. Additionally, Poisson and midSIN algorithms improved statistical robustness and inter-assay consistency. The optimized workflow demonstrated enhanced performance across multiple diagnostically relevant antemortem biospecimens including cerebrospinal fluid, skin, and olfactory mucosal brushings. These findings highlight the potential of quantitatively refined SAAs as powerful biomarker tools for early diagnosis, disease stratification, and therapeutic evaluation in Parkinson's disease and related synucleinopathies.

Keywords: Alpha-synuclein, RT-QuIC, Seed amplification assay, Parkinson's disease, Biomarkers, Synucleinopathies, Neurodegeneration, Protein aggregation, End-point dilution

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Prior to his current role, Dr. Srivastava served as a Senior Postdoctoral Fellow at the National Institute of Allergy and Infectious Diseases (NIAID), National Institutes of Health, USA. He has authored more than 35 peer-reviewed publications in leading journals including *Nature Chemical Biology*, *FASEB Journal*, *PLOS Pathogens*, and several ACS journals.

Dr. Srivastava's research has attracted significant competitive extramural funding from prestigious national and international agencies, including the Anusandhan National Research Foundation (ANRF) Prime Minister's Early Career Research Grant, the Indian Council of Medical Research (ICMR), and the Michael J. Fox Foundation for Parkinson's Research (USA), a testament to the originality and impact of his work.

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Healthcare Biotechnology

Oral Presentation

Combining algae-based biomarkers with AI/ML for sensitive, low-cost point-of-care Alzheimer's screening

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Abstract

Over 55 million individuals are suffering with a progressive neurodegenerative disorder i.e. Alzheimer's disease (AD) worldwide. The accumulation of hyperphosphorylated tau (p-tau) tangles and amyloid-beta (A β) plaque are its key indicators. Traditional techniques of diagnosis of AD such as magnetic resonance imaging (MRI), cerebrospinal fluid (CSF) analysis, and positron emission tomography (PET) have significant drawbacks due to its high cost, invasiveness and late-stage detection. Therefore, present research proposes a sustainable, non-invasive diagnostic approach combining two interdisciplinary platforms such as algae biomarkers with explainable artificial intelligence (XAI)-driven machine learning models to move beyond traditional "black box" models. Parallely, model study included independent and clustered biomedical dataset are random forest classifier (baseline model) & LightBGM, XGBoost classifier. Large Biomedical datasets comprising algae biomarkers such as fucoxanthin response, fucoidan response, phlorotannin response, cellular stress, oxidative stress markers, inflammatory indicators from both effected and non-affected patients (5000) were analyzed. Machine learning models, including Random Forest (baseline), LightGBM, and XGBoost, were implemented. Results showed that XGBoost achieved the highest predictive accuracy (~91–94%), followed by LightGBM (~89–92%), demonstrating robust classification of at-risk individuals. It also explained key contributing biomarkers and threshold values which ultimately enhanced the predictability. Therefore, this integrated approach provides sustainable, non-invasive approach for early AD detection which improved clinical detection.

Keywords: Alzheimer's disease, Algae biomarkers, Non-invasive diagnosis, Machine learning, Explainable AI

One Primer, Multiple Pathogens: A RFLP-Based Approach for Rapid Screening of Smokeless Tobacco Products

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Abstract

Smokeless tobacco (SLT) products are widely consumed in India and may act as reservoirs of opportunistic pathogens, posing additional risks to users. Rapid and cost-effective detection of such pathogens is critical in clinical settings where delayed identification can impact infection management. Although Restriction Fragment Length Polymorphism (RFLP) is a well-established and accurate method for bacterial identification, it conventionally requires microbe-specific primers and multiple restriction enzyme combinations. This study presents a simplified RFLP process using a single primer along with restriction digestion using two restriction enzymes; Mnl I and Hae III, followed by PCR for detecting 4 clinically relevant pathogens-*Pseudomonas aeruginosa*, *Enterococcus faecalis*, *Acinetobacter baumannii* and *Staphylococcus aureus*. A total of 23 heterogeneous SLT samples were analyzed using this simplified RFLP+PCR approach. The method enabled identification of three opportunistic pathogens-*Pseudomonas aeruginosa*, *Enterococcus faecalis*, and *Staphylococcus aureus*-in $\approx 70\%$ SLT samples. *P. aeruginosa* was the most prevalent (52.9%), followed by *E. faecalis* (35.3%), while *S. aureus* was detected in 11.8% of samples and none showed presence of *Acinetobacter baumannii*. Distinct and reproducible RFLP patterns confirmed reliable differentiation of bacterial species. The proposed approach demonstrates a streamlined and cost-effective alternative to conventional RFLP protocols, reducing the need for multiple primer sets and enzyme combinations while maintaining specificity. The presence of opportunistic pathogens in SLT products highlights a potential, often overlooked, source of microbial exposure. Identification of such sources may assist clinicians in infection risk assessment and deciding their therapeutic strategies at early stages improving clinical outcomes.

Keywords: Smokeless tobacco, RFLP, Opportunistic pathogens, *Pseudomonas aeruginosa*, *Enterococcus faecalis*, *Staphylococcus aureus*, Infection risk, Cost-effective diagnostics

Animal Disease Diagnosis Using Molecular Biotechnology

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Abstract

Animal diseases pose significant threats to livestock productivity, wildlife conservation, and global public health. Molecular biotechnology has emerged as a powerful approach for the accurate and rapid diagnosis of animal diseases. Techniques such as polymerase chain reaction (PCR), enzyme-linked immunosorbent assay (ELISA), and DNA sequencing enable the detection of pathogens at the genetic and molecular level, even before the onset of visible symptoms. These methods offer high specificity and sensitivity compared to conventional diagnostic techniques, allowing early intervention and effective disease management. Molecular tools are widely used to identify viral, bacterial, and parasitic infections in animals, thereby reducing the spread of zoonotic diseases that can affect humans. Advancements in bioinformatics facilitate the analysis of complex genetic data, improving pathogen identification and tracking disease outbreaks. The integration of molecular biotechnology with veterinary science enhances disease surveillance, supports vaccine development, and promotes animal health and welfare. However, challenges such as high costs, technical expertise, and accessibility in rural areas remain. Continued research and technological advancements are essential to make these diagnostic tools more affordable and widely available for sustainable animal healthcare systems. This study focuses at exploring the role of molecular biotechnology in the early diagnosis and effective management of animal diseases, while addressing the challenges associated with its implementation in resource-limited settings.

Keywords: Molecular Biotechnology, Animal Diseases, PCR, ELISA, Pathogen Detection, Veterinary Diagnostics, Zoonotic Diseases, Bioinformatics

Preparation and Characterization of Nano-liposomal Formulation for Respiratory Disorders

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Abstract

Respiratory diseases have become very common and the severity of the diseases has also increased in the present scenario of air pollution. Many of these diseases are linked to allergies and inflammations which are caused by the irritants present in in-door and out-door air surrounding us. As most of the current day's medicines are linked with several side effects, scientists are currently looking for potential drug molecules from plants. India has a rich culture of plant-based medicines which are combinedly being studied and evaluated in AYUSH system these days. Though scientist have been able to identify potential drug candidates from these natural products the major problem associated with these molecules is that they are commonly known to have low bioavailability, shorter shelf life and easy biodegradability. Use of nanotechnology has been very beneficial to overcome these challenges. The current study was conducted to design nano-liposomal formulation from the plant Eucalyptus and *Adhatoda vasica* to overcome the disease ARDS (Adult Respiratory Distress Syndrome). The nanoliposome of size 70-200 nm were prepared, characterized and were evaluated for the safe dose range. Further it was found that they are able to overcome certain very important features which would help to normalize the respiratory process such as: surface tension inside the alveoli. inflammation and apoptosis. Present study describes the preparation, characterization and evolution of nano-liposomal formulations for respiratory disorders.

Keywords: ARDS, Air pollution, Nanoliposomes, Natural Products, Eucalyptus, *Adhatoda vasica*.

Dissecting Amino Acid Acquisition Pathways in Lyme Disease Spirochetes

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Abstract

Borrelia burgdorferi, the causative agent of Lyme disease, possesses a highly reduced genome reflective of its obligate parasitic lifestyle, yet the mechanisms underlying amino acid acquisition remain poorly characterized. This talk explores how this spirochete navigates the competing demands of peptide-based and free amino acid uptake pathways to sustain viability across ecologically distinct host environments. Prior work established peptide transport as essential for spirochete survival. Expanding on this foundation, BB0401, a putative glutamate transporter, is shown to facilitate uptake of both glutamate and aspartate and is similarly required for viability. Conditional mutant analysis of both transport systems across the enzootic cycle reveals their critical importance during murine infection, while demonstrating a notable dispensability during prolonged tick midgut colonization highlighting how nutritional requirements shift depending on host context. Broad metabolic profiling under amino acid starvation conditions further illuminates the physiological consequences of disrupting these pathways. Strikingly, even under severe amino acid stress, *B. burgdorferi* does not engage the canonical (p)ppGpp-driven stringent response, pointing to fundamentally distinct adaptive strategies compared to other bacterial pathogens. These findings collectively advance understanding of how *B. burgdorferi* satisfies its nutritional demands and identify acquisition pathways as potential targets for intervention.

Key words: *Borrelia burgdorferi*, Lyme disease, Amino acid acquisition, Peptide transport, Enzootic cycle

Nephroprotective Potential of *Tinospora cordifolia*: Phytochemical Profiling and Antioxidant Protection Against Glucose-Induced Oxidative Stress

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Abstract

Diabetic nephropathy (DN) is a microvascular complication associated with diabetes mellitus and a significant cause of end-stage renal disease, caused by hyperglycemia-induced oxidative stress and inflammation. Current therapeutic strategies offer little protection against DN, underscoring the need for more effective and targeted interventions. *Tinospora cordifolia* is a medicinal plant extensively used for traditional purposes that possesses strong antioxidant and nephroprotective actions. In this study, the nephroprotective action of *Tinospora cordifolia* has been assessed through phytochemical analysis and its ability to protect against oxidative stress induced in DN. Analysis indicated the presence of various bioactive compounds such as alkaloids, flavonoids, glycosides, and phenols, which have proven therapeutic significance. It was found that treatment with *Tinospora cordifolia* significantly reduced oxidative stress indicators such as ROS levels and lipid peroxidation, and increased the activity of antioxidants, including superoxide dismutase (SOD), catalase, and glutathione peroxidase. Furthermore, treatment was observed to have a beneficial effect on renal function parameters and helped reduce histopathological changes such as glomerular hypertrophy and tubular damage. On a mechanistic level, the renoprotective properties of *Tinospora cordifolia* can be attributed to a balance in oxidative stress and inflammation signaling, resulting in a reduction in pro-inflammatory cytokine expression and fibrosis. From these results, it can be concluded that *Tinospora cordifolia* is a promising candidate in protecting against kidney damage caused by diabetes.

Keywords: Diabetic nephropathy, *Tinospora cordifolia*, Nephroprotection, Oxidative stress, Glucose-induced oxidative stress.

BBD and ML-based optimization and prediction of *Curcuma caesia* mediated copper oxide nanoparticles with enhanced bioactivity

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Abstract

Medicinal plants being integral part of agriculture significantly contributes to national GDP. Despite high economic value their therapeutic potentials are constrained by limited stability and bioavailability. To overcome this nanotechnology plays a crucial role by enhancing the functionality of bioactive compounds into highly efficient and biologically applicable nanoscale formulations with improved efficiency at lower concentrations. However, this needs a precise optimization of parameters. In this context, copper oxide nanoparticles were synthesised using *Curcuma caesia* via green unipot approach. Further, synthesis parameters of nanoparticles were optimized followed by predicting the yield using machine learning models including random forest and support vector machine. Model performance and prediction accuracy was evaluated using coefficient of determination (R^2) and root mean square error (RMSE). Further, SVM exhibited the highest model performance with $R^2=0.94$ and RMSE=0.14. Overall, this study integrates green synthesis with advanced ML-driven optimization, offering a robust approach for developing efficient nanomaterials for biomedical applications.

Keywords: Machine learning, Nanoparticles, Optimization, Random Forest, Support vector machine

Genomic Insights and Functional Characterization of a Probiotic Strain for Non-Dairy Fermented Food Fortification

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Abstract

The increasing demand for plant-based functional foods has accelerated the exploration of probiotic strains suitable for novel fermented products. The present study explores the molecular regulation of probiotic-mediated juice fermentation and the enhancement of its nutritive properties. The functional annotation enabled the identification and segregation of metabolic pathways, highlighting genes associated with carbohydrate metabolism, stress response, and bioactive compound synthesis. Notably, genomic analysis revealed the presence of genes linked to bacteriocin production, suggesting potential antimicrobial activity. To validate the functional relevance of genomic predictions, fermentation studies were conducted using a plant-based matrix, specifically sea buckthorn juice. Comparative analysis of unfermented and fermented juice samples demonstrated significant biochemical and functional changes. Parameters such as total phenolic content, total flavonoid content, and antioxidant activity were evaluated, indicating enhanced bioactivity post-fermentation. These findings establish a correlation between genomic potential and phenotypic expression of functional traits.

Keywords: Probiotic, Non-dairy fermentation, Bacteriocin, Functional food

Thermoacoustic studies of Bifonazole and Tween 20 Interactions using hydroethanolic solvent systems

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Abstract

Bifonazole is a versatile azole antifungal drug that is effective for a wide range of fungi. It belongs to the class of imidazole derivatives which are the newer class of antifungal agents showing higher efficacy and safety. Thermoacoustic studies investigated for density (ρ), ultrasonic sound velocity (μ) in two binary mixtures of bifonazole and Tween 20 measurements to probe molecular interactions, micellization, and solubilization of drugs in surfactant micelles—critical for optimizing drug delivery formulations. The experiments were conducted using four distinct hydro-ethanolic concentrations, namely 20% v/v, 40% v/v, 60% v/v, 80% v/v, and 100% v/v, with a range of five temperatures (ranging 20°C, 25°C, 30°C, 35°C and 40 °C) with three different drug concentration (1mg, 5mg and 10mg). From the experimental density and speed of sound data, the apparent molar volume (ϕ_v) and apparent molar compressibility (ϕ_k). The acoustic studies highlighted the existence of hydrophobic and electrostatic interactions within the system. These investigations were significantly used for examining the magnitude of interactions within the system, which can be used for an optimal concentration of bifonazole and surfactant to prepare the formulations for topical delivery.

Keywords: Thermoacoustic studies, Apparent molar volume (ϕ_v), Ethanol, Bifonazole, Micelles.

Exploring the interaction and thermodynamic behaviour of Benzimidazole using Rhamnolipid as bio-surfactant in hydroethanolic system

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Abstract

Benzimidazole is a versatileazole antimicrobial drug that is effective for a wide range of microbes. Benzimidazole is a nitrogen containing heterocyclic compound composed of fused benzene and imidazole rings, known its Broad spectrum antimicrobial Application. The thermodynamic studies of the Benzimidazole was done by using Rhamnolipid as bio-surfactant. The experiments were done using four different hydroethanolic concentrations, as 30% v/v, 50% v/v, 70% v/v and 90% v/v with a range of four temperatures (ranging as 15°C, 25°C, 35°C and 45°C) with three different drug concentrations (1mg, 5mg and 10mg). This study shows the complete analysis of important physicochemical parameters, including density, surface tension, contact angle, and surface free energy, for the better understanding of the surface and interaction properties of the system. Optical Theta Lite Tensiometer has been used for calculating the surface tension, contact angle and surface free energy. These parameters were further used to evaluate other thermodynamic properties, such as the standard enthalpy change (ΔH°_m), standard entropy change (ΔS°_m), and standard Gibbs energy change (ΔG°_m) of micellization. The critical micelle concentration (CMC) was determined using surface tension measurements. These experiments were essential for studying the extent of interactions within the system and identifying the optimal concentrations of benzimidazole and biosurfactant required for the preparation of topical delivery formulations. The reduction in surface tension with increasing surfactant concentration indicated the micelle formation and provided insight into the self-assembly behaviour of the components. Also, the obtained CMC values helped in selecting a stable and efficient formulation with improved stability for enhanced topical application.

Keywords: Benzimidazole; Rhamnolipid; standard enthalpy change; contact angle; standard Gibbs energy change; critical micelle concentration.

Biotech Startups: Innovators Transforming Healthcare

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Abstract

Biotech startups are reshaping healthcare through breakthrough innovations in precision medicine, artificial intelligence (AI), gene therapy, and immunotherapy. Accelerated by the COVID-19 pandemic, these agile firms are moving beyond traditional “one-size-fits-all” treatments toward personalized and technology-driven healthcare solutions. One major trend is precision medicine, where genomic data helps tailor treatments to individual patients, improving outcomes and reducing side effects. AI-powered drug discovery is also transforming the industry by reducing the time and cost required to identify promising drug candidates. Similarly, advances in mRNA and gene therapy are enabling startups to address genetic disorders and develop next-generation therapies. Cell therapy and immuno-oncology further represent revolutionary approaches in treating cancers and chronic diseases. Despite their promise, biotech startups face significant challenges, including high research costs, lengthy development timelines, regulatory hurdles, and high failure rates in clinical trials. To overcome these barriers, many collaborate with large pharmaceutical firms, use AI to improve success rates, and rely on venture capital and strategic partnerships for funding. These startups also offer important leadership lessons in resilience, agility, innovation, and collaboration. Their adaptive approach demonstrates how organizations can thrive in uncertain and high-risk environments. In India, emerging biotech firms are contributing to affordable healthcare innovations and strengthening self-reliance in pharmaceuticals. Overall, biotech startups are not only revolutionizing healthcare delivery but also serving as models of strategic innovation and entrepreneurial leadership in a rapidly evolving global landscape.

Keywords: Biotech Innovation, Entrepreneurship, Precision Medicine, Artificial Intelligence, Health care, Strategic Agility.

Development And Characterization of Vitamin D₃ Nanoformulation for Enhanced Therapeutic Efficacy in Chronic Diseases

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Abstract

Vitamin D₃ plays a crucial role in maintaining calcium-phosphate balance, neuromuscular function, and immune regulation. Deficiency of vitamin D₃ has been increasingly linked to a range of chronic and degenerative diseases. The present study focuses on exploring the molecular association of vitamin D₃ deficiency with seven major diseases rickets, Parkinson's disease, Alzheimer's disease, breast cancer, asthma, systemic arterial hypertension, and inflammatory bowel syndrome (IBS) to identify common molecular targets. Gene datasets for each disease were retrieved from NCBI and key hub genes were identified through CytoHubba, and MCODE was employed to detect functional clusters. Functional enrichment analysis (GO and KEGG) revealed significant involvement of these genes in immune regulation, inflammatory response, oxidative stress, and calcium homeostasis. A nano emulsion was also prepared using vitamin D₃-sesame oil mixture was combined with Tween-80 and Span-80 surfactants in a specific mixture. The formulation was further characterized through FTIR, DLS and Zeta potential. Cytotoxicity of Nanoformulation, doxorubicin and a combination of doxorubicin and formulation was analyzed using MTT Assay. Although conventional supplementation strategies exist, the therapeutic efficacy of Vitamin D₃ remains limited due to its lipophilic nature, poor water solubility, instability under light and heat, and variable bioavailability. To address these limitations, nano-based formulations, particularly nano emulsions have emerged as an alternative, offering enhanced solubility, improved absorption, controlled release, and increased bioefficacy. Some of the key findings of this research work are multiple genes which are common in both the disease and VDR pathways, which establishes a molecular link between them. 12% s-mix and 4% oil based nano emulsion has the smallest size i.e., 86.7 nm. MTT assay was done to optimize the dose and cell viability of MCF-7 cell line, the combination of doxorubicin and Nanoformulation has better results than doxorubicin or nano formulation alone.

Keywords: Vitamin D₃, Nanoemulsion, Deficiency, Gene Analysis, Therapeutics.

A Simulation Framework for the Design and Optimization of Electrochemical Biosensors for Enhanced Sensitivity

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Abstract

Computational modeling before electrode fabrication provides an effective way to understand electrochemical behavior and support better design decisions. In this study, a two-dimensional electrochemical model was developed using COMSOL Multiphysics to study diffusion-controlled processes at the electrode–electrolyte interface. The model combines the Nernst–Planck equation with Butler–Volmer kinetics to represent mass transport and charge transfer within the system. A parametric analysis was carried out by varying scan rate, analyte concentration, and electrode geometry to examine their effect on the electrochemical response. The simulated cyclic voltammetry (CV) curves were used to determine key parameters such as peak current (I_p) and peak potential (E_p). The results indicate that the current response is strongly influenced by diffusion behavior and electrode dimensions, with higher scan rates resulting in increased peak currents. Overall, the model captures expected electrochemical trends and provides clear insight into the relationship between mass transport and reaction kinetics. These findings can help guide the electrode fabrication process in future work by enabling more informed design choices. In this way, simulation can reduce the need for extensive experimental trials and support the development of more efficient electrochemical systems.

Keywords: Electrochemical simulation, COMSOL Multiphysics, cyclic voltammetry, diffusion-controlled processes, electrode design optimization

***Madhuca longifolia* flower: A rich consortia of therapeutic and nutritional relevance and potential substrate for fermentation**

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Abstract

Research done in the last few years has revealed that *Madhuca longifolia* also known as (Mahua) is being used as a food item by the tribes living in Asia. In India, *M. longifolia* tribes of Jharkhand, Chhattisgarh, Bihar, West Bengal and Odisha use every part of the *M. Longifolia* plant. The *M. longifolia* flowers contain a large amount of sugar (glucose, fructose, sucrose) the amount of sugar (40-45%). A large amount of protein, fat, minerals and vitamins are also found in it. The aqueous and alcoholic extracts of the Mahua flower are utilized for their analgesic properties. It is also noted for its hepatoprotective effects. The juice extracted from the flowers is beneficial for treating skin ailments. Additionally, the flowers serve as a tonic, pain reliever, and diuretic. Roasted flowers are known to aid in alleviating coughs. Mahua is effective in helping with skin conditions. Our goal is to use in vitro, pharmacological, and in Laboratory research with lactic acid bacteria strain to determine the beneficial action of *M. longifolia* leaves and make a mahua *Longifolia* flower extraction based probiotic food. Some phytochemical tests have shown that the flowers of *M. longifolia* contain bioactive compounds like steroids, flavonoids, saponins and glycosides. These compounds can have both positive and negative effects on the human body, depending on their quantity and use. The current study aimed at evaluating the phytocompound consortia of the commercially available flower extract and determining the secondary metabolites of therapeutic importance using chromatographic and spectrophotometric analyses. Further the extracted juice was fermented using food grade bacteria and the growth kinetic parameters along with phytocompound consortia, after fermentation, were compared. The results showed the use of flower juice extract as a potential substrate for bacterial fermentation and changes in the phytocompound composition thereof. The results will highlight the changes in the phytocompound composition and associated bioactivities

Keywords: Probiotic, antioxidant, Total phenolic Content, Therapeutic.

Qualitative Analysis of Human Breath for Disease Detection

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Abstract

Medical advancements in the current era have set out new medical practices that eliminate the need for hospital-based medical diagnosis techniques while employing modified systems for medical decision-making based on data generated to improve medical practices. Medical sensor technology has been developed in terms of progressing analog techniques to nanotechnology-based complex systems for providing on-demand, perpetual observation of physiological and biochemical inputs. This analysis attempts to estimate the utilization of nanotechnology and artificial intelligence together, which has the potential to provide innovative medical sensors. The unique physicochemical properties offered by the high surface-to-volume ratios of nanomaterials, such as the presence of nanometals, nanometal oxides, carbon nanomaterials, and nanohybrids of polymeric nanomaterials, provide an exceptional sensing ability together with excellent biological compatibility. These nanomaterials are known to provide the detection of even trace amounts of biomarkers. This metabolic information is dealt with complex nano-sensing inputs, including inputs with varied dimensions, noise, and non-linear patterns, requiring smart analytical systems for efficient sensing analysis. These systems integrate artificial intelligence concepts, including machine learning, deep, and reinforcement learning for effective signal analysis, feature extraction, dimensionality, and intelligent adaptive analysis. The chapter offers the classification of diagnosis based on supervised, also known as conventional, deep learning approaches for the analysis of continuous sensor readings, as well as reinforcement learning for the calibration of sensors in a real-time, stable fashion. There are also details on the advancement in surface engineering, plasmonic sensing, quantum sensing, and nanofabrication, which are significant enablers for high-quality, label-free sensing. Precision medicine, ongoing surveillance, and self-management are made possible by the scalable platform provided by the combination of AI approaches with nanotechnology for medical devices and sensors.

Keywords: Artificial Intelligence, Biosensing, Digital Healthcare, Medical sensors, Nanotechnology.

Cloning, Recombinant Expression And Surface Display Of Linoleic Acid Isomerase For Enhanced Conjugated Linoleic Acid Production

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Abstract

Conjugated linoleic acid (CLA) is a bioactive fatty acid known for its significant health-promoting properties, including anti-carcinogenic, anti-obesity, and immunomodulatory effects. The present study aimed to screen high CLA-producing lactic acid bacteria (LAB), clone and express the linoleic acid isomerase (LAI) gene responsible for CLA production, and develop both recombinant *Escherichia coli* and surface-engineered *Lactiplantibacillus plantarum* systems for enhanced CLA biosynthesis. A total of 78 LAB isolates were screened for CLA production, and *Lactiplantibacillus plantarum* LP-6 and LP-8 were identified as promising candidates. Among all isolates, LP-6 produced the highest CLA (3.20 ppm) by GC analysis. The full-length LAI gene was amplified and cloned from LP-6. For heterologous expression, LAI was cloned into the SnapGene-designed pET-22b(+) vector and transformed into *Escherichia coli* BL21(DE3), where protein expression was optimized at 18°C and 37°C. Purification was performed using Ni-NTA affinity chromatography, followed by dialysis and enzymatic activity analysis. Parallely, for native surface expression, LAI was cloned into pSIP403 with a signal–MCS–anchor cassette and transformed into *Lb. plantarum* LP-6 using a protoplast-mediated method. Recombinant LAI expression in *E. coli* BL21(DE3) yielded soluble protein (~89 kDa), with significantly higher expression at 18°C. Purified enzyme showed activities of 4.87 U and 8.74 U, with specific activities of 829.8 U mg⁻¹ and 745.3 U mg⁻¹, respectively. In *Lb. plantarum*, successful GUS reporter activity confirmed functionality of the pSIP403 system, while SDS-PAGE demonstrated inducible LAI expression in selected transformants. This study successfully established both heterologous and native expression platforms for LAI production, providing a promising strategy for enhanced microbial CLA production and future development of functional probiotic systems.

Keywords: Conjugated linoleic acid (CLA), Linoleic acid isomerase (LAI), *Lactiplantibacillus plantarum*, Recombinant protein expression, Surface display.

Personalized Drug Recommendation via Stacking Ensemble and K- Means clustering

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Abstract

In today's digital world rapid advances in healthcare and the rise of the internet have enabled us to look online at various medicines available in the market for a particular disease. The internet helps us to make an informed decision when buying medicines and also look for alternatives. However, when looking online, patients often encounter irrelevant medicines or medicines which are not suited to their needs. The medicine may even contain side effects which we may not even know about. This project aims to propose a machine learning based drug recommender system that considers the patient's profiles when recommending a drug. Unlike traditional systems, our system accounts for factors that comes when deciding to recommend a medicine like age, gender, side effects, user review etc. In this way we ensure that the drug recommended is truly what the person requires while also accounting for side effects.

Keywords: Machine learning, recommender system, medicine, side effect, age, gender

Fractal-Enhanced Bidirectional Temporal Graph Networks for Multi-Disease Neurodegenerative Disorder Detection Using EEG

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Abstract

Neurological disorders collectively constitute the second-leading cause of death and primary cause of disability worldwide, with schizophrenia, Alzheimer's disease, frontotemporal dementia, and Parkinson's disease representing four highly prevalent yet diagnostically overlapping conditions whose simultaneous automated classification from a single framework remains largely unexplored. This study presents a bidirectional temporal graph convolutional network-transformer framework for unified multi-disease neurological disorder classification from resting-state EEG signals. A comprehensive 14-feature set per channel was extracted across 19-channel recordings, comprising three time-domain statistics; four fractal dimension measures, including Higuchi, Petrosian, Katz FD, and detrended fluctuation analysis; and seven frequency-domain features, including spectral entropy and band powers across delta, theta, alpha, beta, and gamma bands, capturing nonlinear cortical complexity alterations pathologically divergent across all four target conditions. The bidirectional architecture processes forward and backward temporal streams using GCN-Transformer fusion layers, with graph-constrained multi-head attention on dynamic temporal adjacency matrices and sinusoidal positional encodings that capture inter-epoch dependencies across a 13-epoch sliding context window. Six datasets spanning all four neurological conditions were standardized to a unified 19-channel, 250 Hz pipeline, enabling cross-condition comparability within a single instrumentation framework. The system achieves $98.16 \pm 0.21\%$ five-class accuracy under 10-fold cross-validation, with disease-specific evaluations yielding 99.54% on schizophrenia, 98.34% on AD/FTD, and 99.56% on Parkinson's disease, outperforming all state-of-the-art benchmarks simultaneously. With only 800k parameters, the proposed framework is 28 times more parameter-efficient than NeuroFormer (23M parameters), achieving 1.24% higher accuracy while enabling practical deployment in resource-constrained clinical settings.

Keywords: EEG, Bidirectional GCN-Transformer, Neurological disorders, Fractal dimension

Heteroplasmic Variation and Gene-Level Functional Heterogeneity in Mitochondrial Genome of Indigenous Cattle

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Abstract

Mitochondrial genetic variation performs a crucial role in understanding of maternal lineage diversity and evolutionary dynamics in livestock populations. In this study, 46 cattle animals from six distinct geographical locations of India were considered to investigate heteroplasmic variation. A total of 221 variable sites were identified, of which 206 (93.21%) were restricted to individual samples, while only 15 sites were shared across populations, indicating a strong predominance of lineage-specific variation. The mean number of samples per variable site was low (1.10), further supporting the highly individualized distribution of variants. Allele frequency analysis revealed a mean heteroplasmy level of 0.1026 ± 0.14 , with a median of 0.0808 and a range spanning 0.0293 to 0.6, reflecting generally low-to-moderate heteroplasmic abundance across sites. Functional annotation reflects 108 non-synonymous and 34 synonymous substitutions, yielding a non-synonymous to synonymous ratio of 0.76, consistent with the influence of purifying selection acting on mitochondrial protein-coding genes. Comparative gene-level analyses with Kruskal–Wallis test reveals variation in heteroplasmy distribution across mitochondrial genes, indicating a statistically significant overall difference among genes ($\chi^2 = 45.06$, $df = 23$, $p = 0.0039$). While pairwise Wilcoxon tests with Benjamini–Hochberg correction did not reveal robust significant differences between most gene pairs indicating a lack of gene-wise heterogeneity in heteroplasmy distribution. Overall, the results demonstrate that mitochondrial heteroplasmy in these cattle populations is largely structured at the individual level with minimal evidence of strong breed- or gene-specific partitioning. The predominance of individual variants and the low frequency heteroplasmy supports a model of high within-population diversity and weak breed-specific mitochondrial structuring.

Keywords: Mitochondrial Heteroplasmy, Allele Frequency, Purifying Selection, Maternal Lineage

A Hierarchical Transfer Learning Framework for Subject-Independent Infant Cry Classification

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Abstract

Infant crying is the main way babies communicate their physical and emotional needs. However, interpreting these cries manually is often subjective. This inconsistent interpretation can have severe consequence if the cry is due to underlying pain or trauma. This study aims to address these limitations by developing a hierarchical classification framework for automated cry analysis that does not depend on the person interpreting it. The research uses a compiled dataset of 9,961 audio samples from four public datasets, including Donate-a-Cry and CryCeleb. The methodology employs transfer learning via YAMNet, a convolutional neural network pretrained on AudioSet, to extract 1024-dimensional acoustic embeddings. The proposed architecture operates in two stages. In the first stage, a binary classifier distinguishes between cries and non-cries. Next, it uses a multiclass classifier to sort cries into categories: hunger, discomfort, pain, tiredness, or burping. To ensure robust generalization and prevent identity leakage, the model was evaluated using subject-independent splits and cross-dataset validation. The results show that the hierarchical system significantly outperforms baseline models like Random Forest and CRNN, achieving 78% accuracy in subject-independent tests. The Stage 2 subtype classifier achieved 95% validation accuracy, demonstrating how well the transfer-learned embeddings capture important prosodic and spectral features. Furthermore, the study uses SHAP (Shapley Additive exPlanations) analysis to provide local interpretations, transforming the "black box" nature of deep learning into a transparent system suitable for clinical use. The feasibility of the system was demonstrated through a real-time Streamlit interface. This work lays a foundation for AI-assisted neonatal monitoring and highlights the potential for deploying explainable, high-performance models in pediatric healthcare.

Keywords: infant cry classification, transfer learning, YAMNet, subject-independent evaluation, explainable AI

Structural and morphological features of the liver in the development of metabolically associated steatotic liver disease under conditions of experimentally induced obesity

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Abstract

Metabolically associated steatotic liver disease (MASLD) represents a spectrum of liver pathology driven by obesity and metabolic dysregulation. The present study aimed to evaluate the structural and morphological liver changes during MASLD development under experimentally induced obesity. A prospective controlled experiment was conducted on 24 sexually mature outbred male white rats randomized into experimental (n=12) and control (n=12) groups. The experimental group received a hypercaloric high-fat diet (60% fat, 1% cholesterol) for 12 weeks, while controls were maintained on a standard diet. Body weight was monitored weekly. Liver tissue was collected at 4, 8, and 12 weeks for histological analysis using hematoxylin and eosin. Steatosis (grade 0–3), inflammatory activity (0–3), ballooning degeneration, and fibrosis stage (METAVIR) were assessed by two blinded morphologists. Serum ALT, AST, total cholesterol, triglycerides, and glucose levels were measured. By week 12, experimental animals demonstrated significant weight gain compared to controls ($p < 0.01$), hepatomegaly, and macroscopic features of fatty infiltration. Histologically, early microvesicular steatosis at week 4 progressed to predominant macrovesicular steatosis with lobular inflammation and ballooning degeneration by week 12. Steatosis grade was significantly higher in the experimental group (2.4 ± 0.5 vs 0.3 ± 0.2 , $p < 0.001$), accompanied by early perisinusoidal fibrosis (METAVIR F1–F2). Biochemical analysis revealed elevated transaminases, dyslipidemia, and hyperglycemia, correlating with morphological severity. The findings confirm that prolonged high-fat, cholesterol-enriched feeding induces progressive metabolic and structural liver remodeling consistent with MASLD, providing a translationally relevant experimental model for pathogenetic and therapeutic research.

Keywords: Experimentally induced obesity, High-Fat Diet, Steatosis, Steatohepatitis, Macrovesicular Steatosis.

Plant-derived Antimicrobial Peptides from *Ocimum sanctum* against *Streptococcus pneumoniae* and its role in treating infections

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Abstract

Respiratory tract infections caused by multidrug-resistant bacteria represent a major global health concern, creating an urgent need for alternative antimicrobial agents. The present study evaluated the antimicrobial potential of methanolic leaf extracts of *Mentha piperita* and *Ocimum sanctum* against selected respiratory pathogenic bacteria through in vitro analysis. Plant leaves were collected, shade dried, extracted using methanol, and subjected to phytochemical screening, GC-MS, FTIR, antimicrobial assays, FESEM analysis, and cytotoxicity evaluation. Phytochemical analysis confirmed the presence of alkaloids, flavonoids, tannins, saponins, and terpenoids in both extracts. GC-MS profiling revealed major antimicrobial constituents including eugenol in *O. sanctum* and isopulegol/terpenoid compounds in *M. piperita*. Antibacterial activity was assessed against *Escherichia coli*, *Pseudomonas aeruginosa*, *Burkholderia cepacia*, *Staphylococcus aureus*, *Stenotrophomonas maltophilia*, and *Streptococcus pneumoniae* using agar well diffusion, minimum inhibitory concentration (MIC), and minimum bactericidal concentration (MBC) assays. At 30 mg/mL concentration, *O. sanctum* exhibited the highest antibacterial activity against *E. coli* and *S. aureus* with inhibition zones of 27.67 mm, while *M. piperita* demonstrated strong activity against *S. aureus* (27 mm) and *S. pneumoniae* (26 mm). MIC values ranged from 31.2–250 µg/mL for plant extracts, indicating broad-spectrum antibacterial efficacy. FESEM analysis demonstrated severe structural damage, membrane disruption, and deformation of *S. pneumoniae* cells after treatment with plant extracts, suggesting bacteriolytic mechanisms of action. Cytotoxicity assessment using human red blood cells showed acceptable safety profiles at lower concentrations, with toxic effects observed only at comparatively higher doses. The findings conclude that both *O. sanctum* and *M. piperita* possess significant antimicrobial activity against respiratory pathogens, including antibiotic-resistant strains, and may serve as promising natural alternatives for the development of plant-based antimicrobial therapeutics.

Keywords: Antimicrobial peptides, MBC, Respiratory pathogens, *Ocimum sanctum*.

Manikaran Hot Spring Isolates as Novel Sources of Thermostable L-Asparaginase for Cancer Treatment

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Abstract

L-asparaginase (LA) is an important chemotherapeutic enzyme used in the treatment of acute lymphoblastic leukemia (ALL), functioning by hydrolyzing L-asparagine into L-aspartic acid and ammonia, thereby depriving leukemic cells of a critical nutrient. However, currently available formulations from *Escherichia coli* and *Erwinia chrysanthemi* suffer from limitations such as poor thermal stability, short half-life, and immunogenic side effects, necessitating the exploration of more robust alternatives. In this study, thermophilic bacterial isolates obtained from hot spring samples of Manikaran, Himachal Pradesh, were screened for LA production. Among ten isolates, RWS-I exhibited the highest enzyme activity (16.52 U/mL), followed by SWS-II (14 U/mL), RSS-II (6.82 U/mL), and SSS-I (4.69 U/mL). Thermal stability of the crude enzyme was evaluated by incubating the culture supernatant at 37°C and 60°C for time intervals ranging from 0 to 60 minutes, followed by activity determination using the Nesslerization method. The enzyme from RWS-I, RSS-II, and SWS-II retained significant activity up to 60 minutes at both temperatures, whereas SSS-I showed rapid loss of activity beyond 20 minutes. The observed stability profiles of RWS-I, RSS-II and SWS-II suggest that thermophilic LA maintains structural integrity under elevated temperatures, which can be attributed to its conserved quaternary and tertiary architecture. These findings highlight the superior thermostability and activity of selected isolates, making them as potential candidates for further purification, biochemical characterization, and evaluation of anticancer potential in cell-line studies.

Keywords: L-asparaginase, thermophilic bacteria, acute lymphoblastic leukemia, enzyme stability, anticancer ther

Safety studies on the engineered endolysin with enhanced bactericidal activity against *Escherichia coli*

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Abstract

The rapid emergence of multidrug-resistant (MDR) *Escherichia coli* poses a severe global health threat, complicating the treatment of highly infectious diseases. Therefore, there is an urgent need to discover new class of antimicrobials with lower incidences of resistance development. Endolysins are bacteriophage-derived enzymes that degrade the peptidoglycan (PG) layer of the bacterial cell wall without causing any significant dysbiosis of the local microbiota population. In this study, we aimed to engineer and optimize endolysin capable of eradicating clinically significant MDR *E. coli*. We conducted a comparative study utilizing endolysins (E1 and E2) fused with antimicrobial peptides (AMP1 and AMP2). To maximize conformational stability and catalytic efficiency, we systematically varied the linker size connecting the AMP to the endolysin domain. The engineered endolysin demonstrated potent antibacterial activity, achieving a complete reduction in bacterial viability of $\sim 7-8 \log_{10}$ in ATCC25922 *E. coli* strain at a concentration of $\sim 60 \mu\text{g/ml}$ and $55 \mu\text{g/ml}$ (pH 7.4), respectively. To establish relevance of these endolysins in the environment where these may be applied, we tested their efficacy in the biological fluids, i.e., milk and serum. The bactericidal activity ($\sim 7-8 \log_{10}$ reduction) was fully preserved when tested in the presence of milk, however, serum in itself showed complete killing of the pathogens. Our constructs exhibited less than 1% hemolysis, indicating negligible toxicity against red blood cells. The strategic fusion of AMPs to endolysins via optimized linkers could successfully bypass the Gram-negative outer membrane barrier and could provide a new strategy to counter Gram-negative MDR pathogens as alternative treatment for severe MDR *E. coli* infections.

Keywords: MDR, *E. coli*, Endolysin, Antibacterial activity

Design, Expression, and Functional Assessment of Mini-Mub Proteins from *Lactobacillus reuteri*

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Abstract

Bacterial mucus binding proteins (Mub) mediate adherence to the intestinal mucosa but are challenging to study due to their extraordinary large size. Mub *Limolactobacillus reuteri* is constituted of 4200 residues (353 kDa). This study aimed to design, clone, and express the truncated domains of *L. reuteri* Mub protein to understand structural and functional competency.

Three Mub-domains (D1, D2, D3) were expressed in *E. coli*. DSC confirmed that all domains maintained structural integrity across the pH range, including that prevalent in gastric conditions. Mub unfolding exhibited reversible denaturation across the pH range. The D3 domain comprising of D1 and D2 showed the highest thermal stability suggesting interdomain interaction. Single X-ray structures determined at 1.9Å showed a linear alignment of D1 and D2 domains, which suggested that the extended conformation might provide extensive interaction for binding with the host's enteric cells.

Functional assays demonstrated robust binding of D3 to HT-29 enteric epithelial cells, fibroblasts, and mouse intestinal mucus. The D3 exhibited potent exclusion of *Salmonella typhimurium* binding to HT-29 cell line by ~85%.

Our results showed that the truncated Mub domains maintain structural stability and functional mucus-binding/pathogen-exclusion properties and could serve as the lead molecule for developing an antimicrobial agent. These findings establish a promising foundation for developing D3 as a novel protein-based nutraceutical or prophylactic agent to competitively inhibit enteric pathogens and enhance gastrointestinal health.

Keywords: Mub-Mucus binding protein, DSC-Differential Scanning Calorimetry, kDa-kiloDalton

An electrochemical microRNA biosensor integrated with machine learning for early detection of non-small-cell lung cancer

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Abstract

Lung cancer remains the leading cause of cancer-related mortality worldwide, with non-small-cell lung cancer (NSCLC) accounting for the majority of cases and most often detected at advanced stages where curative options are limited. Circulating microRNAs (miRNAs) are stable and minimally invasive biomarkers, yet single-miRNA assays lack the specificity needed for reliable early screening. This study reports a label-free electrochemical biosensor coupled with a machine learning classifier for simultaneous quantification of an NSCLC-associated miRNA panel (miR-21, miR-155, miR-210 and miR-486-5p) in serum. Screen-printed gold electrodes were functionalised with thiolated locked-nucleic-acid capture probes, and target hybridisation was transduced using differential pulse voltammetry and electrochemical impedance spectroscopy. The platform achieved a femtomolar limit of detection across a wide linear dynamic range with strong selectivity against single-base mismatches. Voltammetric features extracted across the panel were used to train and benchmark several supervised models, and a stacking ensemble was optimised through stratified cross-validation, with SHAP analysis quantifying the diagnostic contribution of each miRNA. The integrated panel-plus-ML approach separated early-stage NSCLC from healthy and benign controls with substantially higher accuracy, sensitivity and area under the curve than any single biomarker, while retaining performance in spiked clinical samples. The compact, low-cost and CMOS-compatible architecture supports translation into a point-of-care diagnostic device. These findings demonstrate that combining multiplexed electrochemical biosensing with interpretable machine learning offers a practical route to rapid, affordable and reliable early lung cancer detection, with direct relevance to population-scale screening in resource-limited settings.

Keywords: Lung cancer; microRNA biosensor; electrochemical detection; machine learning; point-of-care diagnostics

Healthcare Biotechnology

Poster Presentation

Developing Novel Strategies Against Biofilm-Forming Proteins in Multi-Drug-Resistant Diarrheal *E. Coli* Strains

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Abstract

Diarrhea is a condition marked by passage of watery stools more than thrice a day and it is the 3rd leading cause of death among children and it is persistent even now in India. Multidrug-resistant (MDR) diarrheagenic *Escherichia coli* (DEC) strains are considered a significant worldwide health concern as the conventional method of treatment using antibiotics became difficult to treat due to the capabilities of the pathogen to get resistant to all the three generations of the antibiotic regime. Formation of the biofilms is one of the strategies deployed by the pathogen that shield them from host defenses and antimicrobial drugs. Biofilm associated proteins like curli regulators (CsgD), autotransporter adhesins (AIDA-I, TibA), Intimin (eae), and flagellar structures (FliC) play important role in the formation of Biofilm. A potential approach for preventing biofilm formation and efficiently maintaining treatment responsiveness is to target these proteins using aptamers-based strategy. Aptamers, are one of the classes of short, single stranded nucleic acids that can fold into different 3D structures and binds to the targeted protein with high specificity thereby serve as best substitute to the antibiotics. The rationale of this study is to design and select aptamers and evaluation of selected aptamers against key biofilm-forming proteins in MDR diarrheal *E. coli*. Systemic Evolution of Ligand by Exponential Enrichment (SELEX) will be used to synthesize high throughput Aptamers which binds to Biofilm Associated Proteins. Real time PCR and fluorescence microscopy were used to assess binding specificity and affinity of aptamers. The efficiency of particular aptamers to impede initial adhesion, inhibit or eradicate biofilm will be analyzed using quantification assays like crystal violet assay and using advanced microscopic assays (AFM, SEM, CLSM). The outcome of this study will pave a pathway for the future potential of aptamer-based treatments as an alternate, non-antibiotic approach to treat infections linked to biofilms formation and preventing antimicrobial resistance in diarrheal *E. coli*.

Keywords: SELEX- Systematic Evolution of Ligands by Exponential Enrichment, MDR- Multi Drug Resistant, DEC- Diarrheal *E. coli*

Dual Targeting Strategy Against Conserved Proteins to Combat Antimicrobial Resistance in *Klebsiella pneumoniae*

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Abstract

The growing global concern over Multiple Drug Resistance (MDR) *Klebsiella pneumoniae* has prompted extensive research aimed at identifying novel molecular targets. In this context, our integrated approach—combining whole-genome comparative analysis, Shannon entropy-based variability assessment, and structure-based high-throughput screening (HTS)—enabled the identification of two promising molecular targets: L-asparaginase (L-asp) and the Cell Division Activator (CedA) protein. Both proteins are found evolutionarily conserved across diverse pathogens and also in drug-resistant and susceptible isolates of *K. pneumoniae*. Our findings emphasize the indispensable roles of both proteins in bacterial growth and survival, thereby underscoring their significance as promising therapeutic targets. Besides, screening of the natural product, Traditional Chinese Medicine (TCM), and FDA-approved drug libraries yielded 3 potential binders to L- Asp of *Klebsiella* with binding energies ranging from ~11.5- 12.0 kcal/mol. While extensive, in vitro and ex vivo testing is in progress, our findings so far highlight L-asparaginase and CedA as novel, conserved molecular targets for mitigating *K. pneumoniae* infection.

Keywords: Antimicrobial Resistance, Drug discovery, Therapeutics

Role of Nucleic Acid Binding in Modulating Optineurin Aggregation

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Abstract

Optineurin (OPTN), a multifunctional and ubiquitously expressed cytoplasmic protein, contains two nucleic acid-binding domains - a Leucine zipper domain and a Zinc finger motif. OPTN's association with Amyotrophic Lateral Sclerosis is well established by its accumulation in pathological aggregates. These aggregates may stem from its intrinsically disordered regions, driving a protein's aggregation by initiating liquid-liquid phase separation (LLPS). Although OPTN's LLPS has been studied *in vivo*, the underlying mechanism and the factors driving this behaviour remain unclear. We have expressed and purified OPTN from a heterologous organism (*E. coli*), followed by establishing OPTN's chaperone-like activity, consistent with the heat shock elements present in its promoter. We also demonstrated that OPTN displays strong nucleic acid-binding capability, likely mediated by its nucleic acid-binding domains. Based on evidence of OPTN's chaperone-like activity, LLPS *in vivo*, and affinity for nucleic acids, we hypothesize that OPTN-nucleic acid interactions significantly contribute to both its chaperoning function and phase-separation behaviour—two key factors that may influence OPTN's aggregation propensity. We also plan to examine the chaperoning activity and nucleic acid affinity of disease mutants of OPTN. Overall, this study aims to illuminate the mechanisms underlying OPTN aggregation and its relevance to disease onset.

Keywords: Optineurin, Aggregation, Liquid-liquid phase separation, Nucleic acid binding domains, Chaperone.

Bioactive Pure Molecules as Modulators of Pancreatic β -Cell Function and Oxidative Stress in Diabetes

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Abstract

Diabetes mellitus is characterized by impaired insulin secretion and β -cell dysfunction, primarily driven by chronic hyperglycemia and oxidative stress. The present study explores the therapeutic potential of selected bioactive pure molecules in improving pancreatic β -cell function and mitigating glucotoxicity-induced cellular damage. *In vitro* cytotoxicity was evaluated using the MTT assay, confirming the dose-dependent safety of the molecules in pancreatic cell MIN-6. Functional efficacy of the selected bioactive molecules was assessed through glucose uptake assay, which demonstrated enhanced cellular glucose uptake and utilization following treatment. To mimic diabetic conditions, oxidative stress was induced using high-glucose exposure, leading to elevated intracellular reactive oxygen species (ROS). Subsequent treatment with the selected bioactive molecules resulted in a significant reduction in ROS levels, indicating their antioxidant potential. Furthermore, glucose-stimulated insulin secretion (GSIS) assays revealed improved insulin release upon glucose challenge, suggesting enhanced β -cell responsiveness and functional recovery. To complement *in vitro* findings, *in vivo* safety profiling was conducted in Wistar rats through acute and subacute toxicity studies. The results indicated no significant adverse effects on physiological or biochemical parameters, supporting the safety of the molecules. Overall, this study demonstrates that these bioactive pure molecules effectively improve β -cell function, enhance glucose handling, and reduce oxidative stress under diabetic conditions. These findings support their potential as promising candidates for diabetes management through modulation of pancreatic cell function and redox balance.

Keywords: Diabetes mellitus, β -cell function, Oxidative stress, Glucose uptake, Pure molecules, Pancreatic modulation.

Multi-Mechanistic Anticancer Evaluation of *Ammania baccifera* Using In Vitro Models and In Vivo Toxicity Assessment

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Abstract

Natural products remain a pivotal resource in oncology due to their multi-targeted efficacy and favourable safety profiles. This study presents a comprehensive preclinical evaluation of *Ammania baccifera*, integrating advanced phytochemical profiling with rigorous *in vitro* and *in vivo* assessments. Quantitative analysis through TPC and TFC, and FTIR fingerprinting, revealed a robust reservoir of bioactive phenolics and flavonoids. The anticancer efficacy was evaluated across a spectrum of breast cancer cell lines (MCF-7, MDA-MB-231, and T47D), using HEK cells to establish a favourable selectivity index. MTT assays demonstrated dose-dependent cytotoxicity, while functional assays, including colony formation, wound healing, and 3D spheroid models, confirmed significant inhibition of proliferation and metastatic potential. Mechanistic investigations revealed that *A. baccifera* triggers the intrinsic apoptotic pathway, characterized by increased intracellular reactive oxygen species (ROS) generation, disruption of mitochondrial membrane potential (MMP), and nuclear fragmentation. Crucially, *in vivo* toxicological screening revealed no significant adverse effects on physiological or behavioural parameters, suggesting a broad therapeutic window. Collectively, these findings elucidate the molecular basis of *A. baccifera*'s selective anticancer activity, positioning it as a promising candidate for the development of standardized plant-based therapeutics against breast carcinoma.

Keywords: *Ammania baccifera*, Phytochemical profiling, Anticancer activity, Apoptosis, *In vivo* Toxicity

Host-Directed Enhancement of Macrophage-Mediated Intracellular Bacterial Clearance by Thymol

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Abstract

The rise of antimicrobial resistance necessitates alternative strategies that enhance host immune responses against intracellular pathogens. This study evaluates the potential of thymol, a natural bioactive compound, in modulating macrophage-mediated bacterial clearance at low concentrations. We hypothesize that thymol enhances intracellular bacterial elimination primarily through host-directed mechanisms rather than direct antibacterial activity. Antibacterial activity was initially assessed using agar well diffusion and time-kill assays, demonstrating dose-dependent inhibitory effects at higher concentrations. However, at a lower concentration, thymol did not exhibit direct bactericidal activity. Biofilm assays revealed reduction in biofilm formation upon thymol treatment at higher concentration. To investigate intracellular survival, macrophages were infected and subjected to a gentamicin protection assay, followed by colony-forming unit (CFU) enumeration. Thymol treatment resulted in a marked decrease in intracellular bacterial load compared to untreated controls. To explore host responses, reactive oxygen species (ROS) and nitric oxide (NO) production were quantified. Thymol-treated macrophages showed enhanced ROS generation, while nitric oxide levels remained comparable to control, indicating selective modulation of antimicrobial pathways without excessive inflammatory activation. Cell viability assays confirmed that the concentration of thymol used was non-cytotoxic to host cells. In conclusion, thymol at low concentration enhances macrophage-mediated intracellular bacterial clearance through host-directed modulation of antimicrobial responses, independent of direct bactericidal activity. These findings suggest its potential as an adjunct therapeutic candidate targeting host-pathogen interactions. Further studies are required to elucidate the underlying molecular mechanisms.

Keywords: Thymol, Macrophages, Intracellular bacteria, Immunomodulation, ROS

Identification and Prioritization of Conserved Essential Drug Targets across the *Mycobacterium tuberculosis* Complex: A Machine Learning Approach

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Abstract

Mycobacterium tuberculosis complex (MTBC), including organisms like *Mycobacterium tuberculosis*, *Mycobacterium bovis*, *Mycobacterium canetti*, *Mycobacterium microti* etc are a serious global disease-causing health threat, attributed in part to high genomic conservation and drug resistance. Here, conserved biomarkers and prioritized high-confidence drug targets across the MTBC were identified using a machine learning driven approach. An encoded dataset of 42,134 proteins isolated from 7 MTBC species were evaluated using engineered sequence-based biophysical properties such as hydrophobicity (GRAVY), isoelectric point (pI), molecular weight, and instability indices. We implemented a supervised learning approach that compared Random Forest (RF) and support vector machine (SVM), with validation based on 5-fold cross-validation. The RF-based model showed the best discriminative performance at 100% accuracy (vs. 98.69% for the SVM) and showed that both GRAVY and molecular weight are the most important biomarkers that can support target prioritization. This study identified 3,944 high-confidence drug targets with a confidence score of 1.0 and were able to identify key conserved proteins, such as those from siderophore biosynthesis (mbtI) or enoyl-ACP reductase (InhA). Feature correlation heatmaps validated the independence of proteomic descriptors and achieved a strong classification boundary. This scalable computational pipeline offers a structured and comprehensive pipeline for tuberculosis treatment and precision medicine by detecting fundamental biological pathways, primarily cell wall biology and metabolic control that are conserved throughout the rest of the MTBC. These findings highlight the potential of combining machine learning and proteomic feature engineering to expedite the identification and targeted finding of translational targets for tuberculosis diagnosis and therapy.

Keywords: *Mycobacterium tuberculosis* complex (MTBC), Genomic Biomarkers, Machine Learning Classification, Drug Target Discovery

Comparative Analysis of Stress Study in Wild Type *Mycobacterium fortuitum* and Transposon-mediated Mutants

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Abstract

Mycobacterium fortuitum is a proliferative, pathogenic, mycobacteria other than tuberculosis (MOTT) that can infect human bones and joints as well as the skin. It is a non-motile, rod-shaped, gram-positive bacterium that is mostly found in soil and water. The bacterium is resilient to different environments, and can survive in a variety of adverse conditions. *M. fortuitum* possess a complex cell wall structure enriched with mycolic acids which are key to its physiology and pathogenicity. The present study was designed for comparative analysis of stress conditions between wild type *M. fortuitum* and mutant strains generated by transposon mutagenesis. Transposon mutants were generated by electroporation of vector pRT291 into wild type strain of *M. fortuitum*. The transposon facilitates random insertion of gene sequence throughout the bacterial genome creating a mutant, enabling identification of essential gene for the molecular characterization. The mutant generated was screened alongside the wild type *M. fortuitum* under multiple stress condition namely, Oxidative stress and Nitrosative stress. Mutants exhibiting reduced growth would indicate that the mutated gene is responsible for stress survival. The comparative screening and survival studies followed by molecular analysis would lead to identification of specific genetic elements responsible for the survival of the bacterium under constraints conditions in environment as well as the within the host. This study would help to gain insight about the molecular mechanism underlying stress adaptation, and may also contribute to the understanding the physiological conditions of *M. fortuitum* under adverse conditions, which underlying expectation of identification of potential therapeutic targets for devising better treatment strategies against *M. fortuitum* and related pathogens.

Keywords: *Mycobacterium fortuitum*, stress study, pRT291, Transposon mutagenesis, Oxidative stress, Nitrosative stress.

Anti-Biofilm Activity of ZnO Nanoparticles Against *Mycobacterium smegmatis*: A Concentration-Dependent Study

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Abstract

Nontuberculous mycobacteria (NTM) are bacteria can still cause serious infections, especially in population with immuno-compromised condition and pre-existing lung diseases. NTM infections are difficult to treat as these bacteria have the ability to form biofilms, a protective layer that helps the bacteria to survive on surfaces and inside the human body. Antibiotics often fail to penetrate the robust biofilms formed by these bacteria making them resistant to antibiotics and contributing to Antimicrobial- resistance (AMR). In this study, we used *Mycobacterium smegmatis* which is a fast-growing, non-pathogenic mycobacterium; often used as a model organism to study mycobacterial biofilms. Zinc oxide nanoparticles (ZnO NPs) were chemically synthesised using Zinc Chloride and NaOH in the laboratory and characterized for their physicochemical properties. To evaluate their anti-biofilm potential, biofilm formation was assessed using a 96-well microplate assay, where cultures were treated with a series of ZnO NP concentrations starting from 128 µg/mL with two-fold, alongside positive control (Ciprofloxacin) and negative control (DMSO). Our results demonstrated that ZnO NPs significantly inhibited biofilm formation in *M. smegmatis* in a concentration-dependent manner, with higher concentrations showing greater inhibition, offering a promising non-bactericidal strategy to combat NTM infections. These findings suggest that ZnO NPs could serve as potent anti-biofilm agents that disrupt protective bacterial layers without promoting antimicrobial resistance, potentially enhancing the efficacy of existing clinical treatments.

Keywords: NTM, *Mycobacterium smegmatis*, Biofilm formation, Zinc nanoparticles, Anti-biofilm strategies

Psychobiotics and the Microbiota-Gut-Brain Axis: Emerging Microbial Strategies for Mental Health Modulation

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Abstract

The rising rates of stress, anxiety and depression with other neuropsychiatric disorders have increased the need to find safer and more effective therapeutic approaches. Psychobiotics function as a special type of probiotics which can control the microbiota-gut-brain connection to treat mental health disorders. The beneficial microorganisms establish two-way communication between the gut and central nervous system through their control of neural pathways and endocrine pathways and immune pathways and metabolic pathways. Recent studies demonstrate that psychobiotics can regulate neurotransmitter production, including gamma aminobutyric acid (GABA), serotonin, dopamine, and short-chain fatty acids, thereby influencing emotional and cognitive functions. The research on microbiomes has progressed to demonstrate how psychobiotics reduce neuroinflammation, restore gut microbial balance, strengthen intestinal barrier function and regulate hypothalamic pituitary adrenal (HPA) axis activity. Targeted psychobiotic supplementation according to clinical and preclinical evidence helps people reduce their stress response while they also experience better sleep and stronger emotional resilience and decreased depressive and anxiety symptoms. The development of omics technologies together with metabolite profiling methods is enabling researchers to investigate how gut-brain signalling pathways operate at the molecular level and how microbes generate neuroactive metabolites. Despite the current research shows potential through its progress but it still encounters obstacles which include specific strain efficiency testing and microbiome differences between people and the need to establish standardized treatment dosages and prove clinical results over extended periods. Future research should focus on personalized psychobiotic formulations and integrated multi-omics analysis and microbiome-based functional food development for mental healthcare. The combination of microbial biotechnology with neuroscience and nutritional science together establishes psychobiotics as a modern approach to maintain mental health and provide therapeutic solutions.

Keywords: Psychobiotics, Microbiota-gut-brain axis, Neurotransmitters, Depression, Gut microbiota, Neuroinflammation, Functional foods

Development of An Oral Vaccine Platform Using Nanovesicles

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Abstract

Newcastle disease virus (NDV) continues to pose a significant challenge to the health of poultry. The primary challenges in poultry disease management include inadequate diagnostic capabilities and unavailability of effective vaccine delivery platforms. While vaccination remains a cornerstone of disease prevention in the poultry industry, traditional injection-based vaccines face significant limitations. So, there is a requirement for an efficient vaccine delivery platform. Oral vaccine delivery platforms offer an alternative to conventional methods, eliciting mucosal immunity crucial for protection against respiratory and enteric pathogens. Here we present the development of an oral vaccine delivery platform in the form of nanovesicles based on outer membrane vesicles (OMVs) as delivery vehicles. Recombinant constructs (pBAD, pBAD-GFP, and pBAD-HN) were designed to express green fluorescent protein (GFP) and hemagglutinin-neuraminidase (HN) protein of NDV. OMVs were successfully purified from bacterial cultures that possessed these constructs using the differential centrifugation method. Further, the physical characterization of purified OMVs was carried out by TEM, DLS, and NTA, demonstrating the morphology and size (<200 nm). We have also determined the presence of HN protein in the purified OMVs by western blotting. GFP-tagging was used as a model system to confirm the expression, incorporation, and efficiency of the delivery of proteins. Mice were orally immunized with OMVs to determine their uptake and biodistribution. Our findings suggest effective uptake and biodistribution of OMVs to distant organs as well as mucosal immune cells, which supported the viability of this delivery system. Our work provides a proof-of-concept of OMVs-based oral vaccine delivery systems and demonstrates their potential in delivering NDV antigens like HN. The ability of the platform to significantly uptake OMVs is further validated by the fact that GFP was used as a reporter. Overall, this strategy provides a foundation for effective needle-free vaccination approaches.

Keywords: Outer membrane vesicles (OMVs), Oral vaccine, GFP tagging, Newcastle disease virus

Exploring the Antiviral Potential of *Catharanthus roseus* Against SARS-CoV-2

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Abstract

Coronavirus Disease 2019 (COVID-19), caused by SARS-CoV-2, continues to pose a major global health challenge due to the emergence of new viral variants and limitations in existing therapeutic options. Therefore, the identification of effective antiviral agents targeting essential viral proteins remains a priority. In this context, medicinal plants rich in bioactive phytoconstituents have gained considerable attention as potential sources of antiviral compounds owing to their structural diversity and broad pharmacological properties. In the present study, a comprehensive in silico approach was employed to investigate the antiviral potential of phytochemicals derived from *Catharanthus roseus* (Sadabahar) against the SARS-CoV-2 papain-like protease (PLpro), a key viral enzyme involved in viral replication and host immune modulation. Molecular docking studies were performed to evaluate the binding affinity and interaction profiles of selected phytocompounds at different allosteric binding sites of PLpro. The top-ranked compounds were further analyzed through molecular dynamics simulations to assess the stability and conformational behavior of the protein–ligand complexes under near-physiological conditions. Additionally, pharmacokinetic properties were evaluated using ADME analysis along with toxicity prediction and LD₅₀ assessment to determine the safety profiles of the shortlisted compounds. The study identified promising *C. roseus* phytocompounds exhibiting strong binding affinity and stable interactions with crucial allosteric residues of PLpro, suggesting their potential role in modulating viral activity. Furthermore, the antioxidant, anti-inflammatory, and immunomodulatory properties of *C. roseus* may aid in reducing cytokine-mediated complications associated with severe COVID-19 infection. Collectively, these findings highlight *Catharanthus roseus* as a promising green source for the development of novel anti-COVID therapeutics.

Keywords: COVID-19, SARS-CoV-2, Molecular docking, Molecular dynamics simulation, Allosteric targeting, Phytochemicals.

Extraction of β -glucans from *Pleurotus* spp.

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Abstract

Mushrooms are the spore forming fruiting bodies of fungi. These are mainly belonging to the phylum Basidiomycota and Ascomycota. Although Medicinal mushrooms are rich source of fiber and bioactive compounds especially β -glucans which helps to promoting health effects. Among these, *Pleurotus ostreatus* & *Pleurotus florida* are widely used for cultivated oyster mushrooms known for their high content of β -1,3 and β -1,6 linked glucans. These are made up of D-glucans. These polysaccharides are mainly extracted from hot water extraction/ethanol precipitation. The FTIR spectra of *Pleurotus ostreatus* & *Pleurotus florida* showed the presence of specific absorption peaks of β -glucan functional groups. The broad absorption bands in the vicinity of 3200-3400 cm^{-1} . The presence of polysaccharides with O-H stretching vibrations as well as the absorption bands around 2920 cm^{-1} indicated the presence of C-H stretching vibrations. Absorption bands at 1600-1650 cm^{-1} indicated polysaccharide related functional groups and bound water. Peaks are observed between 1000–1200 cm^{-1} , which were identified as C–O–C stretching vibrations characteristic of glucan structures. Characteristic peaks of β -glycosidic linkage, located around 890 cm^{-1} , supported the presence of β -linked glucans in both species. The study showed that both mushroom species are good sources of β -glucans which have a high structural and biological significance. The characteristic peaks of *Pleurotus ostreatus*, however, were more intense than that of *Pleurotus florida*, suggesting that it may contain a higher number of β -glucans, which contributes to increased structural integrity. β -glucans in these mushrooms exhibits notable **immunomodulatory**, **antioxidant**, **anti-inflammatory**, and **antitumor** activities. It mainly used for functional foods, nutraceuticals and therapeutic conceptualization.

Keywords: *Pleurotus ostreatus*, *Pleurotus florida*, β -glucans, Immunomodulatory activity, antioxidant activity, anti-tumour activity, therapeutic potential.

Synthesis and characterization of Lutein-based nano-formulation for ocular health

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Abstract

The advancement in the digitalization and information technology leads to the development of ocular disorders and poor macular health. Lutein is yellow-colored xanthophyll carotenoid pigment, which is present in the macula of the eye in the highest concentration in the body. It is also found in retina, human lens, breast milk, brain, adipose tissue etc. It cannot be synthesized in the body and therefore can only be obtained from diet. Its dietary sources include green leafy vegetables like kale, spinach, yellow-colored foods like carrots, papaya and egg yolk etc. Lutein's most abundant source in nature is marigold flower petals but it is also found in daylily flower petals, some photosynthetic microalgae like *Tetrademus obliquus*, *Desmodesmus spp.* It is comparatively more polar than carotenes due to the presence of oxygen atoms in it. Being a macular pigment, lutein shows a positive correlation with the diseases like age – related macular degeneration, cataract, diabetic retinopathy etc. Lutein possesses anti-oxidant, anti-inflammatory and neuroprotective properties, useful in skin health and food industry. Despite its significant benefits, its application is restricted due its instability, oxidative degradation and low bioavailability. Being fat soluble, it is unable to mix in the aqueous medium of the digestive system, reducing overall absorption. In this study, lutein was extracted from sources like *Tetrademus obliquus* (microalgae), *Tagetes spp.* (Marigold Flower). The methods used for extraction included solvent extraction (by different solvents like acetone, methanol, hexane) and oil-based extraction (coconut oil) followed by spectroscopic analysis. This study aims to formulate and characterize a nano formulation using a food grade surfactant Tween 80, and sesame seed oil which is a long-chain triglyceride with anti-oxidant, anti-inflammatory properties, known to increase the stability and solubilization of the active compound.

Keywords: Macular health, Algal pigment, Marigold, retinopathy, Neuroprotective, Nano formulation

qPCR Analysis Reveals Cytochrome C Upregulation in *Saccharomyces boulardii* Under Anaerobic Conditions

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Abstract

Saccharomyces boulardii is a clinical vital fungal probiotic known for its proven efficacy against gastrointestinal dysbiosis. The yeast must survive the physiochemical changes from oxygenated environment to anaerobic environment inside the mammalian gastrointestinal (GI) tract. A property that makes *Saccharomyces boulardii* a well-known probiotic is its high stress tolerance, tracking its precise transcriptomic adaptation during shifting of environment is fundamentally important for improvement of available clinical strain its viability and other commercial uses. This study is focused on the transcriptomic analysis of *S. boulardii* from oxygen rich (aerobic respiration) to oxygen free (anaerobic fermentation) environment. Successfully analysing this transition is essential for understanding the yeast's molecular adaptability, with broader prospectus for optimization, industrial fermentation, and probiotic viability. This study performed a transcriptomic analysis of key genes involved in the respiratory chain and oxidative stress response to characterize the metabolic reconfiguration of *S. boulardii* during anaerobic adaptation. Cultures were subjected to aerobic and induced anaerobic condition, cDNA synthesis followed by qPCR quantification of target genes, including Cytochrome c, Glutathione Synthetase, Aldehyde Dehydrogenase, and Pyruvate Kinase. qPCR analysis revealed a metabolic shift, with significant upregulation in fermentation-related genes ALDH and Pyruvate kinase. Most notable finding was, Cyt c expression increased 485-fold, suggesting its role in electron reservoir for mitochondria, during anoxia marker GSH showed a slight downregulation prioritizing the metabolism of other factors for cell survival, these results provide essential transcriptomic validation of the adaptive strategies employed by *S. boulardii* to maintain redox homeostasis and serve as molecular benchmarks for assessing probiotic robustness within the healthcare biotechnology sector.

Keyword: *Saccharomyces boulardii*, Transcriptomic profiling, Metabolic adaptation, Quantitative PCR (qPCR), fermentation.

Protective effectiveness of *Ganoderma lucidum* on isolated rat liver cells exposed to damage from alcohol and fatty acid

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Abstract

Background: Prolonged exposure to ethanol and fatty acids results in gradual damage to the liver. *Ganoderma lucidum* thrives in high-altitude environments and offers various health advantages and therefore hypothesized to be effective liver injuries associated with ethanol and fatty acid prolonged exposures. Objectives: This study aims to investigate the disruption of metabolic and apoptotic pathways caused by fat exposure (4mM palmitic acid) and ethanol exposure (100 mM ethanol), along with the potential reversal using an aqueous extract of *Ganoderma lucidum*. Methods: Hepatocytes were treated with ethanol or fatty acids in the presence or absence of the extract for 24 hours, after which the metabolic and apoptotic markers were assessed. Results: Following the exposure of liver cells to ethanol, there was a noticeable disturbance in the expression of several metabolic markers, including hsp90, alcohol dehydrogenase, eNOS, CYPE1, CD31, along with apoptotic markers, like superoxide dismutase and CXCL. Additionally, liver cells treated with 4 mM palmitic acid exhibited disruption in the expression of metabolic markers such as FAS, PPAR-A, CPT, LRAT, CD36, DGTA, and SREBP, along with notable changes in apoptotic markers like BCL2 and CXCL. The administration of *Ganoderma lucidum* aqueous extract to rat liver cells exposed to either ethanol or palmitic acid was able to counteract all the negative effects observed. Conclusions: Overall, the indicators of metabolism and programmed cell death that were disrupted by alcohol and fatty acids could be restored with the use of the extract treatment. The results indicate that *Ganoderma lucidum* may serve as a promising agent for addressing different types of liver damage.

Keywords: Hypoxia, Ethanol, Fatty acid, Apoptosis, *Ganoderma lucidum*.

Epitope mapping using proteome for designing peptide allergen shots targeting *Aspergillus terreus*

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Abstract

Aspergillus terreus is an opportunistic fungal pathogen associated with allergic manifestations and invasive infections, yet its allergen repertoire remains insufficiently explored, limiting the development of targeted immunotherapies. This study aims to identify potential peptide-based candidates for allergen-specific immunotherapy using a comprehensive **proteome-wide in silico approach**. The complete proteome of *Aspergillus terreus* was explored and subjected to systematic screening to identify antigenic and non-homologous proteins, thereby minimizing the risk of host cross-reactivity. Proteins with significant similarity to the human proteome were excluded to enhance safety profiles. Subsequently, prioritized proteins were analysed for subcellular localization, with emphasis on secreted and surface-associated proteins due to their higher immunogenic potential. B-cell and T-cell epitope prediction was performed using established immunoinformatic tools, and high-affinity MHC class I and II binding peptides were shortlisted based on binding affinity, antigenicity, and predicted population coverage. Particular focus was placed on identifying short T-cell epitopes with minimal IgE-binding potential to reduce the likelihood of hypersensitivity reactions while promoting immune tolerance. Structural modelling and epitope mapping confirmed the surface accessibility and stability of selected peptides. Comparative analysis with experimentally characterized allergens, including Asp t 36, supported the biological relevance of the predicted epitopes and validated the computational pipeline. In conclusion, this study provides a systematic immunoinformatic framework for the discovery of safe and effective peptide-based allergen shot candidates against *Aspergillus terreus*. The proposed epitopes represent promising leads for next-generation allergen immunotherapy, further the data generated provides a strong platform for *in vitro* and *in vivo* validation studies.

Keywords: Fungal allergens, Immunogenic peptides, Drug resistance, Allergens and *Aspergillus*.

Comparative Evaluation of Antimicrobial and Antibiofilm Activity of Furfural in Model Bacterial Systems

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Abstract

Background: Furfural, a biomass-derived furan aldehyde, has gained attention for its renewable origin and antimicrobial potential. However, its antibiofilm activity and comparative efficacy across different bacterial systems remain insufficiently explored. **Objectives:** The present study aimed to evaluate the antimicrobial and antibiofilm activity of furfural against representative Gram-negative and Gram-positive model organisms, including *Acinetobacter baylyi*, *Pseudomonas fluorescens*, and *Staphylococcus epidermidis*. **Methods:** Antimicrobial activity was determined using broth microdilution assays to establish minimum inhibitory concentrations. Antibiofilm efficacy was quantified using a crystal violet assay, and growth kinetics were analyzed to assess time-dependent effects on bacterial proliferation. Molecular docking analysis was performed to assess potential interactions with the target. **Results:** Furfural exhibited concentration-dependent antimicrobial and antibiofilm activity across all tested organisms. Antimicrobial activity reached 95% inhibition at 1 mg/mL for *A. baylyi* and *S. epidermidis*, and 92% for *P. fluorescens*. Similarly, strong antibiofilm activity was observed at 1 mg/mL, with 92% inhibition in *A. baylyi* and *S. epidermidis*, and 90% in *P. fluorescens*. Growth kinetic analysis supported these findings, showing suppressed growth at MIC and partial recovery at sub-MIC levels, indicating a bacteriostatic effect. Molecular docking showed modest binding affinity. **Conclusion:** Furfural exhibited consistent, concentration-dependent antimicrobial and antibiofilm activity across both Gram-positive and Gram-negative model bacteria, indicating a broad-spectrum effect. Growth kinetics supported a predominantly bacteriostatic mode of action against selected bacteria.

Keywords: Antibiofilm activity; Antimicrobial activity; Comparative analysis; Growth kinetics; Furfural; Molecular docking

Vd3-Based Nano-Formulation: A Therapeutic Approach for Diseases Associated with Vd3 Deficiency

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Abstract

Vitamin D₃ plays a crucial role in maintaining calcium-phosphate balance, neuromuscular function, and immune regulation. Deficiency of vitamin D₃ has been increasingly linked to a range of chronic and degenerative diseases. The present study focuses on exploring the molecular association of vitamin D₃ deficiency with seven major diseases rickets, Parkinson's disease, Alzheimer's disease, breast cancer, asthma, systemic arterial hypertension, and inflammatory bowel syndrome (IBS) to identify common molecular targets. Gene datasets for each disease were retrieved from NCBI and key hub genes were identified through CytoHubba, and MCODE was employed to detect functional clusters. Functional enrichment analysis (GO and KEGG) revealed significant involvement of these genes in immune regulation, inflammatory response, oxidative stress, and calcium homeostasis. A nano-emulsion was also prepared using vitamin D₃-sesame oil mixture was combined with Tween-80 and Span-80 surfactants in a specific mixture. The formulation was further characterized through FTIR, DLS and Zeta potential. Cytotoxicity of nano-formulation, doxorubicin and a combination of doxorubicin and formulation was analyzed using MTT Assay. Although conventional supplementation strategies exist, the therapeutic efficacy of Vitamin D₃ remains limited due to its lipophilic nature, poor water solubility, instability under light and heat, and variable bioavailability. To address these limitations, nano-based formulations, particularly nano-emulsions have emerged as an alternative, offering enhanced solubility, improved absorption, controlled release, and increased bio-efficacy. Some of the key findings of this research work are multiple genes which are common in both the disease and VDR pathways, which establishes a molecular link between them. 12% s-mix and 4% oil-based nano-emulsion has the smallest size i.e., 86.7 nm. MTT assay was done to optimize the dose and cell viability of MCF-7 cell line, the combination of doxorubicin and nano-formulation has better results than doxorubicin or nano-formulation alone.

Keywords: Vitamin D₃, Nano-emulsion, Deficiency, Gene Analysis, Therapeutics.

Cracking the Influenza Code - A dual approach targeting Nucleoprotein and host-directed antiviral strategy

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Abstract

Background & Aim: Neuraminidase inhibitors have been the main anti influenza virus therapy (IV therapy) but their widespread use and concern about resistance, and on the other hand, limited effectiveness of current vaccine is because of its poor coverage against emergent drift and shift strain virus, making targeting conserved components of influenza virus such as NP along with critical host factors a valuable alternative. Here, we aim to identify small molecule inhibitors against NP (virus-directed) and its interacting host factors (host-directed). **Methods:** A structure-based in silico method was employed using crystal structure of NP protein of Influenza A/WSN/1933 (H1N1). The crystal structure was subjected for molecular dynamic simulation to obtain stabilized structure which was followed by virtual screening, docking and ligand based studies. We then prioritized and ranked the screened compounds based on binding affinity, stability, and drug likeness. The selected antiviral agents were assessed for activity using plaque assays, qRT-PCR and western blot. NP-host interactions were predicted using co-immunoprecipitation and LC-MS technique, and then analyzed by bioinformatic methods. Host factors were characterized and the one interacting in NP-dependent pathways was targeted. **Results:** In our screen, we identify novel small molecule inhibitors which exhibited more than 90% inhibition across various strains of influenza viruses (H1N1 and H3N1). The key host factor interaction networks of viral NP protein are found to be involve in pathways that regulates RNA metabolism, immune response, and nuclear-transport. Functional validation was confirmed for a pro-viral role of an RNA surveillance protein, which was further targeted to identify the novel small molecule inhibitor with significant antiviral effect. We demonstrate novel dual acting antivirals targeting NP along with interacting host factors and present a unique poly-pharmacological approach for the development of broad spectrum antiviral drugs against influenza viruses.

Keywords: Influenza nucleoprotein (NP), Host-directed antivirals, Structure-based virtual screening, Broad-spectrum antivirals, Poly-pharmacological approach

Overexpression of the ADRB2 Gene in *Mus musculus*: Construction and Validation of a Molecular Cloning System

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Abstract

Aging is a complex biological process characterized by progressive decline in physiological functions and increased susceptibility to diseases. The β 2-adrenergic receptor gene (ADRB2), a G-protein-coupled receptor involved in cellular signaling and stress response, has been implicated in aging and age-related disorders. This study aimed to construct and validate an ADRB2 overexpression system in *Mus musculus* as a preliminary step toward investigating its role in aging-related molecular pathways. The experimental workflow included RNA isolation from RAW mouse macrophage cells, followed by cDNA synthesis and PCR amplification of the ADRB2 gene. A specific amplicon of approximately 1256 bp was obtained, with optimal amplification achieved at an annealing temperature of 62°C. The amplified product and EGFP plasmid vector (~7656 bp) were subjected to double restriction digestion using XbaI and BamHI, followed by purification and ligation using T4 DNA ligase. The ligation mixture was transformed into chemically competent *Escherichia coli* cells using the heat-shock method. All intermediate molecular cloning steps were successfully performed and validated. However, no bacterial colonies were observed following transformation, indicating possible inefficiencies in ligation or transformation processes. Despite this limitation, the study establishes a standardized workflow for ADRB2 gene cloning and highlights critical parameters requiring optimization. This work provides a basis for future functional studies aimed at understanding ADRB2-mediated signaling in aging.

Keywords: ADRB2, ageing, molecular cloning, gene overexpression, *Mus musculus*

Fluoride-induced hepatotoxicity: Insights into Oxidative stress, Inflammation and Apoptotic Pathways

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Abstract

Fluoride (F⁻), a pervasive environmental contaminant, exerts toxic effects on multiple organ systems upon chronic exposure, with the liver being particularly susceptible due to its central role in metabolism and detoxification. Prolonged F⁻ exposure induces significant histopathological alterations, including hepatocellular degeneration, sinusoidal dilation and necrosis, reflecting compromised hepatic architecture. Biochemically, increased serum levels of alanine aminotransferase (ALT) and aspartate aminotransferase (AST) indicate disruption of membrane integrity and impaired liver function. Mechanistically, oxidative stress plays a pivotal role, characterized by excessive generation of reactive oxygen species (ROS), enhanced lipid peroxidation and depletion of endogenous antioxidant defenses such as superoxide dismutase (SOD), catalase and reduced glutathione (GSH), leading to redox imbalance and mitochondrial dysfunction. Furthermore, F⁻ activates inflammatory signaling pathways, particularly NF-κB, resulting in the upregulation of pro-inflammatory cytokines, while simultaneously triggering apoptotic pathways via mitochondrial depolarization, cytochrome c release and caspase activation. In addition, F⁻ interferes with hepatic metabolic processes by altering enzyme activity and gene expression, thereby exacerbating cellular dysfunction. Collectively, these findings demonstrate that F⁻-induced hepatotoxicity is a multifactorial process involving oxidative damage, inflammation and apoptosis, underscoring the need for deeper mechanistic insights to facilitate the development of effective therapeutic and preventive strategies, especially in regions with high environmental F⁻ exposure.

Keywords: Fluoride, hepatotoxicity, oxidative stress, inflammation, apoptosis

Therapeutic potential and targeted delivery of *Paris Polyphylla* saponins in breast cancer management

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Abstract

Breast cancer remains a global health problem; new subtypes like triple negative breast cancer are becoming more common & conventional treatments have toxic side effects. Steroidal saponins derived from plants can be used as anti-cancer drugs as they target multiple pathways & appear to be less toxic than other chemotherapy agents. Specifically, the polyphyllins isolated from *Paris polyphylla* are gaining attention for their potential use in treating all molecular subtypes of breast cancer. This review provides an overview of recent literature regarding the anticancer activity and mechanisms of action of major polyphyllins including Polyphyllin I, II, III, D and Paris Saponin VII. Additionally, computational studies supporting these findings and nanotechnology-assisted delivery systems will also be discussed. Polyphyllin I causes DRP1 mediated mitochondrial division and leads to mitophagy through PINK1. Polyphyllin II is a PI3K/AKT inhibitor which has been shown to decrease cellular glycolysis. Polyphyllin III is a ferroptosis inducer through ACSL4. Polyphyllin D induces acute ER stress and apoptosis. Lastly, Paris Saponin VII is an activator of the Hippo pathway leading to cytotoxic autophagy. Molecular docking and molecular dynamics were used to validate these compounds' ability to bind to multiple known oncogenes such as estrogen receptor alpha (ER α), EGFR, and PI3K. Although there are many in vitro models that show great potential for treatment of breast cancer, the poor aqueous solubility and limited oral availability of polyphyllin saponins prevent their use clinically. However, recent advances in nanotechnology have provided nanoparticle-based drug delivery systems that may improve upon these limitations. These have shown increased pharmacokinetic stability, targeted delivery to tumors, and decreased systemic toxicity when compared to free forms of polyphyllin saponins. Overall, our studies indicate that polyphyllin saponins derived from *Paris polyphylla* could be utilized as future generations of breast cancer treatments and warrant further translational and clinical evaluation.

Keywords Saponin · Breast cancer · Polyphyllin · Bioinformatics · Nanotechnology

Untargeted LC–MS Analysis of Toxigenic *Aspergillus flavus* Extracts for Secondary Metabolite Identification

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Abstract:

The aflatoxins are extremely toxic and carcinogenic secondary metabolites that are produced by *Aspergillus flavus*, which have serious impacts on food safety and human health. The current study examined a toxigenic strain of *Aspergillus flavus* (BT-05) to profile comprehensively its metabolite composition using liquid chromatography-mass spectrometry (LC-MS) analysis. *A. flavus* was inoculated in PDB at 120 rpm, 25 °C for 3 days, metabolites were extracted using solvent extraction method to obtain crude extracellular extract. The analysis of the extract by LC-MS led to a total of 194,216 metabolites identification. To minimize redundancy, compounds whose mass-to-charge (m/z) ratios equalized with their scores and retaining the best compounds. Downstream analysis resulted into total of 743 unique compounds. Further analysis of these compounds, using spectral matching and chemical properties, indicated the presence of multiple metabolites with structural and functional similarities to established aflatoxins and associated secondarily metabolites. The research offers an extensive metabolomic perspective regarding the toxigenic profile of *A. flavus* BT-05 and also highlights the diversity of potentially hazardous compounds other than traditionally studied aflatoxins. These results add to the better comprehension of the complexity of fungal metabolites and can be used to develop improved methods to detect toxins and assess their risk.

Keywords: Secondary metabolites, *Aspergillus flavus*, Downstream

Analysis of wound-induced gene expression in *Schmidtea mediterranea* following *Pseudomonas* infection

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Abstract

Regeneration is a complex biological process that enables organisms to restore lost or damaged tissues through cellular and molecular mechanisms. This study investigated the molecular basis of regeneration in *S. mediterranea* by focusing on three regeneration-associated genes, *fos-1*, *follistatin*, and *jun-1*. The study further examined the effect of *Pseudomonas aeruginosa* infection on the expression of these genes during regeneration, assessing how an external bacterial challenge may influence the molecular mechanisms associated with regeneration. For this study, healthy planarians were maintained under controlled laboratory conditions and subjected to transverse amputation to generate tail fragments. Regenerating fragments were collected at multiple time points (2 to 48 hours) post amputation, to analyse the wound response dynamics. Total RNA was isolated using the Trizol method, followed by cDNA synthesis and gene-specific PCR amplification. The amplified products were cloned into pGEM-T vector, verified through blue and white screening, colony PCR, plasmid isolation and sequencing. The confirmed constructs were used for *in-vitro* transcription to generate digoxigenin-labelled RNA probes for *in-situ* hybridization. The study successfully standardized molecular workflow for gene cloning, probe generation and detection of regeneration-associated transcripts by *in situ* hybridization, supported only by the expression of *fos-1* gene at wound site only under control condition. Furthermore, comparative examination of infected and control fragments suggested that bacterial challenge may influence wound-associated gene expression but requires further optimization for conclusive interpretation. Overall, this study provides a useful experimental framework for analysing regeneration-related genes in planarians and highlights the importance of integrating wound biology with host pathogen interaction in regeneration research.

Keywords: *Pseudomonas aeruginosa*, *Schmidtea mediterranea*, regeneration, infection

Advancing Diabetic Wound Management Using *Psidium guajava* Hydro-Alcoholic Fruit Extract

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Abstract

Diabetic wounds constitute a substantial healthcare concern due to their poor healing and susceptibility to infection. *Psidium guajava*'s therapeutic properties have long been recognized by traditional medicine. This study utilized fruits of *P. guajava* that have been less explored in terms of diabetic wound healing. The phytochemical composition and effects of *P. guajava* hydro-alcoholic fruit extract (PGHE) on different parameters influencing diabetic wound healing were comprehensively investigated including: anti-inflammatory effects, antibacterial properties, antioxidant activity, anti-diabetic properties, and fibroblast proliferation. The findings of this study demonstrated that PGHE has strong anti-diabetic effect, including a significant inhibition of α -amylase activity (73.70%) and 124.8% increase in 2-NBDG uptake in McCoy cells. PGHE demonstrated considerable antioxidant activity, inhibiting DPPH (IC₅₀: 0.044 mg/mL) and ABTS (IC₅₀: 0.043 mg/mL) free radicals. In *in vitro* wound healing studies employing PGHE revealed a significant increase in McCoy fibroblast proliferation by 1.55-fold. With inhibition zones varying from 12.9 mm to 14.1 mm, PGHE demonstrated variable anti-bacterial activity against all investigated bacterial strains. It efficiently reduced heat-induced RBC hemolysis, with anti-inflammatory effect of 69.70% at 0.2 mg/mL. In conclusion, this evidence-based pharmacological study highlights the promising potential of PGHE in facilitating the healing of diabetic wounds, offering a topical approach to address this challenging healthcare issue.

Keywords: Diabetic wounds; *Psidium guajava*; anti-oxidant; anti-bacterial; anti-inflammatory; topical approach

Impact of Hypobaric Hypoxia on Rat Liver: Cellular and Molecular Adaptations

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A low-oxygen environment triggers the activation of mechanisms that sense oxygen and respond differently across various tissues, initiating adaptive pathways through hypoxia-inducible factor 1 alpha, which serves as a key regulator of hypoxia. This research focuses on examining the molecular and cellular responses to hypoxia in the liver of rats subjected to low-pressure hypoxia at an altitude of 7620 meters over periods of 1, 3, and 7 days. After exposure to hypobaric hypoxia, liver tissues were removed to assess the redox status, overall antioxidant capacity, and molecular markers of adaptation, including hypoxia-inducible factor 1 alpha (HIF-1 α), vascular endothelial growth factor (VEGF), and erythropoietin (EPO). The total antioxidant capacity in the liver showed a significant reduction on the 3rd and 7th days of exposure, while HIF-1 α and its related factors displayed varying expression patterns in the liver. HIF-1 α levels rose on the 1st and 7th days, and VEGF concentrations increased on these same days of hypobaric hypoxia exposure. Additionally, erythropoietin played a role in the liver's adaptive response. In summary, low-pressure hypoxia activates various elements of the HIF-1 α signaling pathway in the liver at different exposure times, indicating a time-sensitive reaction to hypobaric hypoxia.

Keywords: Hypobaric hypoxia, Hypoxia inducible factor, Oxygen sensing, Liver

Novel Therapeutic Inhibitor Targeting Dysregulated Kinase Signaling in Tau-Mediated Neurodegeneration

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Abstract

Tauopathies, including Alzheimer's disease, are characterized by progressive neuronal degeneration driven by abnormal hyperphosphorylation of tau protein, leading to microtubule destabilization and neurofibrillary tangle formation. Dysregulated kinase signaling pathways, particularly those involving glycogen synthase kinase-3 β (GSK-3 β), cyclin-dependent kinase 5 (CDK5), and mitogen-activated protein kinases (MAPKs), play a critical role in mediating tau pathology and disease progression. Among these, the MAPK/ERK signaling pathway, particularly ERK1/2, plays a central role in tau phosphorylation, neuronal plasticity, and neuronal survival, making ERK1/2 a clinically relevant therapeutic target for disease modification. In this study, an integrative in silico approach was employed to investigate kinase signaling networks associated with tau-mediated neurodegeneration and to identify potential therapeutic inhibitors targeting ERK1/2. Protein protein interaction network analysis was performed to identify key regulatory nodes within kinase driven pathways. Structure based molecular docking was conducted to evaluate the binding affinity of selected natural compounds against the ERK1/2 target. Among the screened compounds, Baicalein demonstrated strong binding affinity toward ERK1/2, with favorable docking scores indicating stable interactions within the active site. The compound also exhibited consistent binding across multiple cavities, suggesting its potential to effectively inhibit ERK1/2 mediated phosphorylation pathways. Clinically, these findings position Baicalein as a promising lead candidate for disease modifying intervention in tauopathies. Targeted inhibition of ERK1/2 signaling may attenuate tau hyperphosphorylation, thereby reducing neurodegenerative burden, slowing neuronal dysfunction, and preserving memory, learning ability, and daily cognitive performance. This study underscores the therapeutic importance of ERK1/2 inhibition and supports further preclinical and translational evaluation of Baicalein in tau-mediated neurodegeneration.

Keywords: Tauopathies, Alzheimer's disease, MAPK/ERK1 signaling, kinase dysregulation, tau hyperphosphorylation, Baicalein, molecular docking, CB-Dock, in silico drug discovery, therapeutic inhibitors, neurodegeneration, disease-modifying therapy.

Bipolar Disorder: An Integrated Neuroscience and Neuropsychological Study

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Abstract

Recent global data indicate that people with bipolar disorder die, on average, nearly 13 years earlier than the general population due to psychiatric and physical health complications. Current literature often treats the neuroscientific and neuropsychological aspects of bipolar disorder as parallel fields. This review bridges that gap by synthesizing synaptic-level neurobiological changes with cognitive and behavioural outcomes, providing a unified mechanistic understanding of the disorder in light of recent advances in neuroscience research. At the neurobiological level, bipolar disorder is associated with dysregulation of key brain regions, including the prefrontal cortex, amygdala, and hippocampus, along with alterations in neurotransmitter systems such as dopamine, serotonin, and glutamate. Emerging evidence also highlights the role of neuroinflammation, mitochondrial dysfunction, and impaired synaptic plasticity in disease progression. From a neuropsychological standpoint, patients exhibit persistent cognitive deficits, particularly in executive function, attention, memory, and emotional regulation, even during euthymic phases. Advances in neuroimaging and molecular research have enabled the identification of disrupted neural circuits underlying mood instability and cognitive impairment. Furthermore, integrating findings from neuroscience with clinical neuropsychology enhances early diagnosis, improves therapeutic targeting, and supports the development of personalized treatment strategies. This review emphasizes the need for a multidimensional framework that bridges molecular mechanisms, brain circuitry, and behavioral outcomes to better understand and manage bipolar disorder.

Keywords: Cognitive Dysfunction, Prefrontal Cortex, Amygdala, Neurotransmitters, Synaptic Plasticity, Executive Function, Mood Disorders

Agriculture Biotechnology

Oral Presentation

A Web Based Intelligent Decision Support System for Precision Irrigation Using Hybrid Deep Learning Models

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Abstract

Agriculture is the major source of freshwater withdrawals in the world (70 percent). Conventional irrigation methods are very inefficient which causes wastage of water in a large quantity and reduced crop yields. The Intelligent Decision Support System, as described in this paper is a web-based system uses hybrid generative methods of deep learning to give accuracy-irrigation recommendations. The suggested system combines Convolutional neural networks (CNN) and Long Short-Term Memory (LSTM). To interpret multiple-source data, adding soil moisture gauges, weather conditions and so on et cetera. LSTM networks are applied, parameters, and crop imagery. The CNN-LSTM hybrid model is good at capturing both the spatial and time-varying characteristics of data, which allow to predict the soil moisture and crop water correctly stress detection. The deployed system is a three-tier responsive web application system. providing it to farmers through standard web made tools. Performance appraisal based on. The benchmark datasets prove that the hybrid model is highly predictive in terms of R². Soil moisture prediction values more than 0.94 and classification accuracy greater than 95% values on crop stress detection. It is an irrigation-advice system, offering actionable advice in general, based on simulation studies, showing possible 20-25% saving of water used in comparison with traditional irrigation systems. This work helps to democratize precision agriculture so that AI-derived irrigation proves to be a matter of fact. Verdicts may be provided by software alone which removes cost concerns and is making. Sustainable production methods those are reachable by the smallholder farmers. The paper presents a new model of The Precision Irrigation Company, based on Deep Learning and CNN-LSTM, to support the creation of a web- based decision support system (DSS).

Keywords: Precision Irrigation, Deep Learning, CNN-LSTM, Decision Support System, Web Application, Soil Moisture Prediction

Blockchain-Enabled Agricultural Value Chains in Himachal Pradesh: A Decentralized Framework for Enhancing Farmer Income and Market Transparency

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Abstract

There are still structural problems with agricultural marketing systems in Himachal Pradesh, including fragmented market linkages, multiple intermediaries, little transparency in price discovery and delays in settlement of payments. The state is predominantly composed of small and marginal farmers engaged in high-value horticulture particularly apples, stone fruits, off-season vegetables, and organic crops. Market distortions in these sectors lead to income instability, weak bargaining power, delayed payments, limited traceability and related challenges for farmers in Himachal Pradesh. This study looks into the block-chain based decentralized framework that may be built for the hill agricultural systems of Himachal Pradesh. The proposed model involves a permissioned blockchain network of farmers, FPOs, traders, storing units, logistic service providers and government departments. This information, once validated, is on a blockchain in an electronic platform thus ensuring speedy market linkages with the farm gate with greater transparency. The potential of IoT-backed quality assessment devices and geotagging further enhances traceability in reference to apple and certified organic crops of reputed economic value. The framework also comes up with the idea of tokenized warehouse receipts that would enable farmers to draw institutional credit against their stored produce. The system is likely to enhance farm-gate price realization and mitigate post-harvest inefficiency by shortening the transaction process and improving information flow. The pilot is proposed under relevant state agencies in coordination with agricultural universities and digital partners. With appropriate policy support, blockchain-based systems can enhance income stabilization and market transparency in Himalayan agriculture.

Keywords: Blockchain, Farmer Income, Market Transparency, Himachal Pradesh.

Optimizing biofertilizers to improve the survival percentage of tissue culture-raised *Costus igneus* (Insulin plant)

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Abstract

The Insulin plant (*Costus igneus*) is widely known for its anti-diabetic properties; therefore, there is a need for fast and large-scale multiplication of the plant. Micropropagation is one of the most efficient techniques in obtaining disease-free and genetically identical plants but is limited by the low survival of plantlets after acclimatization in vitro. The present study was planned to optimize the bio stimulants along with PGPMs to improve the survival percentage of *Costus igneus* during this critical stage. Propagation of *Costus igneus* plantlets was first done using MS medium with IBA and Kinetin for shoot proliferation and half-strength MS with IBA for rooting. Although strong roots and shoots had developed in vitro, there was evidence of stress in plantlets following acclimatization as a result of abrupt change of environment which is responsible for decreasing survival rates. To overcome these PGPM based biofertilizers were applied at the time of acclimatization. Some microbial strains having nitrogen fixing, phosphorus solubilizing and IAA producing capabilities were supplemented in media or roots. The application of PGPMs in such cases has resulted in significant improvement in the growth of plantlets by enhancing the uptake of nutrients, promoting root elongation, increasing chlorophyll concentration and reducing transplantation shock. Plantlets under microbial treatment have been observed to have better resistance towards environmental stress thus resulting in effective hardening of the plants as compared to the control group. This paper highlights the need of inclusion of biological inputs in the traditional micropropagation techniques for developing sustainable and effective micropropagation technique of *Costus igneus*. Future studies are needed for field trials of the bio-fertilizers and optimization of microbial consortia and their interaction with the plants. It can be concluded that micropropagation, along with PGPM based biofertilizer, is an effective technique in general.

Keywords: *Costus igneus*, Acclimatisation, Plant growth-promoting microorganisms (PGPMs)

A Comprehensive Review on Podophyllotoxin Production from *Podophyllum hexandrum*: Advances in Semisynthetic, Microbial, and Plant Cell Culture Approaches

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Abstract

Podophyllotoxin, often referred to as “Himalayan Gold,” is a vital secondary metabolite with significant medical importance. It is primarily obtained from the endangered medicinal plant *Podophyllum hexandrum*, whose declining populations are threatened by slow natural propagation, excessive harvesting in the Himalayan region, and increasing demand. This lignan serves as a key precursor in the semi-synthesis of several widely used chemotherapeutic agents. However, its complex chemical structure limits large-scale synthetic production, making extraction from natural sources the primary means of supply. This review highlights the crucial role of endophytes associated with *Podophyllum hexandrum* as promising alternative producers of podophyllotoxin, offering potential to reduce dependence on traditional extraction methods. It also examines structural modifications of podophyllotoxin derivatives in modern therapeutics, along with recent advances in biotechnology that support enhanced production. Furthermore, the review explores future prospects involving genomics and green chemistry approaches aimed at sustainable and scalable production. Emphasis is also placed on biodiversity conservation strategies to ensure the long-term availability of this valuable anticancer compound.

Keywords: Podophyllotoxin, *Podophyllum hexandrum*, Semisynthetic Derivatives,

Proteomics Explains the Role of Autophagy in Fruit Ripening and Ethylene Production

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Abstract

Fruit ripening is a critical determinant of agricultural productivity, directly influencing food supply and quality worldwide. This developmental process is governed by physiological, biochemical, and molecular mechanisms that modulate colour, texture, and flavour. Recent studies suggest that autophagy may regulate fruit ripening through crosstalk with ethylene signalling. However, the underlying molecular mechanisms remain poorly understood. This study intended to investigate the role of autophagy in tomato fruit ripening and to determine how suppression of the key autophagy gene *SlATG4* affects ethylene production, ripening progression, and the abundance of ripening-promoting proteins. Ripening-specific suppression of *SlATG4* gene was achieved by generating transgenic tomato lines carrying an RNAi construct under E8 ripening-driven promoter (E8:*SlATG4*-RNAi). Two independent lines, L9 and L18, representing weak and strong silencing were taken into consideration. Parameters like fruit ripening progression, coloration and ethylene production were analysed. Proteomics analyses were conducted at Turing (T) and Red Ripe (RR) stages in wild-type, L9, and L18 fruits to identify molecular cues associated with *SlATG4* silencing. We found that autophagy restricts tomato fruit ripening via repression of ethylene production. Notably, L18 fruits, showing strong silencing, exhibited accelerated ripening, reaching full coloration seven days earlier than WT and L9 fruits. This phenotype was accompanied by elevated ethylene production and an earlier onset of the climacteric phase. Proteomics analyses showed that *ATG4* silencing exerted pronounced effects at the RR stage, with significant stabilization of ripening-promoting proteins, including *SlEXP1*, *PSY1*, *SlSGR1*, and the ethylene biosynthetic enzymes *SlACO1* and *SlACO6*. The finding provides compelling evidence that autophagy restricts tomato fruit ripening by repressing ethylene production.

Keywords: Ripening-specific promoter, *SlATG4*, Autophagy

Selection of Native Bacterial Isolates from Degraded Soil for Soil Conditioner Formulation

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Abstract

Land degradation affects nearly 2 billion hectares of land globally, reducing soil fertility, crop productivity, and ecosystem sustainability. With increasing population and food demand, maintaining soil health is essential for sustainable agriculture. Microbial soil conditioners offer an eco-friendly approach for restoring degraded soils. Therefore, this study aims to isolate and characterize native bacterial isolates of degraded soils for their potential use in microbial bioformulation as soil conditioners. Soil samples were collected from four sites: Hindon Riverbank, Hindon River wet sediment zone, leather tannery degraded soil from Kanpur industrial area, and petrochemical degraded soil from IFP Petro Products, Ghaziabad industrial area. Physicochemical analysis was performed to assess the level of soil degradation. Bacterial isolates were obtained using serial dilution and spread plate techniques, purified, and maintained as pure cultures, for further study. The isolates were screened for antioxidant potential and PGPR traits including phosphate solubilization, IAA production, and siderophore production. Results showed that petrochemical degraded soil had the highest pH (8.5), low organic carbon (0.5–0.75%), and low nitrate nitrogen content (5–10 kg/acre), indicating severe degradation. A total of 24 bacterial isolates were obtained, among which 6 isolates showed the highest antioxidant potential, while 13 isolates showed positive phosphate solubilization. These findings demonstrate the potential of native bacterial isolates from degraded soils for the development of efficient microbial bioformulations as sustainable soil conditioners, contributing to soil restoration, improved soil fertility, and long-term agricultural sustainability while supporting SDG 2, 12, 13, and 15.

Keywords: Soil Degradation, Soil Conditioners, Native Bacterial Isolates, Plant Growth Promoting Rhizobacteria (PGPR), Microbial Bioformulation.

Exploring the Chemical Composition and Biological Activities of the Indian Medicinal Plants

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Abstract

Medicinal plants have gained significant attention as potential sources of safer and cost-effective therapeutic agents, especially in the context of increasing drug resistance and adverse effects associated with the synthetic compounds; their comparative chemical profiling and biological evaluation remain insufficiently explored. In this study, *Rosa damascena* Herrm (Gul-e-Surkh), and *Jasminum sambac* (L) Aiton (Jasmine) were analysed to investigate their chemical composition and biological potential. Chromatographic techniques, including high-Performance thin-layer chromatography and high-performance liquid chromatography, were employed to generate and characterise chemical fingerprints, while nuclear magnetic resonance spectroscopy provided insights into the structural features of the compounds present. The antioxidant capacity of these extracts was evaluated using ABTS and Nitric oxide scavenging assays, followed by antimicrobial and cytotoxic evaluation using the MTT assay. The results show significant variation in chemical profiles among the extracts, which was reflected in their biological activities. Extracts exhibiting stronger antioxidant activity also demonstrated enhanced cytotoxic and antimicrobial effects, indicating a potential correlation between the chemical composition and functional properties. Overall, this study highlights the potential of medicinal plants as promising sources of biologically active compounds for future pharmaceutical applications.

Keywords: Antimicrobial, Antioxidant, Cytotoxicity, HPLC, Natural products

Enhancement of Nutritional and Functional Properties of Kalanamak rice Through Controlled Fermentation and Microbial Characterization

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Abstract

Kalanamak rice is an indigenous aromatic rice variety valued for its rich nutritional composition and traditional therapeutic significance. The present study explored its potential as a functional fermented food through controlled fermentation and microbial characterization. Proximate and mineral analyses of raw Kalanamak rice revealed appreciable levels of essential micronutrients, particularly iron, zinc, potassium, and magnesium, indicating its potential role in combating micronutrient deficiencies and improving dietary quality. Fermentation was optimized using different rice-to-water ratios (1:10 and 1:20) and incubation periods of 12 and 24 h. A gradual decline in pH during fermentation confirmed active microbial metabolism and organic acid production. Microbial enumeration demonstrated increased microbial growth during the initial stages of fermentation, followed by a reduction after 24 h, likely due to increased acidity and nutrient depletion. Five non-pathogenic bacterial isolates obtained from fermented rice broth were selected for further characterization and bioactivity analysis. Although antimicrobial activity against the tested pathogens was not observed, molecular identification using 16S rRNA gene sequencing revealed the predominance of *Bacillus* spp., which are commonly associated with traditional fermentation processes and production of beneficial bioactive metabolites. The presence of these bacteria suggests the probiotic and functional potential of the fermented product. The findings demonstrate that controlled fermentation can improve the functional and microbiological attributes of Kalanamak rice while supporting beneficial microbial communities. This study provides scientific evidence supporting the use of traditionally fermented Kalanamak rice as a promising probiotic-enriched functional food with potential nutritional and health-promoting applications.

Keywords: Kalanamak rice, Fermentation, Functional food, Probiotic potential, *Bacillus* spp.

Unveiling The Metabolomic Profile and Deciphering Bioactive Phytocompounds from In-Vitro Propagated *Picrorhiza Kurroa*

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Abstract

Lifestyle transitions from old to modern patterns accompanying globalization reflected by dietary shifts, less physical activity and increased stress have significantly contributed to the development of disease etiology, worldwide. Around 4% annual deaths have been reported worldwide due to liver related diseases by World Health Organization. The paradigm shifts towards wide acceptance of alternative therapies, due to associated side effects with conventional drugs, has taken the world with stride. Medicinal plants enriched in phytocompounds are gaining consumer acceptance due to availability, efficacy and minimum or no side effects. *Picrorhiza kurroa*, a hepatoprotective plant from family *Plantaginaceae*, has been a focus of interest among agronomist and cultivars due to high global demand. However, the dynamic metabolite profile regulated by abiotic cultivation conditions are instrumental in showing variations in therapeutic efficacies. It is pertinent to develop an association between phytocompound composition and abiotic factors during controlled and uncontrolled plant propagation. Current study evaluates the role of micropropagation conditions toward the dynamic phytocompounds pool. The results will highlight the exploration of metabolomic profile of in-vitro propagated *Picrorhiza Kurroa*.

Keywords: Hepatoprotective, *Picrorhiza kurroa*, metabolomic.

Phytochemical and Biological Evaluation of Leaf Extracts of *Moringa oleifera* and *Catharanthus roseus*

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Abstract

Medicinal plants are rich in phytochemicals and have been used in traditional medicine. These can be an alternative source of antimicrobial compounds in the treatment of infectious diseases. The present study attempts to critically assess *Moringa oleifera* and *Catharanthus roseus* by involving integrated phytochemical characterization and antibacterial activity. Preliminary phytochemical screening of former mentioned medicinal plants showed the presence of alkaloids, flavonoids, saponins, tannins, and triterpenes. The antibacterial activity of ethanolic plant extracts of both plants also exhibited notable inhibition, especially against *E. coli* ATCC 25922 (25 ± 0.4 mm). The MIC values ranged from 6.25 to 50 µg/ml, indicating variable antibacterial potency. GC–MS profiling of *M. oleifera* indicated 4H-Pyran-4-one, 2, 3-dihydro-3, 5-dihydroxy-6-methyl- (34.80%) as the predominant compound followed by Erythritol (24.00%). GC–MS profiling of *Catharanthus roseus* indicated Phytol (36.84%) as the predominant compound followed by n-Hexadecanoic acid (10.89%). The results validate the traditional use and highlight the potential of both plants as a natural, safe, and effective alternatives or complementary agents to conventional antibiotics.

Keywords: *Phytochemical, Minimum inhibitory assay, GC-MS analysis, antibacterial activities, Gram-negative bacteria*

Assessment of Genetic Diversity and Phytochemical Profiling of selected Medicinal Plant species from Agra region using RAPD profiling and HPLC chromatogram

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Abstract

This study evaluates the genetic diversity and phytochemical analysis of ten medicinal plant species collected from four natural sites Bharatpur, Dholpur, Hathras, and Farah of Agra (Uttar Pradesh, India). After the plant sample collections taxonomic identification and calculation of biodiversity index were performed. Medicinal plant selected for the present study were *Calotropis procera*, *Calotropis. gigantea*, *Datura. metel*, *Datura stramonium*, *Euphorbia hirta*, *Coccinia. indica*, *Acacia nilotica L.*, *Solanum. xanthocarpum*, *Solanum nigrum*, and *Withania. Somnifera*. Molecular profiling was assessed using Random Amplified Polymorphic DNA (RAPD) markers and biochemical characterization of plants were done by Reverse Phase -High Performance Liquid Chromatography (RP-HPLC). RAPD markers are widely used for detecting genetic variability due to their simplicity and efficiency. A total of ten RAPD primers generated 40 scorable bands, of which 65% were polymorphic, indicating moderate genetic variability among the studied taxa. The presence of polymorphic bands demonstrates genetic diversity both within and among populations across the four sites. In contrast, the appearance of monomorphic bands suggests some degree of genomic conservation, possibly reflecting shared ancestry or evolutionary stability in specific loci among the plant species. HPLC with reverse phase column, a reliable method for phytochemical characterization, revealed the presence of multiple bioactive compounds. Across all analyzed samples, saponin was consistently present, indicating its widespread occurrence in these medicinal plants. Other bioactive compounds such as gallic acid, rutin, and p-coumaric acid showed variation. The present study is very important with respect to biodiversity of wild plant species in Agra region and also suggest the conservation of species based on molecular, phytochemical and biodiversity index analysis.

Keywords: RAPD, HPLC, genetic diversity, medicinal plants, phytochemicals.

Integration of Plant Microbial Fuel Cell and Vertical Hydroponics Tower for Enhanced Bioelectricity Production and System Efficiency Performance Evaluation

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Abstract

Plants Microbial Fuel Cells (PMFCs) have shown up as reliable renewable-energy production, alongside reducing the carbon footprint. However, the conventional PMFCs have few constraints, such as low electrical output, large spatial requirements, and reproducibility. In this study, a vertical hydroponics tower, integrated with a PMFC, was developed for enhanced bioelectricity production by employing *Solanum lycopersicum* in this setup, cultivated in Hoagland nutrient medium under recirculating hydroponic conditions. On the 11th day of germination, a total of 48 plants were transferred into the setup. The nutrient reservoir functioned as a bioelectrochemical reactor containing anodic and cathodic chambers. The aerobic chamber consists of a cathode, where electrons are accepted, and reduction occurs; and another anaerobic chamber consists of an anode, where electrons are released, and oxidation occurs. Carbon-fiber cloth electrodes were employed as anode and cathode, due to their high electrical conductivity, corrosion resistance, chemical stability, biocompatibility, and large surface area, which enhanced microbial colonization and electron-transfer efficiency. The anodic chamber was established using wetland soil collected from Tughlaqabad Biodiversity Park to provide electrochemically active anaerobic microbial communities. These microbial communities feed upon plant root exudates (exudates released from tomato roots served as natural substrates) and excrete electrons as their metabolic product. These electrons are then transferred from the anaerobic anode to the oxygen-rich cathode, resulting in bioelectricity production. The voltage and current were measured using the digital multimeter over the span of 3 months, and power density was calculated. The peak power density achieved as a result of this integration was 213.78mW/m². A polarization curve analysis was also carried out to evaluate the operational behavior, internal resistance, and charge-transfer.

Keywords: Plant Microbial Fuel Cell (PMFC), Polarization curve, Hydroponics Technology

From Morphology to Sustainability: Taxonomic Keys of Genus *Chasmina* (Noctuidae) for Precision Pest Identification

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Abstract

Accurate species identification is essential for effective pest monitoring and biodiversity assessment in agroecosystems. The Family Noctuidae is highly diverse and ecologically significant, yet species of the genus *Chasmina* are difficult to distinguish based solely on external morphology. This study presents a detailed taxonomic assessment of *Chasmina rejecta* (Fabricius), *Chasmina judicata* Walker, *Chasmina tibialis* (Fabricius) and *Chasmina candida* (Walker), based on male genitalic attributes. Specimens were collected from the Western Ghats, India. Male genitalia slides were prepared using standard KOH maceration and examined under a microscope to analyse diagnostic structures, including the valva, uncus, vinculum, juxta, and aedeagus. Information on host plant associations, pest status, and the distribution of the genus *Chasmina* was synthesised from available literature and regional records. A novel dichotomous key is proposed for the first time, providing a reliable tool for species identification. The study highlights the importance of integrating taxonomy with ecological data to support sustainable pest monitoring and biodiversity conservation.

Keywords: *Chasmina*, Noctuidae, Male genitalia, Taxonomy, Dichotomous key.

Physicochemical Characteristics of Black Rice–Based Yoghurt Stabilized by Red Palm Oil Pickering Emulsion

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Abstract

The development of stable and functional plant-based yogurt alternatives remains challenging due to the absence of dairy proteins that contribute to structure and stability. This study aimed to evaluate the effect of red palm oil (RPO) concentration on the physicochemical, functional, and microbiological properties of a black rice–based yogurt drink stabilized using a Pickering emulsion system. Emulsions containing 0–5% RPO were incorporated into black rice milk and fermented using lactic acid bacteria. The resulting products were analyzed for color, pH, titratable acidity, total soluble solids, viscosity, water-holding capacity, antioxidant activity (DPPH), total phenolic content (TPC), moisture, ash content, and microbial viability. The results showed that increasing RPO concentration significantly influenced physicochemical properties, particularly enhancing lightness (L^*) and yellowness (b^*) due to carotenoid content. pH increased with higher RPO levels, while titratable acidity remained relatively stable. Viscosity and pseudoplastic behavior improved with RPO addition, indicating enhanced structural integrity of the emulsion system. Antioxidant activity increased significantly, with the highest value observed at 4% RPO, whereas TPC remained unaffected, reflecting the distinction between lipophilic and hydrophilic antioxidant fractions. Moisture content decreased and ash content increased with higher RPO levels, indicating compositional changes in the matrix. All samples maintained probiotic viability above the minimum standard (>7 log CFU/mL), although higher oil concentrations slightly reduced bacterial counts. Overall, moderate incorporation of RPO (3.5–4%) provided optimal balance between stability, antioxidant enhancement, and microbial viability. These findings demonstrate that RPO-stabilized Pickering emulsions can serve as an effective strategy to improve the quality and functionality of black rice–based plant yogurt drinks, supporting the development of clean-label, nutritionally enhanced dairy alternatives.

Keywords: Black rice, Emulsion, Fermentation, Pickering.

Agriculture Biotechnology

Posters

Structural, Functional, and Physicochemical Modifications in Starches of Three Minor Millets Induced by Heat–Moisture Treatment: A Comparative Investigation.

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Abstract

This study investigates the cultivar-dependent effects of heat–moisture treatment (HMT) on the structural, physicochemical, functional, and digestibility properties of starches extracted from three small millets—finger millet (FMS), little millet (LMS), and barnyard millet (BMS). Native starches were isolated using alkaline extraction and subjected to HMT at 100 °C for 30, 90, and 150 min. HMT significantly modified functional properties, with notable increases in swelling index (LMS: ~5.67 to 9.90), solubility (up to ~9.84% in BMS), oil absorption capacity (LMS: 1.37 to 2.42 g/g), and freeze–thaw stability (LMS: 0.88 to 1.69 g/g). Structural analyses (XRD, FTIR, and SEM) confirmed crystalline rearrangement, partial granule disruption, and enhanced molecular ordering without altering the fundamental chemical structure. Thermal analysis revealed increased gelatinization temperatures (e.g., BMS peak temperature up to 119.63 °C), indicating improved thermal stability. Rheological studies showed reduced peak viscosity and breakdown values, suggesting strengthened internal bonding and restricted granule swelling. Digestibility analysis demonstrated a significant decrease in rapidly digestible starch (RDS) (e.g., LMS: 0.376% to 0.149%) and an increase in slowly digestible starch (SDS) (up to 3.8%), while resistant starch (RS) remained stable (~46–48%). These changes indicate improved potential for low-glycemic food applications. Among the cultivars, LMS treated for 150 min exhibited the most balanced improvements in functional stability, hydration properties, and digestibility profile. Multivariate analysis (PCA, PLSR) further confirmed strong correlations between structural rearrangements, reduced hydration capacity, and enhanced starch digestibility behavior. Overall, HMT proved to be an effective, clean-label, non-chemical modification technique for tailoring millet starch functionality.

Keywords: Minor millets, Heat-moisture treatment, Resistant starch, Functional food

Baseline Salt Stress Response Profiling in Mustard (*Brassica Juncea*) and Spinach (*Spinacia Oleracea*) for Climate-Resilient Agriculture

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Abstract

Soil salinity is a critical abiotic stress that significantly constrains crop productivity and threatens global food security under changing climatic conditions. The present study aims to evaluate the impact of (sodium chloride) induced salinity stress on two economically important crops, mustard (*Brassica juncea*) and spinach (*Spinacia oleracea*). Plants were subjected to varying concentrations of NaCl under controlled conditions to assess their tolerance and adaptive responses. Growth parameters, including seed germination, root and shoot length, biomass accumulation, and chlorophyll content, were examined to determine the effect of salinity on plant development. In addition, key biochemical indicators such as proline accumulation, antioxidant enzyme activity, and membrane stability were analyzed to understand the underlying stress mitigation mechanisms. The study provides a comparative assessment of salt stress responses in mustard and spinach, highlighting crop-specific variations in tolerance levels. These findings contribute to a better understanding of plant adaptation to salinity and establish a foundational basis for developing sustainable strategies aimed at improving crop resilience under saline environments. The outcomes are expected to support future efforts in designing effective biological interventions for climate-smart agriculture.

Keywords: Salinity stress, NaCl treatment, Mustard, Abiotic stress, Plant physiology, Climate-Resilient agriculture

Optimization of Spent Mushroom Substrate (Sms) Amendments for Enhancing Soil Health and Growth Performance of Spinach (*Spinacia Oleracea* L.)

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Abstract

The sustainable valorization of agro-industrial residues has emerged as a promising strategy to improve soil quality, enhance crop productivity, and promote circular agricultural systems. Among such residues, spent mushroom substrate (SMS), a by-product of mushroom cultivation, represents a nutrient-rich organic resource with significant potential for agricultural reuse. The present study evaluates the effectiveness of SMS as an organic soil amendment for the cultivation of spinach (*Spinacia oleracea* L.) under controlled pot conditions. Experimental treatments were established by incorporating SMS into soil at different rates (5, 10, 15, and 20% v/v), using three amendment formulations comprising mixtures of three SMS types, four SMS types, and a combined mixture of seven SMS types. Plant responses were assessed through germination percentage, vegetative growth parameters, biomass accumulation, and overall crop performance to determine the influence of SMS application on plant development. In parallel, soil physicochemical properties, including pH, electrical conductivity, organic carbon content, and nutrient status, were analyzed to evaluate improvements in soil fertility. Furthermore, key soil enzymatic activities associated with nutrient cycling and microbial functioning were measured to assess the biological enhancement of soil systems following SMS incorporation. The study systematically examines the combined effects of amendment rate and substrate diversity on plant growth and soil functional attributes. The results are expected to identify optimal SMS application levels and combinations that support sustainable spinach production while improving soil health. Overall, this work highlights the potential of SMS as an eco-friendly, cost-effective soil amendment and contributes to the development of sustainable waste management strategies in agriculture.

Keywords: Spent mushroom substrate, SMS, spinach, soil amendment, soil enzymes

Next-Generation PhytoMycoBiological Formulation: Integrating Novel Botanical Extracts with *Trichoderma* Metabolites for Sustainable Control of Soil-Borne Fungal Pathogens

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Abstract

Plant fungal pathogens *Fusarium oxysporum* and *Macrophomina phaseolina* significantly constrain agricultural productivity due to their persistence, wide host range, and resistance to synthetic fungicides. The present study advances PhytoMycoBiological (PMB) strategies by evaluating the antifungal potential of three phytobiological extracts *Achyranthes aspera*, *Ricinus communis*, and *Datura stramonium* along with *Azadirachta indica* as a reference control, across three concentrations (0.128 g/ml, 0.256 g/ml, and 0.384 g/ml) under in vitro conditions. The results revealed a clear concentration-dependent inhibition of radial mycelial growth in both pathogens. Among all treatments, *Ricinus communis* demonstrated the highest antifungal efficacy at all tested concentrations, exhibiting greater compatibility and consistently higher inhibition percentages compared to *Achyranthes aspera*, *Datura stramonium*, and *Azadirachta indica*. The superior performance of *Ricinus communis* is attributed to its rich phytochemical profile, including alkaloids, phenolics, and other bioactive compounds that interfere with fungal cell membrane integrity and metabolic processes. Comparative analysis confirmed a hierarchical efficacy pattern, with *Ricinus communis* emerging as the most potent phytobiological agent. This study highlights the potential of concentration-optimized plant extracts as eco-friendly and sustainable alternatives to synthetic fungicides for the effective management of soil-borne fungal pathogens.

Keywords: Phytobiological extracts, *Macrophomina phaseolina*, *Fusarium oxysporum*, Biocontrol, Sustainable agriculture

Nanoparticle-Conjugated Insecticides; Next-Generation Tools for Enhanced Pest Control in Agriculture

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Abstract

Agricultural productivity is under constant threat from insect pests, resulting in significant crop losses and reduced yield. Although conventional chemical insecticides remain the primary tool for pest management, their extensive use has raised serious concerns regarding environmental pollution, non-target toxicity, and the rapid emergence of resistance in insects. These limitations necessitate a transition towards more efficient pest management approaches. Nanoparticle-conjugated insecticides will be redefining the limits of pest control by transforming conventional molecules into precision-engineered delivery systems with amplified biological performance. By integrating nanotechnology with insecticidal chemistry, these formulations may unlock enhanced efficiency, potency, and target interaction at remarkably low doses. Metallic nanoparticles such as copper oxide will serve not only as carriers but also as active enhancers, exhibiting a synergistic mode of action that are expected to amplify overall insecticidal efficacy. In this study, the insecticide Spinosad is being used for conjugation with CuO nanoparticles. The successful conjugation will be confirmed via physical characterization methods. Conjugation of insecticide with nanoparticles is expected to enhance stability against environmental degradation and improve cuticular penetration, enabling efficient delivery of active ingredients to target sites. The conjugated efficacy of insecticide will be evaluated using model insect in bioassay experiments. If successful, this piece of research can provide a proof of the concept for development of metal nanoparticle-conjugated insecticides as next-generation tools for achieving superior pest control in agriculture.

Keywords: Nanoparticles, Insecticides, Spinosad, Conjugation.

A Circular economy approach of utilizing Bacterial Cellulose towards textile application

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Abstract

Bacterial Cellulose (BC) has proven to be a sustainable biomaterial that has numerous industrial uses like textile, food packaging, and biomedical uses. Orange peel waste-based bacterial isolate was utilized to produce BC through a circular economy approach using pea pod and kitchen waste as an organic and nitrogen source in a sustainable manner. Pea pod powder was acid hydrolyzed using H_2SO_4 and used hydrolyzed broth as a carbon source for BC production and resulted in 14.5g/L BC yield under static submerged condition of 6.0 pH in 7 days. BC pellicle formation on air-liquid interface was initiated after 3rd day of incubation and fully grown on 7th day. The proposed approach showcases the cheaper strategy for BC production using environment-burden wastes as cheap-raw materials for BC production for subsequent usage in textile industries as sustainable polymer with reduced ecological footprint. Although these findings seem to be preliminary but showcases the WtP abilities of agricultural and food waste towards the high-value textile entity with subsequent additional studies towards the streamline textile process application.

Keywords: Bacterial Cellulose Production, Pea pod, static fermentation

Technology-Driven Authentication of Herbal Materials: Integrating Molecular, Analytical, and Computational Approaches

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Abstract

Increasing fraudulent practices such as adulteration and substitution in herbal products urges the immediate need for a reliable authentication strategy. Apart from posing serious health risks, these fraudulent practices also undermine public trust in regulatory bodies and pharmacovigilance systems. Several conventional and advanced approaches including molecular, analytical, and more sophisticated AI-based computational techniques have been developed to authenticate herbal products. Currently applied approaches include sequencing-based (DNA barcoding, DNA-Mini barcoding, DNA-metabarcoding, super barcoding), and non-sequencing-based molecular tools (Bar-HRM), analytical techniques such as chromatographic (TLC, HPTLC, HPLC, GC), spectroscopic (FTIR, NMR), spectrometric (MS, ICP), and hyphenated platforms (LC-MS, GC-MS, ICP-MS), selected in accordance to sample complexity and processing level. Parallely, AI-based approaches such as digital image processing using transfer learning models such as DenseNet and MobileNet, and chemometric analyses using supervised and non-supervised learning models such as PLS-DA and PCA are currently being explored for the interpretation of molecular and chemical profiling data. However, no single method serves as a universal strategy across sample types and processing levels. Therefore, a multidisciplinary strategy focusing on integrative framework is increasingly advocated to complement the shortcomings of alternate methods and build a robust authentication system that enhances detection accuracy and reliability during quality control.

Keywords: Adulteration, Substitution, Authentication

Formulation and Optimization of Millet Based Fermented Foods for Enhanced GABA Production

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Abstract

The formulation and optimization of millet-based fermented foods for enhanced γ -aminobutyric acid (GABA) production have gained increasing attention due to the functional and therapeutic benefits of GABA. This bioactive compound is synthesized through the decarboxylation of L-glutamic acid by glutamate decarboxylase (GAD), primarily mediated by lactic acid bacteria (LAB) during fermentation. Millets, being rich in proteins, fibres, key minerals have functional health benefits. They are precursor elements of amino acid particularly glutamate, serve as promising substrates for GABA-enriched functional foods. Recent studies demonstrate that indigenous LAB strains isolated from millet ecosystems exhibit strong probiotic potential and metabolic adaptability, enhancing nutrient bioavailability and bioactive compound synthesis. Optimization of fermentation parameters—including pH, (30–37°C), incubation time, and inoculum size—significantly influences GABA yield. Supplementation with monosodium glutamate (MSG) and Pyridoxal 5-phosphate (PLP) further enhances production by increasing substrate availability for GAD activity. Comparative research on cereal and pseudocereal fermentation highlights that higher protein content and glutamate availability correlate with increased GABA levels, as observed in fermentation studies using *Levilactobacillus brevis*. Additionally, pre-treatments such as germination, soaking, and thermal processing modify amino acid profiles, improving fermentation efficiency and GABA accumulation. Overall, integrating optimized fermentation conditions with suitable millet selection and microbial strains can significantly enhance GABA production. This approach supports the development of nutritionally enriched, functional millet-based fermented foods with potential applications in managing neurological and metabolic disorders.

Keywords: γ -Aminobutyric Acid (GABA), Millet-based fermented foods, Fermentation optimization, Lactic acid bacteria (LAB)

Harnessing Root Nodule Endophytic Bacteria to Mitigate Drought Stress in Central Indian Soybean Cultivars

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Abstract

Glycine max (soybean) is a globally vital crop for protein and edible oil production; however, its sustainable yield is increasingly constrained by climate change-induced droughts. While *Bradyrhizobium* species are the primary nitrogen-fixing symbionts of soybean, root nodules also harbor diverse non-rhizobial endophytes (NREs) that can significantly influence plant health and stress resilience. This study aimed to harness root-endophytic bacteria to enhance drought tolerance in soybeans. Following the isolation and screening of bacteria from six commercial cultivars for plant growth-promoting (PGP) traits and mutual compatibility, three elite NREs (NRE-202, 208, and 272) and one rhizobial endophyte (RE-11) were selected for *in planta* evaluation. A controlled pot experiment was conducted using seven microbial treatments across two moisture regimes (100% and 75% field capacity) on drought-sensitive (JS9560) and drought-tolerant (JS9752) soybean cultivars. Morpho-physiological and biochemical assessments at 45 days after sowing revealed that drought stress (75% FC) significantly impaired growth and physiology, particularly in uninoculated controls. Conversely, bacterial inoculation mitigated these effects, promoting greater biomass, expanded root architecture, and improved physiological markers, including relative water content, chlorophyll retention, and membrane stability index. Furthermore, inoculated plants exhibited bolstered antioxidant defenses, characterized by elevated CAT, POX, and SOD activities, and a corresponding reduction in oxidative damage (lipid peroxidation, DPPH, and FRAP assays). Notably, the synergistic four-strain consortium (NRE-202, NRE-208, NRE-272, and RE-11) consistently outperformed the single-strain inoculations across all measured parameters. These findings underscore the agronomic potential of integrating NREs with rhizobial symbionts to develop robust and multifaceted bioformulations for climate-resilient agriculture.

Keywords: Soybean, Drought Stress, Microbial Consortium, Root Nodule

Effect of *Azospirillum*-based synergistic combinations under drought and nutrient stress on root architecture of pearl millet (*Pennisetum glaucum* L.)

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Abstract

Pearl millet (*Pennisetum glaucum* L.), a staple cereal of semi-arid regions, faces chronic productivity constraints due to recurrent drought and poor soil fertility, conditions under which root architecture becomes a critical determinant of water absorption, nutrient foraging, and biomass accumulation. *Azospirillum*, a well-established plant growth-promoting rhizobacterium, is recognized for stimulating root elongation and lateral root development, yet its synergistic interactions with other beneficial microorganisms remain underexplored. The present study aimed to evaluate *Azospirillum*-based synergistic combinations for their ability to modulate root system architecture and enhance plant growth of pearl millet under combined drought and nutrient stress. The pot experiment was conducted at the National Phytotron Facility, IARI, under two moisture regimes viz., 75% and 50% field capacity (FC) each with two different nutrient levels; 75% and 50% Recommended Dose of Fertilizer (RDF). The treatments included uninoculated controls, inoculation with *Azospirillum* alone and four synergistic combinations (SC1, SC2, SC3 and SC4 selected based on previous experiments). Growth parameters and root architectural traits (analysed using root scanner), were recorded at 45 days after sowing. Combined stress (50% FC + 50% RDF) significantly suppressed root development relative to optimal conditions (75% FC + 75% RDF). However, inoculated plants under stress exhibited improved root architecture, characterized by greater root biomass and enhanced overall plant growth. Among all treatments, the synergistic combination SC2 consistently outperformed single *Azospirillum* inoculation and uninoculated treatments. These findings highlight root architectural plasticity as a key mechanistic link between microbial inoculation and improved plant performance under stress, positioning *Azospirillum*-based synergistic formulations as effective and sustainable bioinputs for dryland pearl millet cultivation in climate-vulnerable agroecosystems.

Keywords: Pearl millet, *Azospirillum*, Plant growth-promoting bacteria, Moisture.

From Chilling Deficits to Human Crisis: Climate-Induced Occupational Stress, Burnout, and the Role of Emotional Intelligence Among Apple Farmers of Himachal Pradesh

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Abstract

Over ₹6,000 crore is generated by the apple economy in Himachal Pradesh, supporting over 300,000 smallholder families on 100,000 hectares. Reduced winter chilling accumulation is worsening the climate crisis. Temperate apple cultivars need "chilling hours," or periods below 7°C, for consistent bud break, flowering, and fruit set. This study uses IMD gridded datasets and ERA5 reanalysis products, using the Utah and Dynamic Models, to quantify chilling hour trends (1970–2025) in six prominent apple-producing districts: Shimla, Kullu, Kinnaur, Mandi, Sirmaur, and Lahaul & Spiti. It uses bias-corrected CMIP6 outputs under the SSP2-4.5 and SSP5-8.5 scenarios to predict deficits until 2060. Mann-Kendall trend tests will show statistically significant declines across elevation strata (1,000–3,000 m amsl), while GIS-integrated suitability maps will show upward altitudinal shifts in apple cultivation zones. Goleman's Emotional Intelligence (EI) framework in a mixed-methods study Emotional intelligence (EI) will be assessed as a mediating and moderating variable in the association between climate stress and burnout. This novel interdisciplinary framework integrates climate science with human resource management by combining objective bioclimatic data with farmer psychological well-being. Shimla and Kullu are expected to fall below critical thresholds for standard apple cultivars under SSP5-8.5 by 2040 due to statistically significant decreasing chilling accumulation in mid-hill elevation zones. Farmers with high emotional self-regulation have lower burnout rates due to climate stress. The results will provide an evidence-based framework for targeted psychosocial interventions, emotionally intelligent extension services, climate-adaptive varietal transition programs, and resilience-focused horticultural policies for at-risk Western Himalayan Mountain farming communities.

Keywords: Chilling hours, CMIP6 climate projections, occupational stress, burnout, emotional intelligence.

Integrative Taxonomy of *Yepcalphis dilectissima* from the Western Ghats, India

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Abstract

Accurate species identification is essential for biodiversity conservation and effective pest management. The family Noctuidae represents one of the most diverse groups of Lepidoptera; however, several genera remain taxonomically unresolved due to insufficient genital study. The genus *Yepcalphis* Felder is one such poorly studied group with limited morphological and ecological documentation. The present study reports *Yepcalphis dilectissima* (Walker) for the first time from the Western Ghats of India. A comprehensive taxonomic assessment was conducted, integrating adult morphology, wing venation, and a detailed examination of male and female genitalia. Specimens were collected from Western Ghats habitats and were prepared using standard KOH-based dissection protocols, followed by detailed microscopic examination. Key diagnostic features, including uncus, valva, vinculum, juxta, and aedeagus in males, and corpus bursae, ductus bursae, and signum in females, were critically analysed to establish reliable identification criteria. Additionally, host plant associations and updated distributional records were documented to elucidate the ecological significance of the species. The integration of taxonomy with ecological insights enhances species resolution and supports biodiversity assessment, pest monitoring, and sustainable agricultural management under changing environmental conditions.

Keywords: *Yepcalphis dilectissima*, genitalic morphology, Noctuidae taxonomy, host plant association, Western Ghats biodiversity.

Seasonal Dynamics of Moth Diversity in Kinnaur District of Himachal Pradesh

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Abstract

Lepidoptera is one of the most diverse groups of insects. It plays an important role in the ecosystem as pollinators, herbivores, and indicators of environmental changes. This study looks at the seasonal and altitudinal patterns of moth diversity in Kinnaur District, Himachal Pradesh. This area is climate-sensitive and features steep environmental changes and a variety of plant life. We carried out a year-long survey from March 2025 to February 2026 across sixteen sites. These sites represented forested, agricultural, and human-influenced habitats using light traps. We recorded a total of 290 specimens, which included 73 species, 25 subfamilies, and 9 families. Erebidæ was the most common family at 38%, followed by Noctuidæ at 30% and Geometridæ at 16%. This shows their ability to adapt to different ecological conditions. We noticed seasonal variation in moth activity, with peak abundance occurring in summer at 55%. This was followed by post-monsoon at 31%, monsoon at 10%, and minimal activity in winter at 3%. These trends reflect temperature changes and the availability of resources. In terms of altitude, we found the highest diversity at mid-elevations between 1,800 and 2,800 meters. Alpine zones supported fewer species due to harsher climatic conditions. The diversity indices, like Shannon–Wiener H' at 1.56 and Simpson's index at 0.73, indicate moderate diversity and a fairly balanced community structure. This study provides the first detailed account of seasonal moth dynamics in Kinnaur. It also establishes a baseline for future ecological monitoring. We highlight the need to conserve altitudinal habitats to maintain Lepidopteran diversity in the western Himalaya.

Keywords: Moth diversity, Seasonal dynamics, Species richness, Kinnaur District, Himachal Pradesh.

Bio pesticial Potential of *Nerium oleander*: A Toxicological study using *Drosophila melanogaster*

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Abstract

The need for safer, more environmentally friendly alternatives has been brought to light by the growing resistance to synthetic pesticides and their detrimental impact on the environment. In this regard, the current study assesses the biopesticidal potential of *Nerium oleander*, an ornamental plant widely distributed mainly in subtropical and tropical regions worldwide. To determine the main bioactive components of *N. oleander*, methanolic and ethanolic extracts were made and subjected to qualitative and quantitative assay followed by GC-MS analysis. Using *Drosophila melanogaster* as a model organism, taking advantage of its close biological and physiological similarities to agriculturally relevant pest species such as *Drosophila suzukii* and *Zaprionus* species. To evaluate the impacts of this selected plant, toxicological tests were carried out involving various biological parameters such as mortality, fecundity, egg hatching, and larval locomotion. The findings showed that the extracts had considerable biological activity with the ethanolic extract exhibiting more potent effects than the methanolic extract. Strong oviposition deterrent and a significant decrease in fecundity and egg hatching were noted. Additionally, there was a dose-dependent impact on larval locomotion activity. Potential insecticidal compounds, some of which are identified by GC-MS analysis, are responsible for the reported effects. According to the results, the future prospects of *Nerium oleander* lie in its potential development as an eco-friendly, plant-based biopesticide through improved formulations, targeted pest control, and integration into sustainable pest management strategies.

Keywords: *Drosophila*, Fecundity, Growth inhibition, Plant-based biopesticide, Synthetic insecticide, Toxicology

Microbial inoculation–mediated modulation of root exudates under moisture and nutrient stress in pearl millet

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Abstract

Root exudates constitute a critical chemical interface governing plant–microbe interactions and play a significant role in plant adaptation to abiotic stresses. The present study focuses on understanding how microbial inoculation influences root exudate metabolite profiles under combined moisture and nutrient stress conditions. Pearl millet (*Pennisetum glaucum* L.), a staple cereal of semi-arid regions, is frequently exposed to water deficit and low soil fertility, which collectively constrain productivity. Microbial inoculants, particularly *Azospirillum*-based combinations, have shown potential in enhancing plant growth and stress tolerance. Previously selected compatible plant growth-promoting bacterial combination were further evaluated in this study for their role in modulating root exudate composition under stress. Plants were grown under controlled conditions with two moisture regimes (75% and 50% field capacity) and two nutrient levels (75% and 50% Recommended Dose of Fertilizer), along with selected microbial co-inoculation treatments at National Phytotron Facility, IARI. Root exudates were collected at 45 days after sowing and subjected to metabolomic profiling. Comparative analysis indicated distinct differences in metabolite composition between stress and non-stress conditions, with notable variations in inoculated treatments. These observations suggest a shift in metabolic processes associated with stress response and plant–microbe interactions. Overall, the study demonstrates that microbial inoculation influences root exudate composition under combined moisture and nutrient stress, highlighting its role in plant adaptive responses. The findings contribute to a better understanding of metabolite mediated plant–microbe interactions and support the development of microbial strategies for improving crop resilience under multiple stress conditions.

Keywords: Pearl millet, Plant growth-promoting bacteria, Moisture and nutrient stress tolerance, Root exudates, Metabolomics.

Development and Characterization of Modified Pearl Millet Starch-Based Films for Sustainable Food Packaging Applications

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Abstract

The rising concerns for the environment over synthetic plastic packaging have fueled global interest in biodegradable, renewable, and agro-based alternatives. Starch has emerged as a promising biopolymer due to its wide availability, biodegradability, potential to form films, and inexpensive cost. Pearl millet, an unexplored yet nutrient-rich cereal extensively cultivated in arid and semi-arid locations, has a high starch content that has largely gone undiscovered for industrial purposes. This study aims to develop and characterize modified pearl millet starch-based films as an environmentally sustainable alternative to traditional food packaging materials, while also fostering opportunities for value addition and the enhancement of agricultural. The research involves the systematic extraction of starch from pearl millet, followed by its modification utilizing physical, chemical and enzymatic procedures. These modification approaches are projected to enhance starch's essential functional qualities, such as structural stability, heat resistance, mechanical strength, and water vapor barrier capacity. To enhance the films' functional performance, postbiotics—non-viable microbial metabolites renowned for their antibacterial and antipathogenic properties—are introduced into the film matrix. The Physicochemical properties of the developed films will be accessed via techniques such as Fourier Transform Infrared Spectroscopy (FTIR), Scanning Electron Microscopy (SEM), tensile strength analysis, moisture susceptibility testing, and measurements of water vapor transmission rate. Furthermore, the efficiency of the films for real food packaging applications will be examined by shelf-life studies on chosen perishable food products such as mushrooms or tomatoes. Beyond scientific development, this research emphasizes the socioeconomic dimension by highlighting pearl millet as a raw resource with significant potential for industrial value addition.

Keywords: Pearl millet starch, Starch Modifications, Biodegradable films, Active packaging, Sustainable Materials.

Next-Generation PhytoMycoBiological Formulation: Integrating Novel Botanical Extracts with *Trichoderma* Metabolites for Sustainable Control of Soil-Borne Fungal Pathogens

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Abstract

Plant fungal pathogens *Fusarium oxysporum* and *Macrophomina phaseolina* significantly constrain agricultural productivity due to their persistence, wide host range, and resistance to synthetic fungicides. The present study advances PhytoMycoBiological (PMB) strategies by evaluating the antifungal potential of three phytobiological extracts *Achyranthes aspera*, *Ricinus communis*, and *Datura stramonium* along with *Azadirachta indica* as a reference control, across three concentrations (0.128 g/ml, 0.256 g/ml, and 0.384 g/ml) under in vitro conditions. The results revealed a clear concentration-dependent inhibition of radial mycelial growth in both pathogens. Among all treatments, *Ricinus communis* demonstrated the highest antifungal efficacy at all tested concentrations, exhibiting greater compatibility and consistently higher inhibition percentages compared to *Achyranthes aspera*, *Datura stramonium*, and *Azadirachta indica*. The superior performance of *Ricinus communis* is attributed to its rich phytochemical profile, including alkaloids, phenolics, and other bioactive compounds that interfere with fungal cell membrane integrity and metabolic processes. Comparative analysis confirmed a hierarchical efficacy pattern, with *Ricinus communis* emerging as the most potent phytobiological agent. This study highlights the potential of concentration-optimized plant extracts as eco-friendly and sustainable alternatives to synthetic fungicides for the effective management of soil-borne fungal pathogens.

Keywords: Phytobiological extracts, *Macrophomina phaseolina*, *Fusarium oxysporum*, antifungal activity, biocontrol, sustainable agriculture

Stress-Tolerant Endophytic Bacteria from Sugarcane (Co 86032) as Potential Bioinoculants for Enhancing Salinity and Drought Resilience

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Abstract

Abiotic stresses such as salinity and drought are major constraints to sugarcane productivity, adversely affecting plant growth, physiological processes, and nutrient acquisition. Endophytic bacteria capable of tolerating such stresses. In the present study, 205 endophytic bacterial isolates obtained from leaf (51), cane (67), and root (87) tissues of sugarcane variety, Co 86032 were systematically evaluated for salinity (5, 10, and 15% NaCl) and osmotic stress tolerance using polyethylene glycol (PEG 6000; 10, 20, and 30%). Based on optical density (OD₆₀₀), isolates were classified as highly sensitive (<0.3), sensitive (0.3–0.39), tolerant (0.4–0.5), and completely tolerant (>0.5). At 10% PEG, 62% of isolates were completely tolerant, whereas tolerance declined significantly ($p < 0.05$) at higher stress levels, with 48% and >85% of isolates categorized as highly sensitive at 20% and 30% PEG, respectively. Only 7% of isolates retained complete tolerance at 20% PEG, while no isolates maintained OD > 0.4 at 30% PEG, indicating a critical osmotic threshold. Tissue-wise comparisons revealed that cane-derived isolates exhibited a significantly higher proportion of tolerant and completely tolerant strains (32%) than root (~1%) and leaf (18%) isolates ($p < 0.05$). Under salinity stress, 92% of isolates tolerated 5% NaCl, 74% tolerated 10% NaCl, and only 28% sustained growth at 15% NaCl, with cane isolates demonstrating superior high-salinity tolerance. Two-way ANOVA confirmed significant effects of stress intensity and tissue origin on bacterial growth response ($p < 0.05$). This study provides a comparative, tissue-specific evaluation of salinity and PEG-induced osmotic stress tolerance in sugarcane endophytic bacteria, identifying elite isolates with dual-stress resilience and bioinoculant potential. The identified stress-tolerant endophytic strains are expected to serve as next-generation bioinoculants for sustainable agricultural systems

Keywords: Endophytic bacteria, Abiotic stress tolerance, Salinity stress, Bioinoculants, Climate-resilient agriculture

Antibacterial Activity of Ethanolic and Aqueous Extract of *Hibiscus rosa-sinensis* Leaves Against Bacteria Isolated from Soil and Plant Samples

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Abstract

The growing prevalence of antibiotic-resistant microorganisms has intensified the search for alternative antimicrobial agents derived from medicinal plants. *Hibiscus rosa-sinensis* is widely recognized for its rich phytochemical composition and traditional therapeutic applications. The present study was undertaken to evaluate and compare the antibacterial activity of ethanolic and aqueous leaf extracts of *Hibiscus rosa-sinensis* against bacterial isolates obtained from soil and plant samples. Bacterial strains were isolated and identified through morphological and biochemical characterization, including *Staphylococcus aureus* (M1), *Pseudomonas aeruginosa* (M3), and *Lactobacillus* (Y1). Leaf extracts were prepared using ethanol (Soxhlet extraction) and distilled water (maceration method). Antibacterial activity was assessed using the agar well diffusion technique, and zones of inhibition were measured. The ethanolic extract demonstrated higher antibacterial activity, with zones of inhibition of 17 mm against *Pseudomonas aeruginosa* and 16 mm against *Staphylococcus aureus*, while the aqueous extract showed comparatively lower activity (16 mm and 12 mm respectively). No significant inhibition was observed against *Lactobacillus*. Phytochemical screening confirmed the presence of tannins, phenols, alkaloids, and saponins, which contribute to antimicrobial activity. The results suggest that the enhanced activity of the ethanolic extract is due to its superior ability to extract bioactive phytochemicals. The study highlights the potential of *Hibiscus rosa-sinensis* as a natural antimicrobial agent and supports further investigation into its pharmaceutical applications.

Keywords: *Hibiscus rosa-sinensis*, Antibacterial activity, Ethanolic extract, Phytochemicals, Antibiotic resistance

Determination of the Mineral Composition of the Krantaus Deposit's Glaucinite Sands, Qualitative and Quantitative

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Abstract

The development of effective and sustainable fertilizers based on regional mineral resources is required due to the rising worldwide need for agricultural productivity, rising production costs, and environmental issues. In order to evaluate their potential as a raw material for the synthesis of complex mineral fertilizers, this study examines the mineralogical composition and phase properties of glauconite sands from the Krantau deposit in the Republic of Karakalpakstan. The mineral phases and their distribution across various particle size fractions were ascertained via both qualitative and quantitative X-ray diffraction (XRD) investigations. MDI JADE 5.0 software was used for phase identification, and Profex 3.9.2, a program based on the Rietveld refinement approach, was used for quantitative analysis. The findings show that the predominant mineral phases are quartz and glauconite, with feldspar minerals (microcline, anorthite, and albite) and clay minerals (kaolinite, muscovite, montmorillonite, and illite) following. Additionally, found were trace amounts of auxiliary phosphate compounds and halite. To identify the mineral phases and their distribution across various particle size fractions, X-ray diffraction (XRD) investigations were conducted both qualitatively and quantitatively. The Rietveld refinement method-based Profex 3.9.2 program was used for quantitative analysis, and MDI JADE 5.0 software was used for phase identification. The findings show that the most common mineral phases are glauconite and quartz, with feldspar minerals (anorthite, albite, and microcline) and clay minerals (illite, muscovite, montmorillonite, and kaolinite) following. There were also trace amounts of accessory phosphate compounds and halite.

Keywords: Quantitative phase analysis, Qualitative X-ray diffraction study, Glaucinite sand

Statistical Optimization Of Conditions For The Extraction Of Ferulic Acid And Vanillin From Rice Bran Hydrolysate Using Box-Behnken Design

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Abstract

Vanillin, a high-value aromatic compound widely used in food, pharmaceutical, and cosmetic industries, is increasingly being produced through sustainable biotechnological approaches. The present study investigates the valorization of rice bran, an underutilized agro-industrial by-product, for the efficient production of vanillin via physicochemical pretreatment and statistical optimization. Initially, a one-factor-at-a-time approach was employed to optimize key hydrolysis parameters, including pH, substrate concentration, autoclaving pressure, and pulping time, for enhanced release of ferulic acid—the primary precursor of vanillin. Maximum yields during preliminary optimization were observed under highly alkaline conditions (pH 13), elevated substrate concentration (15% w/v), moderate pressure (15 psi), and optimal pulping duration (30 min), indicating the critical role of alkaline hydrolysis in disrupting lignocellulosic structures.

Subsequently, Response Surface Methodology (RSM) using a Box–Behnken Design (BBD) was applied to evaluate the combined effects and interactions of the selected variables. A total of 27 experimental runs were conducted to develop second-order polynomial regression models for predicting vanillin and ferulic acid yields. The optimized conditions (pH 13.0, 8% substrate concentration, 20 psi pressure, and 17.5 min pulping time) resulted in a maximum vanillin yield of 1466.07 µg/mL and ferulic acid yield of 454.54 µg/mL. The developed models exhibited high statistical significance, with strong coefficients of determination ($R^2 = 0.9756$ for ferulic acid and 0.8919 for vanillin), confirming model adequacy and reliability.

Validation experiments demonstrated close agreement between predicted and experimental values, further supporting the robustness of the optimization strategy. The study highlights the synergistic influence of physicochemical parameters on biomass depolymerization and phenolic compound release, emphasizing the importance of parameter interaction in maximizing yield.

Overall, this research establishes an efficient, eco-friendly, and economically viable approach for vanillin production from rice bran hydrolysate. The integration of agro-waste valorization with statistical optimization provides a promising platform for sustainable bioprocess development and potential industrial-scale applications.

Keywords: Statistical Optimization, Response Surface Methodology, Vanillin, Box–Behnken Design

Environment Biotechnology

Oral Presentation

Harnessing Spiritual Intelligence for Sustainable Environmental Adaptation to Climate Change: A Pathway to Resilience

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Abstract

This study investigates the impact of spiritual intelligence (SQ) on fostering resilience and eco-conscious behaviors essential for sustainable environmental climate adaptation, addressing a notable gap in adaptation frameworks traditionally centered on technological and policy approaches. The objectives of the research are to investigate the Role of Spiritual Intelligence (SQ) in Climate Adaptation and to Offer Practical Insights for Climate Resilience Frameworks. Through a quantitative analysis of 303 participants, results reveal that a higher spiritual quotient (SQN) is strongly correlated with both spiritual quality of consciousness (SQC) and spiritual quality of resilience (SQR). These findings underscore SQ's role in building intrinsic motivation for adaptive, sustainable behaviors and resilience in the face of environmental climate-related stressors. The study suggests that integrating SQ into organizational and community resilience frameworks offers a promising avenue to enhance personal and collective responses to environmental climate challenges, helping to transform eco-anxiety into proactive environmental stewardship. Additionally, SQ-driven approaches may be particularly beneficial to younger generations experiencing eco-anxiety, providing them with psychological resources to engage meaningfully in climate solutions. This research positions SQ as a powerful, complementary resource for fostering long-term ecological well-being and environmental responsibility. By linking SQ with resilience and environmental responsibility, this study offers new insights into how intrinsic values can drive adaptive behaviors, moving beyond traditional external approaches.

Keywords: Environment, Eco-Consciousness, Spiritual Intelligence, Resilience, Environmental Stewardship.

Simulation-based petri net analysis of central carbon metabolism in *Scenedesmus* for gene level optimization of carbohydrate production

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Abstract

The use of microalgae like *Scenedesmus* for the sustainable production of carbohydrates has been recognized because of their fast growth and effective carbon fixation. Metabolic engineering of such organisms, which involves optimizing the pathway flux towards carbohydrate production, is still an open area of research. Thus, a comprehensive understanding of the central carbon metabolism network is required to achieve success in metabolic engineering of microalgae. This study proposes a modeling approach that utilizes the Petri net method to model the central carbon metabolic network of *Scenedesmus*. The proposed model includes the glycolytic pathway, pentose phosphate, Calvin cycle and tricarboxylic acid cycles. Network analysis through reachability and state-space studies was conducted to investigate the dynamic behavior of the network, identify the system bottlenecks. The model was used to identify key metabolic reactions that govern carbon partitioning. A target gene was found where its modification can result in improved carbohydrate production with no adverse effect on the system. Simulation results show that manipulation of the target gene promotes carbohydrate accumulation without compromising other biological processes. In general, this study offers an effective *in silico* method for identifying targets for gene manipulation aimed at increasing the efficiency of carbohydrates production by microalgae. The accumulated carbohydrates can serve as a carbon feedstock for the biosynthesis of polyhydroxyalkanoates (PHA), offering an environmentally friendly alternative to conventional plastics.

Keywords: Petri net, Mathematical modelling, *Scenedesmus*, Central Carbon Metabolism, Polyhydroxyalkanoates (PHA).

Isolation and Screening of Triclosan Degrading Microorganisms

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Abstract

Pharmaceuticals and Personal Care Products (PPCPs) are a class of emerging pollutants that have gained significant attention due to their continuous release and persistence in aquatic environments. Among these, triclosan is a widely used antimicrobial agent found in various consumer products such as toothpaste, soaps, detergents, toys, and surgical disinfectants. Its presence in aquatic systems raises concerns due to its potential to accumulate in lower trophic organisms and subsequently transfer through the food chain, thereby affecting higher organisms. The present study focuses on the isolation and screening of triclosan-degrading microorganisms from water samples collected from the Hindon River. Selective enrichment techniques were employed to isolate potential degraders, followed by primary and secondary screening to identify microorganisms capable of utilizing triclosan as a substrate. The degradation potential of selected isolates was evaluated by monitoring microbial growth patterns and assessing triclosan concentration over time. Further characterization of efficient isolates was carried out using morphological, biochemical, and molecular analyses to determine their taxonomic identity and functional capabilities. The results demonstrated a decline in viable cell count with increasing triclosan concentration, decreasing from 1.2×10^3 CFU/mL in the control to 300 CFU/mL at 100 mg/L and 11 CFU/mL at 500 mg/L. Additionally, the isolates exhibited clear halo zone formation on triclosan-containing media, indicating their potential biodegradation activity.

Keywords: Pharmaceuticals and Personal Care Products (PPCPs), Triclosan, Biodegradation, Microbial Isolation, Bioremediation.

Bacterial Cellulose Production by *Komagataeibacter saccharivorans*: Influence of Culture Media Composition

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Abstract

Bacterial cellulose (BC) is an extracellular polysaccharide produced by acetic acid bacteria. It is known for high purity, biodegradability, high mechanical strength, good water-retention ability, and a distinctive fibrillar nanostructure. Unlike plant cellulose, BC lacks lignin and hemicellulose, making it an ideal choice for medical, food, environmental, and industrial applications. This study aimed at exploring the effect of culture media on bacterial growth kinetics and bacterial cellulose production by *K. saccharivorans* under static culture conditions. We selected three culture media, namely HS medium, YPM medium, and Referred Son medium. Overnight grown bacterial culture was inoculated in culture media flask (100 mL) and incubated under static conditions at 30°C for 7 days. BC sheets developed at the air-liquid interface were recovered and purified by alkali treatment method and successive washes to remove residual bacterial cells and medium constituents. The purified cellulose was dried and subjected to yield comparison and structural analysis. Results showed that the composition of the medium significantly impacted the BC thickness and its yield. Physicochemical characterization using UV-Vis and FTIR analysis was conducted to characterize the chemical structure of cellulose. The FTIR results showed the presence of functional peaks corresponding to hydroxyl groups (-OH), C-H stretching, and β -1,4 glycosidic bonds, indicating successful production of BC from all the different media. These findings highlight the potential of optimizing culture media composition to enhance bacterial cellulose yield without compromising its fundamental physicochemical properties.

Keywords: Bacterial Cellulose, FTIR, *Komagataeibacter*, Culture media, Static culture.

Sustainable and environment friendly Biopolymer plastics from the Chips industry waste

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Abstract

The aim of this study is to produce biodegradable biopolymer plastics from organic waste of chips-industry, banana and potato peel waste. As in India, banana and potato chips are enjoyed by many consumers, and their waste has not been used properly. Food industry wastes can be considered a fascinating and profitable source of synthesis of packaging materials. Firstly, we dried raw banana peels and potato peels in an oven for overnight at 50-70°C, grinded them into fine powdered, and dissolved them into an alkaline solution of Sodium Hydroxide for degrading lignin, hemicellulose, micellulose, and other complex polymers in plant biomass. And used bio-based binding agents for casting like glycerol, a plasticizer; sodium alginate along with carboxymethyl cellulose (CMC) as a binding agent to enhance the flexibility. Bioplastics were black in color (without adding bleaching agents like H₂O₂ or NaOCl) and showed heat resistance, water resistance and microbial growth resistance properties to a greater extent. Further, the molecular structure is investigated and confirmed by FTIR spectroscopy. The study proves that a combination of raw banana peels, which are abundant in cellulose, hemicellulose, lignin, polyphenol and pectin leads to high flexibility and elongation. Whereas potato peels, which contain starch like amylose and amylopectin contribute to high tensile strength and elasticity. This project is helpful in recycling food waste into a valuable product which can be expanded by exploring relatable fields such as biochar, biofuel, and bio composting, supporting a sustainable zero waste future.

Keywords: Food waste, Biodegradable biopolymer, Potato peel, Banana peel.

Towards Sustainability: Innovations and Environmental Impacts in Leather Manufacturing for the Textile Industry

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Abstract

The textile industry can utilise all kinds of resources available in nature, from animals to plants and to microbes. But evolution of textile materials has intensely hampered nature as well. From very ancient times people are attracted by animal leather and fur for their aesthetics and practical qualities, but in recent years, these materials have become a subject of debate due to increasing awareness of ethical rights and concerns surrounding animal welfare and environmental impact. If we talk about eco-friendly, cruelty-free sustainable fashion then plant-based leather, waste-based leather offers stylish alternatives to traditional leather. This review article discusses about the real-world applications of scalability, cost analysis of the products. This also talks about how sustainable approach of making bio-leathers connects to carbon neutrality, SDG12, and SDG13. This article compares productivity, processing, new approaches and environmental impact related to all types of leathers. This article also deals with life cycle assessment (LCA) of leather industry.

Keywords: Sustainable development alternatives, Bio leather, Life cycle assessment (LCA), Circular Bioeconomy, Plant-based leather, Tensile strength.

Bacteriophage Diversity Across Scales: Structural Insights from MCP and Metagenomic Evidence from the Yamuna River

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Abstract

The global escalation of antimicrobial resistance has driven the exploration of bacteriophages as alternative therapeutics. In this study, the Major Capsid Protein (MCP) was utilized as a conserved structural marker to investigate phage diversity and phylogenetic relationships across multiple clinically relevant bacterial genera. Comparative sequence analysis revealed notable host-specific variation alongside strong conservation, particularly among Enterobacteriaceae-infecting phages, where sequence identity approached ~99%. A substantial proportion (~73%) of these phages exhibited a conserved structural organization corresponding to the 3J7X MCP, indicating its evolutionary persistence. To evaluate functional relevance, molecular docking of the 3J7X MCP with selected disaccharide ligands demonstrated favorable binding interactions, suggesting a role in capsid stability and structural resilience. These findings support the potential application of this MCP framework in designing stable phage formulations and engineered therapeutic strategies. To extend these structural and evolutionary insights to a real-world context, a combined wet-lab and metagenomic investigation of the Yamuna River virome was conducted. This analysis identified 28,993 viral sequences across 21 viral classes, with *Caudoviricetes* as the predominant group (49%). Host assignment indicated that 57% of phages were associated with characterized bacterial hosts, whereas 43% remained unclassified, highlighting substantial unexplored diversity. Among these, 2,642 phages were linked to pathogenic bacteria, including 544 associated with clinically significant ESKAPE pathogens. Overall, this integrative approach provides comprehensive insights into phage evolution, structure, and environmental diversity, underscoring their potential in combating multidrug-resistant infections.

Keywords: Bacteriophages, Docking, ESKAPE Major Capsid Protein, Metagenomics, Phylogenetic.

A Circular Bioeconomy Approach for Sustainable Carbon Capture, Wastewater Valorization and Bioenergy Production via Integrated Algal Biorefinery Systems

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Abstract

The World is generally facing two interconnected challenges the increase in CO₂ level and the growing energy crisis particularly the increasing cost rate and scarcity of conventional fuels such as LPG. With rapid industrialization and agriculture expansion due to Population Explosion nutrient rich waste water discharge is also pose a great environmental challenge to the ecosystem which demands the integrated, cost effective and environment friendly solutions which not only treat waste but generate energy. Conventional methods require more energy to treat waste water and also fails to treat waste as a valuable source rather than garbage, while establishment of carbon capture technologies requires intense cost. The key objectives include algal biomass yield, waste water utilization, CO₂ fixation efficiency of algae and biogas yield. This study proposes a biorefinery system that combine open high-rate algal raceway ponds (HRAPs) having cultivation of microalgae occur, generally fed with nutrient-rich wastewater and anaerobic digestion (AD) to simultaneous reduce CO₂ emission and produce biogas which can serve as a renewable alternative to conventional cooking fuels like LPG. In addition to this it combines carbon capture with wastewater treatment and small-scale bioenergy production, creating a practical solution to the ongoing energy crisis. By turning waste into useful energy, the system helps to reduce their reliance on fossil fuels while also decrease environmental pollution. This research summarizes a sustainable and circular bioeconomy integrated process to convert environmental challenges into opportunities for cleaner energy production and efficient resource recovery.

Keywords: Microalgae, carbon capture, wastewater treatment, circular bioeconomy, biogas production.

Preprocessing techniques for digestate derived from a single-stage biogas plant

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Abstract

Food waste is one of the most common types of organic waste generated across the world, with an amount of 1.05 billion tons, yet managing it effectively continues to be a major environmental challenge. Anaerobic digestion (AD) has emerged as the most promising technology to turn waste into energy. The AD process converts organic waste into a renewable source of energy, i.e., biogas and another byproduct known as digestate. Biogas mainly comprises methane and carbon dioxide and can be used for heating and electricity generation, whereas digestate consists of essential elements such as nitrogen, phosphorus, and potassium (N, P, and K) that can be used in agriculture as a fertilizer and soil conditioner to improve crop productivity. The digestate is applied in both solid and liquid form; however, the liquid fraction of the digestate has suspended, dissolved, and organic solids, which may restrict its efficiency and wider application. In the present study, the food waste digestate was obtained from a single-stage biogas digester located at Jaypee University of Information Technology, Solan, Himachal Pradesh campus. Physical and chemical pretreatment methods were employed to enhance digestate quality, particularly in terms of solids removal. The physical and chemical processes used for the removal of large and fine suspended particles include screening, sedimentation and coagulation-flocculation, and their effectiveness was evaluated using various physicochemical parameters. The study findings indicate that the implementation of different pretreatment techniques can be a sustainable and cost-effective strategy for lowering dependence on chemical-based fertilizers and supporting the circular economy.

Keywords: Food waste, Anaerobic digestion, Biogas, Digestate, Coagulation-Flocculation

Optimization of Bioplastic preparation from Banana Peel waste and their characterization

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Abstract

Today, bioplastics have become an important area of research due to the adverse effects of the conventional plastics such as the use of fossil fuel for their production, they are non-biodegradable and can cause environment pollution. To overcome these problems and for the safety of the environment, plastics needs to be replaced with sustainable substitutes, especially from waste materials which are of little or no use otherwise. In this study, bioplastic has been made using organic waste like banana peels which also contributes to waste management and environmental protection. Peels were collected and washed during the process separately, before pretreatment. Then they were boiled and dried to soften the fiber and starch, and ground into a smooth paste. A plasticizer (glycerol and sorbitol) was added to this paste and the pH was adjusted at 5-7 with 0.5 M HCl and NaOH. The procedure was optimized one by one and several samples of bioplastic were prepared. The results showed that among three different antioxidants and different concentration the lighter color was obtained in the sample containing 10% sodium metabisulfite (SMBS) than other antioxidants (Ascorbic acid and Citric acid). Sorbitol based bioplastics were better than Glycerol based bioplastics in terms of biodegradability, moisture content, mechanical strength and solubility in water and alcohol. The FTIR analysis was performed and showed the presence of functional groups on bioplastics such as hydroxyl (O–H), carbonyl (C=O) and (C–O), which confirmed the presence of polysaccharides in the sample and interaction of biopolymer chains with plasticizers. Ultimately, the bioplastic obtained exhibits positive features and promise as a sustainable alternative of conventional plastics.

Keywords: Bioplastic production, Use of organic waste, Plasticizer, Biodegradability, FTIR Analysis

***Pleurotus ostreatus* as a potent bioremediation agent for the removal of Methylene Blue dye in wastewater and the effect of inducers**

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Abstract

The use of synthetic dyes is widespread in various industrial sectors, and they are often disposed of in water bodies without being properly treated. The complex structure and nature of these dyes make them quite challenging to remove from wastewater; thus, they become potential pollutants that can cause serious damage to the environment. Several methods use white rot fungi and other organisms for dye degradation, therefore becoming a hot topic of research lately. The present study is aimed at identifying the optimum conditions for the growth of *Pleurotus ostreatus* in terms of pH, temperature, and incubation time for maximum biomass production. The study further investigates the efficacy of the fungus, *P. ostreatus*, together with laccase-inducing substances such as copper sulfate, tannic acid, ethanol, Tween-80 and gallic acid, for the efficient elimination of the cationic methylene blue dye. The fungus was cultivated with different laccase inducers and varying concentrations of methylene blue dye. The dye decolorization was noted as a measure of the amount of dye removed in the different treatments of the experiment. The treatment having *P. ostreatus* in media along with tannic acid was the most efficient in methylene blue removal, with rates as high as $99 \pm 0.54\%$. It was also observed that *P. ostreatus*, along with the other inducer treatments, performed better than the control treatment at lower MB concentrations. This implies that *P. ostreatus* has the potential of being a reliable biosorbent and bioremediation agent in the process of textile dye removal. Also, compounds such as tannic acid and copper sulfate may then be used to enhance its performance by stimulating its ligninolytic enzyme system.

Keywords: Wastewater, *Pleurotus ostreatus*, Methylene blue dye

Fabrication and Characterization of Bacterial Cellulose and Chitosan Composites

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Abstract

This review presents a focused overview of the fabrication and characterization of cellulose–chitosan biocomposites developed for food packaging applications. Owing to their biodegradability, biocompatibility, and inherent antimicrobial activity, cellulose–chitosan biocomposites have emerged as promising sustainable alternatives to conventional petroleum-based packaging materials. The review highlights recent fabrication strategies, including solvent casting, electrospinning, layer-by-layer assembly and incorporation of nanoscale reinforcements aimed at enhancing key functional properties such as mechanical strength, flexibility, thermal stability, and barrier performance against moisture and gases. Comprehensive emphasis is given to characterization techniques employed to assess structural, physicochemical, mechanical and antimicrobial properties relevant to food packaging. Furthermore, it provides insights into the role of cellulose–chitosan nanocomposites in extending food shelf life through improved protection against microbial contamination and environmental degradation. This review highlights the current challenges, scalability considerations, and future research directions required to advance the commercial adoption of cellulose–chitosan biocomposites as eco-friendly food packaging materials.

Keywords: Cellulose, Biocomposites, Thermal Stability, Antimicrobial Properties.

Bioplastics from Agricultural Waste: Production, Characterization, and Environmental Sustainability Assessment

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Abstract

The growing environmental impact of traditional petroleum-based plastics, generating more than 400 million metric tonnes of waste each year, highlights the pressing need for sustainable and eco-friendly alternatives. Bioplastics, synthesized from renewable biomass feedstocks, have emerged as a promising solution to mitigate plastic pollution while supporting the transition towards a circular bioeconomy. In this study, we investigate the production, characterization, and environmental performance of bioplastics derived from lignocellulosic agricultural residues, specifically rice husk, sugarcane bagasse, and wheat straw, which are abundantly available in the Indian subcontinent. Two primary biopolymers, polylactic acid (PLA) and polyhydroxyalkanoates (PHA/PHB), were synthesized through microbial fermentation pathways employing *Lactobacillus rhamnosus* for lactic acid production and *Cupriavidus necator* under nitrogen-limited fed-batch conditions for PHA accumulation. Feedstock pretreatment involving alkaline hydrolysis and dilute acid saccharification was optimized to maximize fermentable sugar yields. Recovered polymers were blended at varying PLA/PHA ratios using twin-screw extrusion and reinforced with cellulose nanocrystals to enhance mechanical and barrier properties. Composite materials were characterized by FTIR, DSC, TGA, SEM, and standard ASTM mechanical testing protocols. Biodegradation behavior was evaluated across soil burial (ISO 17556), industrial composting (ASTM D5338), and marine environments (ASTM D6691) over 180 days, confirming controlled degradation without ecotoxicological impact, as validated by *Daphnia magna* acute toxicity assays and seed germination bioassays. Life cycle assessment (ISO 14040) demonstrated a significantly reduced global warming potential and fossil resource depletion compared to conventional PET and polyethylene. Techno-economic analysis projected competitive minimum selling prices at commercial scale, identifying fermentation yield and feedstock cost as primary drivers. These results demonstrate that PLA/PHA biocomposites produced from agricultural waste are practical, eco-friendly, and cost-effective substitutes for conventional fossil-based plastics, with significant potential for use in food packaging, agricultural films, and disposable consumer products.

Keywords: Bioplastics, Polyhydroxyalkanoates (PHA), Polylactic acid (PLA), Agricultural waste valorization, Biodegradation

Evaluation of the Phytoremediation Potential and Bioaccumulation Capacity of *Ocimum basilicum* for Heavy Metal Contaminated Soil

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Abstract

Soil contamination by heavy metals poses a significant threat to ecological integrity and public health. While conventional remediation techniques are often cost-prohibitive and environmentally disruptive, phytoremediation offers a sustainable, "green" alternative by leveraging plant-based mechanisms to sequester or detoxify contaminants. This study evaluates the phytoremediation potential of *Ocimum basilicum* in metal contaminated environment, specifically targeting Lead (Pb), Cadmium (Cd), and Nickel (Ni). A 21-day pot experiment was conducted using soil spiked with increasing concentrations of Pb, Cd, and Ni. Following the incubation period, metal accumulation in plant tissues was quantified using Inductively Coupled Plasma Mass Spectrometry (ICP-MS). Growth parameters and physiological changes were monitored to assess the plant's tolerance. Statistical analysis and data visualization were performed in R Studio to determine the bioaccumulation capacity and the overall remediation efficiency of *O. basilicum*. Preliminary findings indicate that *O. basilicum* exhibits a robust tolerance to the selected heavy metals, with measurable uptake across all concentration gradients. The plant's physiological response suggested active metabolic adaptation to metal stress, though biomass variations were observed at higher concentrations. The results suggest that *O. basilicum* is a viable candidate for the phytoremediation of Pb, Cd, and Ni. This study underscores the utility of aromatic plants in soil decontamination strategies, providing a dual-purpose approach to environmental management through sustainable botanical interventions.

Keywords: Environment, Heavy metal, Plant, Remediation, Soil, Sustainable

Deciphering the Impact of Alginate and Biochar Immobilization on the Metals-Bioleaching Efficiency of *Chromobacterium violaceum* from Electronic Waste

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Abstract

Soil contamination by heavy metals poses a significant threat to ecological integrity and public health. While conventional remediation techniques are often cost-prohibitive and environmentally disruptive, phytoremediation offers a sustainable, "green" alternative by leveraging plant-based mechanisms to sequester or detoxify contaminants. This study evaluates the phytoremediation potential of *Ocimum basilicum* in metal contaminated environment, specifically targeting Lead (Pb), Cadmium (Cd), and Nickel (Ni). A 21-day pot experiment was conducted using soil spiked with increasing concentrations of Pb, Cd, and Ni. Following the incubation period, metal accumulation in plant tissues was quantified using Inductively Coupled Plasma Mass Spectrometry (ICP-MS). Growth parameters and physiological changes were monitored to assess the plant's tolerance. Statistical analysis and data visualization were performed in R Studio to determine the bioaccumulation capacity and the overall remediation efficiency of *O. basilicum*. Preliminary findings indicate that *O. basilicum* exhibits a robust tolerance to the selected heavy metals, with measurable uptake across all concentration gradients. The plant's physiological response suggested active metabolic adaptation to metal stress, though biomass variations were observed at higher concentrations. The results suggest that *O. basilicum* is a viable candidate for the phytoremediation of Pb, Cd, and Ni. This study underscores the utility of aromatic plants in soil decontamination strategies, providing a dual-purpose approach to environmental management through sustainable botanical interventions.

Keywords: Environment, Heavy metal, Plant, Remediation, Soil, Sustainable

Environment Biotechnology

Posters

Sustainable Remediation of Hexavalent Chromium: Synthesis, Mechanistic Insights, and Performance of Green Iron-Oxide Nanoparticles in Cr (VI) Adsorption

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Abstract

Heavy metals are a significant environmental problem due to their toxicity, bioaccumulation, and persistence. Hexavalent chromium [Cr (VI)] pollution has attracted a lot of attention due to its high mobility, solubility, and possible toxicity. While conventional physical and chemical synthesis techniques provide accessible routes to iron oxide nanoparticles, their utility is frequently limited by high energy consumption, the use of toxic reagents, and poor control over particle morphology. Recently, green synthesis of nanoparticle production has emerged as an alternative for sustainable and environmentally safe remediation. Due to their expansive specific surface area, green-synthesized iron nanoparticles exhibit exceptional efficiency in the remediation of Cr (VI) from aqueous solutions. Hence, this study used spinach (*Spinacia oleracea*), a hyper-accumulator plant extract, to prepare iron oxide nanoparticles and investigated the effects of synthetic conditions on the subsequent remediation performance. In addition, the characterization of the produced nanoparticles was done via DSC, FTIR, XRD, FE-SEM, and TEM. The size of the synthesised nanoparticles turned out to be less than 32 nm. Moreover, batch experiments were conducted to identify the optimal conditions and environment needed for maximum adsorption. The parameters included were pH, temperature, initial Cr (VI) concentration, nanoparticle dose, and contact time. The synthesised nanoparticles were able to remediate >98% Cr (VI). The experimental adsorption isotherms and kinetics were rigorously analysed and subsequently utilized to train a deep learning model, enabling high-accuracy prediction of removal efficiencies across diverse operational parameters.

Keywords: Hexavalent Chromium, Iron, Nanoparticles, Remediation, Adsorption.

Metagenomic and Culture-Dependent Analysis of Yamuna River Microbiota Reveals Native Microplastic-Degrading Bacteria

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Abstract

Microplastic contamination in aquatic environments poses a significant ecological and public health concern due to its persistence and resistance to degradation. This study integrates physicochemical analysis, metagenomic profiling, experimental biodegradation, and molecular docking to evaluate the potential for microplastic degradation. Water samples were collected from the sites of Yamuna River (Delhi NCR) were analysed for key parameters including pH, temperature, dissolved oxygen (DO), biochemical oxygen demand (BOD), and chemical oxygen demand (COD) to assess environmental conditions influencing microbial activity. A 21-day biodegradation experiment using microbes was set up resulted in a significant degradation efficiency of approximately 10%, indicating active microbial involvement. In addition, physicochemical characterization of plastic was analysed by X-ray diffraction (XRD) and differential scanning calorimetry (DSC) and Fourier transform infrared spectroscopy (FTIR). This revealed the changes in crystallinity, thermal stability, and polymer structure and alterations in functional groups, including reduced ester (C=O) peaks and increased hydroxyl (-OH) signals, confirming polymer breakdown. Moreover, Metagenomic analysis based on 16S rRNA sequencing revealed a diverse microbial community dominated by genera such as *Flavobacterium*, with functional predictions indicating the presence of plastic-degrading enzymes and metabolic pathways. Molecular docking studies further demonstrated strong binding interactions between selected enzymes (e.g., PDB ID: 3d2c) and plastic intermediates such as BHET, with binding energies ranging from -5.4 kcal/mol, supporting their catalytic potential. Overall, this study highlights the synergistic role of environmental conditions, microbial diversity, and enzymatic mechanisms in microplastic degradation, providing a comprehensive framework for developing sustainable bioremediation strategies for aquatic ecosystems.

Keywords: Microplastic Pollution, Microbial Biodegradation, Metagenomic Profiling, Molecular Docking, Bioremediation.

Limitations and Challenges of Nanotechnology-Based Heavy Metal Remediation: Bridging Lab-Scale Success to Field Applications

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Abstract

Recent advances in nanotechnology have led to the development of many engineered nanomaterials, such as metal oxides, carbon-based nanostructures, and nanocomposites, for removing heavy metals from polluted water and soil. These materials work very well in the lab because of their large surface area, adjustable surface chemistry, and high reactivity. However, moving these nanotechnology-based methods from the lab to real-world environmental applications remains a major challenge. This review examines the main obstacles to large-scale adoption. Key issues include nanoparticle clumping, lower efficiency in complex environments, limited reuse, and possible ecological risks if nanoparticles are released. Other challenges are scaling up, keeping costs reasonable, ensuring long-term stability, and dealing with unclear regulations. The lack of standardized ways to measure performance and insufficient testing outside the lab also make it harder to use these technologies in practice. This review highlights the gap between lab success and real-world use and stresses the need for teamwork across fields such as materials science, environmental engineering, and risk assessment. It also discusses possible solutions, such as altering material surfaces, using immobilization, combining different systems, and adopting greener production methods. By addressing these issues, this review aims to guide future work toward making nanotechnology-based heavy-metal cleanup more practical and sustainable.

Keywords: Heavy metal remediation; Nanotechnology; Engineered nanomaterials; Field-scale application; Environmental risk assessment.

A Biotechnological Conceptual Model of a Single-Chamber Biofilter for Non-Biodegradable Waste Management in Martian Environments

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Abstract

Non-biodegradable wastes have a significant threat on environmental sustainability and human health. With the prospect of human settlement on Mars, this presents a major challenge in the effective degradation of non-biodegradable wastes that would get accumulated over Martian surface and it remains a critical challenge on Earth. Wastes such as plastics, synthetic compounds, packaging materials, polyethylene are resistant to natural degradation and hence they require effective waste management strategies to ensure sustainable living in extraterrestrial and terrestrial habitats. This study proposes a conceptual design of a single-chamber bioreactor based biofilter which is integrated with a biofiltration unit containing specialized microbial consortia capable of facilitating enzymatic breakdown and biotransformation of non-biodegradable wastes. The system maintains optimal conditions for microbial activity under extreme environmental conditions such as low pressure, limited water availability and high radiation exposure is maintained by the enclosed chamber. The biotransformation unit converts the complex waste materials into simpler and non-toxic by-products, which can be further utilised or safely managed within the habitat systems. This conceptual model is developed through an analysis of existing literature on microbial bioremediation, waste degradation and extremophilic biology. The expected outcomes include reduction in waste accumulation, enhanced environmental sustainability, and resource efficiency in closed-loop systems. Moreover, this idea offers potential applications for addressing non-biodegradable waste challenges on Earth, particularly in isolated or resource-limited settings. This system leverages microbial community behavior and extremophilic adaptation to enable efficient waste biotransformation under Martian conditions and is among the first conceptual integrations of extremophilic bioremediation systems for extraterrestrial waste management.

Keywords: Bioremediation, Extremophiles, Martian habitats, Non-biodegradable waste, Sustainability.

Decoding Plant Tolerance Mechanisms Against Salinity Stress

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Abstract

Recent focus towards intensive high-input agricultural practices to maximize crop yield involves heavy use of fertilizers, pesticides, and irrigation. These methods increase food production but often lead to environmental degradation, including soil erosion, and increased soil salinity. The soluble salt residues build up in the root zone due to uncontrolled irrigation and chemical usages, affecting soil and plant interactions. This increase in salinity leads to osmotic stress, ionic imbalance, and nutrient deficiencies, which eventually affect plant development, metabolism, and production. On the cellular level, salinity elevates the formation of reactive oxygen species (ROS), which cause oxidative damage of lipids, proteins, and nucleic acids, and also serves as signalling molecules and triggers stress responses in plants. Plants counteract these types of challenges by integrating cellular, biochemical, and molecular adaptations that help to sustain cellular homeostasis. The major component of this whole mechanism is the antioxidant defense system, which consists of various enzymatic components (Superoxide Dismutase, Catalase, Peroxidases, Ascorbate Peroxidase, and Glutathione Reductase) and non-enzymatic antioxidants (Ascorbate, Glutathione, Tocopherols, Carotenoids, Phenolics, and Compatible Osmolytes). These systems synergize to control the ROS levels and maintain redox balance in a saline environment. Moreover, salinity stress triggers intricate networks of molecular signalling, which comprise ROS, calcium signalling, and kinase-mediated pathways. Other pathways that maintain ion homeostasis include the SOS signalling system. The combination of these mechanisms helps the plants to maintain metabolic stability and adapt to saline conditions. The present review offers to provide in-depth critical insights of these interdependent responses in plants to understand how they contribute to enhancing stress tolerance and improving crop productivity. Such understanding will be highly valuable for developing strategies to optimize plant responses under rising salinity levels and, consequently, improve crop yield.

Keywords: Salinity stress, Reactive oxygen species (ROS), Antioxidant defense system, Redox homeostasis, Molecular signaling pathways

The Role of Microplastics in Antimicrobial Resistance: A Complex Global Challenge

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Abstract

From usefulness to futility, plastic has evolved into one of the most critical environmental challenges of all time. It gives rise to microplastics (MPs), an invisible, ubiquitous pollutant found everywhere, from the ocean floor to human blood. Antimicrobial resistance (AMR) stands as one of the deadliest public health threats of this century. It projects over 39 million deaths between 2025 and 2050. Both MPs and AMR seem unrelated, yet pose deeply interconnected threats to human life and remain critically underexplored and untapped. This gap is alarming in a developing nation like ours, given the lack of waste management and the extensive misuse of antibiotics. This creates a synergistic storm of microplastic-driven AMR expansion. Microplastics act as vectors due to their hydrophobic surfaces, chemical stability, and larger surface area. This makes them ideal substrates for bacterial colonization, biofilm formation, and transfer of antibiotic genes via horizontal gene transfer. Addressing this synergistic threat requires a multilevel response that includes upgrading wastewater treatment, especially from hospitals to pharmaceutical facilities. This is important to break the plastic-bacteria cycle in waterbodies. Managing landfills and leachate is also crucial. Avoiding the use of microbeads and single-use plastics, and spreading public awareness of the conscious use of antibiotics and plastic, are very important. Shifting to biodegradable alternatives like PHA, which offer a future without a toxic legacy, can bring significant change. These are not just aspirational; they are mandated. In 2022, 175 nations committed to a legally binding plastic treaty through UNEA-5 and WHO's 2024 AMR Global Call to Action, targeting a 10% reduction in AMR deaths by 2030 and collectively advancing UN SDGs 3, 6, 12, 13, and 14. With microplastic production projected to reach 750 million metric tons by 2050, the roadmap exists and must be followed urgently.

Keywords: Microplastics, Antimicrobial resistance, Global challenge.

In Silico Evaluation of Enzyme Peroxidase Interaction with Structurally Diverse Textile Dyes

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Abstract

Textile wastewater containing non-biodegradable synthetic dyes such as azo and triphenylmethane compounds poses a severe environmental threat owing to their persistent toxicity and resistance to conventional degradation processes. Enzyme-based bioremediation has emerged as a promising and eco-friendly alternative; however, a thorough mechanistic understanding of enzyme-dye molecular interactions remains essential for optimizing catalytic efficiency. *Arthromyces ramosus* peroxidase (ARP), a heme-independent peroxidase, has demonstrated broad applicability in the bioremediation of industrial effluents and the oxidative breakdown of synthetic colorants, making it a compelling candidate for in-depth molecular investigation. This study aimed to characterize the molecular binding interactions of ARP (PDB ID: 1ARU) with four commonly encountered textile dyes Indigo Carmine, Crystal Violet, Azo Dye, and Malachite Green to evaluate its potential as a biocatalyst in dye decolorization applications. Molecular docking-based in silico binding analysis was performed to assess binding affinities and elucidate key interaction patterns between ARP and each dye molecule at the active site level. The results demonstrated that Indigo Carmine and Crystal Violet exhibited significantly stronger binding affinities, with docking scores of -9.0 and -8.1 kcal/mol, respectively, compared to Malachite Green at -6.8 kcal/mol, indicating a thermodynamic selectivity of ARP toward specific aromatic structural configurations. These differential binding profiles suggest that the structural and electronic properties of dye molecules play a decisive role in governing catalytic recognition and substrate specificity. In conclusion, this in silico approach provides a valuable mechanistic framework for identifying and screening peroxidase enzymes suited for textile wastewater bioremediation, while establishing a computational platform that can accelerate the rational design and development of environmentally sustainable, enzyme-mediated decolorization technologies for industrial effluent management.

Keywords: Peroxidase, In Silico analysis, Molecular Docking, Textile dye.

Green Synthesis of Zinc Oxide Nanoparticles Using Banana Peel Extract for Efficient Dye Removal from Aqueous Solutions

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Abstract

The textile business is famous for consuming the most water of any industry, utilising about 200 litres for every kilogramme of fabric, and in India, the textile industry alone uses 425,000,000 gallons of water every day. The two primary water-consuming processes in the textile industry are fabric dyeing and fabric washing. The problem is that the fabric is not sufficiently bound to the dye, which leads to the dye being dumped as effluent into water bodies. The high pH, high BOD and COD levels and heavy metals in the effluent also have a detrimental influence on the ecology. Finding effective techniques to treat the effluent before releasing it into water channels is essential, and numerous physical and chemical methods are being applied on a big scale. Banana peels are being utilised to create Zinc Oxide nanoparticles by testing various parameters such as temperature and pH. The final synthesis of ZnO nanoparticles is tracked by monitoring the absorbance spectra with a UV-Visible spectrophotometer, and SEM and FTIR were used to examine the biosynthesized nanoparticles. The current study, which uses a banana peel plant extract to create ZnO nanoparticles, is an effective, environmentally friendly, and simple approach that could have a huge influence in the near future for synthesising metallic nanoparticles on an industrial and commercial scale. Therefore, this project explores an understanding of a combination of less extensively researched and attempted tactics, and the objective was to use a nanoparticle remediation technique to remove a monoazo dye, like Methyl Red. ZnO nanoparticles obtained by green synthesis were employed to rectify methyl red, and for methyl red, we found that ZnO had a decolorization efficiency of almost 23%. The results from this approach can be used in the future for the remediation of more toxic dyes that pollute the environment.

Keywords: Zinc Oxide nanoparticles, Textile industry, dyes, UV–Vis spectroscopy.

Ectomycorrhizal Fungi–Mediated Remediation of Elevated Heavy Metals in Mining-Disturbed Forest Ecosystems

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Abstract

Mining activities often result in the accumulation of elevated concentrations of heavy metals such as iron (Fe), manganese (Mn), aluminium (Al), chromium (Cr), nickel (Ni), lead (Pb), and zinc (Zn) in forest soils, adversely affecting soil quality, plant growth, and ecosystem stability. Although a wide range of heavy metals are present in mining-disturbed ecosystems, this study specifically focuses on zinc (Zn) and nickel (Ni) due to their higher mobility, toxicity, and ecological significance. Ectomycorrhizal (ECM) fungi play a crucial role in enhancing plant tolerance to metal stress through their symbiotic associations and functional adaptations. This study aims to explore the potential of ECM fungi, including *Entoloma*, *Pisolithus*, *Laccaria*, *Lactarius*, *Boletus*, *Russula*, *Suillus*, *Geastrum*, and *Amanita*, in mitigating heavy metal stress in mining-disturbed forest ecosystems associated with *Eucalyptus* spp., *Quercus* spp., and *Pinus* spp. The work focuses on understanding key mechanisms such as metal sequestration, immobilization, extracellular binding, and regulation of metal uptake in host plants. It also evaluates the functional responses of ECM fungi in terms of metabolic activity and their role in improving nutrient acquisition under stress conditions. The study is expected to provide insights into ECM-mediated phytoremediation as a sustainable and eco-friendly approach for restoring soil health and supporting vegetation recovery in metal-contaminated forest ecosystems.

Keywords: Ectomycorrhizal fungi, Mining disturbance, Phytoremediation, *Pisolithus*, *Laccaria*, Forest restoration, Soil contamination.

Eco-Friendly production of chitosan from *Aspergillus niger* cultivated on pineapple peel via solid-state fermentation

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Abstract

A deacetylated derivative of chitin, chitosan has attracted a lot of interest as a result of its many industrial uses, biodegradability and biocompatibility. Sustainable solutions are required since seasonal availability, environmental issues and inconsistent product quality constrain conventional manufacturing from crustacean waste. The synthesis of chitosan from *Aspergillus niger* isolated from naturally grown pineapple was thoroughly examined in this study. Pineapple peel was used as an agro-industrial substrate in solid-state fermentation (SSF) to produce chitosan after the fungal strain was identified based on its morphological, microscopic and molecular characteristics. Optimized alkali-acid extraction was applied to the fermented biomass to enable the chitosan recovery. A maximum yield of around 50–55 mg g⁻¹ (dry biomass basis) was attained, indicating effective biomass conversion and substrate use. FT-IR analysis confirmed the presence of characteristic functional groups associated with chitosan, whereas morphological characterisation by FESEM showed a smooth and fibrous structure, indicating the retention of polymer integrity. A high percentage of reactive amino groups was indicated by the degree of deacetylation (DD), which was found to be in the range of around 75–80% using spectrophotometry. These results demonstrate the possibility of naturally occurring *A. niger* grown on pineapple peel as a sustainable and affordable source of chitosan. The integration of solid-state fermentation with agro-waste valorization provides a promising strategy for scalable biopolymer production aligned with circular bioeconomy principles.

Keywords: Chitosan, *Aspergillus niger*, Agro-waste, Valorization, Circular bioeconomy

Thermodynamic profiling of keratin-surfactant system using anionic surfactant for topical formulation

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Abstract

The improper disposal of chicken feather waste from the poultry industry causes significant environmental issues. Converting this protein-rich biomass into keratin offers a sustainable solution, as keratin is a fibrous structural protein abundantly found in chicken feathers and is widely recognized for its high mechanical strength and biocompatibility. These properties are essential for skin-related applications, including tissue regeneration, wound healing, moisture retention, and antioxidant protection. In the present study, keratin was extracted from chicken feather biomass through alkaline hydrolysis process and characterized to confirm structural and physicochemical properties. The interfacial and physicochemical behavior of keratin solutions (1, 2, and 3% w/v) was systematically investigated in the presence of the anionic surfactant sodium dodecyl sulfate (SDS 0-0.014 mM) at different temperatures ranging from 25°C to 40°C using surface tension, contact angle, and surface free energy analyses. The critical micelle concentration and micelle formation were determined by measuring surface tension, whereas the wettability, spreading, and adhesion of the keratin-surfactant system were examined by contact angle and surface free energy analyses. Thermodynamic parameters such as standard Gibbs free energy change (ΔG_m°), Enthalpy change (ΔH_m°), and Entropy change (ΔS_m°) were calculated to understand keratin-surfactant interactions. The results showed that surface tension and CMC decreased with the increase in SDS concentration at higher temperatures with 2 % (w/v) keratin system demonstrating optimal micelle formation. The range of negative ΔG_m° values confirmed the spontaneous nature of micellization process, whereas positive ΔH_m° and ΔS_m° values indicate an endothermic, entropy-driven process due to favorable interactions of molecules. In addition, Lower contact angle and higher surface free energy reflect improved wettability and adhesion, highlighting the keratin-surfactant system's potential for topical applications.

Keywords: Sodium dodecyl sulfate, Surface tension, Critical micelle concentration, Thermodynamic parameters, Waste valorization

Pine Needles as green material for Removal of Metal Ions and Dyes from Wastewater

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Abstract

A possible low-cost, environmentally responsible, and effective method of eliminating contaminants from water is the work on treating wastewater using pine needles. Numerous contaminants that can be detrimental to human health and the environment, such as chemicals, heavy metals, and organic compounds, can be found in industrial effluent. Numerous health issues, such as skin irritation, respiratory issues, and in extreme situations, cancer, can result from exposure to these contaminants. Natural substances like lignin and tannins, which are abundant in pine needles, have been demonstrated to have a high affinity for binding heavy metals and other contaminants. Pine needles were gathered, cleaned, and dried for the study before being used to assess how well they removed dyes from artificial wastewater solutions. According to the findings, pine needles have a promising future in wastewater dye removal. It was discovered that increasing the pine needle dosage and contact time increased the removal efficiency. Utilizing activated pine needle biochar resulted in a 4.08% increase in efficiency. The study's overall findings demonstrate the potential of employing pine needles as an economical and environmentally beneficial wastewater treatment method.

Keywords: Waste water treatment, Biochar, Pine needles, Sustainability, Waste management

Role of Conserved Regions in PETase-Mediated Degradation

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Abstract

Plastic pollution generated by polyethylene terephthalate (PET) is a major environmental issue due to its high stability and resistance to natural degradation. In the recent years, several bacterial species like *Ideonella sakaiensis*, *Pseudomonas*, *Bacillus*, *Thermobifida*, and *Rhodococcus*, have gain attention due to their ability to degrade PET. A major enzyme PETase has been identified which show an important role in catalytic activity in PET degradation. It also found that PETase enzyme has a conserved region which contain catalytic amino acid triad (-SHD-) for substrate binding and enzyme stability. *R. pyridinivorans* has been identified that has the capability of degradation of PET. Therefore, to decipher the molecular details a biodegradation, a bioinformatic approach was utilized. In this study, we identified the potential PET-degrading enzymes using in silico approach. The available protein sequences of *R. pyridinivorans* were retrieved from NCBI and searched for similarity against PETase enzyme from *Ideonella*. Previous studies revealed an important role of PETase in catalytic activity in PET degradation. The protein sequences which showed significant similarity were further checked for their domains, which showed the presence of PETase (PF12740) and DLH (PF01738), in 2 strain - GF23 and P23. As, the 3D protein structure of PETase is unknown for *R. pyridinivorans* we also generated its 3D structure using Alphafold. Thus, further, to evaluate the accuracy and functional relevance, the predicted significance. This study reveals the conservation of the PETase-associated M5 motif in *R. pyridinivorans*, providing motif level evidence for previously unrecognized PET-degrading and super- potential in a bacterium that degrades PET. These findings indicate to its potential improved applicability in eco-friendly plastic breakdown. on the experimentally validated 3D structure of *Ideonella*.

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

Microbial Valorization of Pomegranate Peel for Antiseptic Formulation

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Abstract:

Pomegranate (*Punica granatum*) peel, an abundant agro-industrial waste, is a rich source of bioactive phytochemicals, especially flavonoids and phenolics. The transformation of agricultural waste into materials for the manufacture of cosmetics and pharmaceuticals is a viable way to produce these products sustainably. This current study investigates the use of pomegranate peel powder as a low-cost carbon source for the microbial fermentation and extraction of phenolic and flavonoid compounds using *Lactobacillus plantarum* under controlled conditions (pH 6.2–6.5, 30–37 °C, incubation up to 24 hours) to facilitate enzymatic hydrolysis and release of bound phytochemicals. The metabolic activity of *L. plantarum*, which includes the production of β -glucosidase and esterase enzymes, contributes to the depolymerization of complex tannins, such as punicalagin, into simpler, bioactive molecules, such as ellagic acid. The bio-valorized extracts were successfully integrated into a stable oil-in-water antiseptic formulation containing aloe vera and almond oil, which exhibited a skin-compatible pH of 7.3 and no dermal irritation. This research demonstrated the potential of *L. plantarum*-mediated fermentation as a sustainable strategy for developing natural, high-performance antiseptic ingredients. The result provides scientific evidence that microbial fermentation enhances the bioactivity of pomegranate peel powder, showing its potential as a sustainable source of natural ingredients for future cosmetic applications.

Keywords: Pomegranate peel, *Lactobacillus plantarum*, Fermentation.

Production of Biolubricant from Waste Cooking Oil (WCO) using immobilized lipase

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Abstract

Biolubricants have immense importance in the automobile and industrial machinery to reduce the friction between metallic surfaces. In this study a commercial lipase was immobilized onto ZIF-8 metal organic framework (MOF) and kaolin clay particles and used for the production of free fatty acids. Amine functionalization of Kaolin clay is crucial for unlocking full potential of lipase from esterification to biolubricant production. Immobilization was optimized by providing abundant, reactive NH_2 site for superior electrostatic or covalent bonding. Waste Cooking Oil (WCO) was procured from different restaurants and food manufacturers and filtration of oil was performed. The production of Bio lubricant typically through the enzymatic transesterification of WCO with complex alcohol typically at 75°C and at a pH of 8. Then the produced free fatty acids were subjected to second transesterification and converted into biolubricants. Initially the feedstock was converted into fatty acid methyl ester (FAME) via transesterification, resulting in a conversion efficiency of 97.16% providing a high purity precursor for subsequent bio lubricant synthesis. The second transesterification step achieved a maximum conversion of 91.1% when lipase immobilized with amine functionalized Kaolin clay, lipase immobilized with ZIF-8/GO shows efficiency of 87.5%, lipase immobilized with kaolin clay shows efficiency of 85% whereas lipase enzyme itself shows efficiency of 68% and comparatively if oil is treated with only catalyst such as PEG 400 it shows efficiency of 75%. So, this analysis confirmed that immobilized lipase maintained high catalytic activity, significantly outperforming, non-functionalized support.

Keywords: Lipase, Immobilization, Activation, Functionalization, Bio lubricant, Waste Cooking Oil, Kaolin clay, FAME, Transesterification.

Fabrication and Characterization of Bacterial Cellulose and Chitosan Composites for Food Packaging

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Abstract

The growing environmental burden of synthetic plastic packaging has accelerated the search for sustainable, biodegradable alternatives derived from renewable resources. In this context, the present study focuses on the fabrication and characterization of bacterial cellulose (BC) and chitosan based composite materials for potential application in food packaging. Bacterial cellulose, produced by microbial fermentation, exhibits exceptional purity, high tensile strength and a nanofibrous network structure, while chitosan contributes antimicrobial properties and film forming capability. The integration of these two biopolymers aims to create a composite material that combines mechanical robustness with functional bioactivity. The composites were fabricated through an In-situ method, followed by controlled drying to ensure uniform film formation. Comprehensive characterization was performed to evaluate structural, physical and functional properties. Techniques such as X-ray diffraction (XRD) and Fourier transform infrared spectroscopy (FTIR) were employed to confirm molecular interactions and crystallinity. Mechanical properties, including tensile strength and flexibility, were assessed to determine suitability for packaging applications. Additionally, water absorption capacity, barrier properties and antimicrobial activity were analysed to evaluate performance under real world conditions. The results demonstrated enhanced mechanical strength, improved moisture resistance and notable antimicrobial activity in the BC-chitosan composites compared to individual components. The synergistic interaction between bacterial cellulose and chitosan resulted in a structurally stable and functionally superior material. These findings highlight the potential of BC-chitosan composites as an eco-friendly alternative to conventional packaging materials, contributing to reduced environmental impact and improved food safety. This study underscores the feasibility of utilizing bio-based composites in sustainable packaging solutions and provides a foundation for further development and large-scale application in the food industry.

Keywords: Bacterial Cellulose, Chitosan, Biopolymer Composites

Ectomycorrhizal Diversity and Functional Metabolic Profiling Across Forest Disturbance Gradients: Implications for Ecosystem Restoration

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Abstract

Ectomycorrhizal (ECM) fungi are essential components of forest ecosystems, where they support plant growth, nutrient uptake, and overall ecosystem stability. ECM diversity and metabolic functioning vary significantly between disturbed and undisturbed forest environments, influencing ecosystem recovery and resilience. Common ECM genera such as *Entoloma*, *Pisolithus*, *Laccaria*, *Lactarius*, *Boletus*, *Russula*, *Suillus*, *Geastrum*, and *Amanita* form symbiotic associations with important tree species including *Eucalyptus* spp., *Quercus* spp. (oak), and *Pinus* spp. (pine). Disturbed ecosystems generally show a decline in ECM diversity along with a shift toward stress-tolerant species, often resulting in reduced metabolic efficiency and nutrient cycling capacity. In contrast, undisturbed forests tend to maintain richer and more stable ECM communities with higher enzymatic activity and functional diversity. Advances in molecular tools, physiological profiling, and enzyme-based approaches have improved the understanding of ECM functional traits and their ecological roles. In addition, factors such as soil properties, host plant diversity, and stages of forest succession play a key role in shaping ECM community structure and function. Adaptable genera like *Pisolithus* and *Laccaria* show strong potential in restoration efforts due to their ability to establish under stressed conditions and support plant establishment. Overall, integrating ECM diversity with metabolic function provides a useful approach for understanding ecosystem responses to disturbance and for developing effective forest restoration and management strategies.

Keywords: Ectomycorrhizal fungi (ECM), Metabolic profiling, Ecosystem restoration, Nutrient cycling, Functional diversity.

Isolation and Biochemical Characterization of Lead (Pb) Tolerant Bacteria from Wastewater

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Abstract

Heavy metal contamination in industrial and municipal wastewater poses significant environmental and public health concerns due to the persistence, toxicity, and bioaccumulative nature of metal like lead (Pb). Heavy metal pollution in wastewater represents a major environmental threat. Biological approaches, particularly the use of metal-tolerant bacteria, offer a sustainable alternative for heavy-metal remediation. The present study aimed to isolate and biochemically identify bacteria capable of tolerating and potentially remediating Pb from contaminated wastewater sources. This research concentrates on the isolation and identification of bacteria that exhibit tolerance to lead (Pb) from wastewater samples. Wastewater was collected from drain areas near various industries in Baddi Himachal Pradesh, and bacterial isolates were obtained using serial dilution and plating on nutrient agar amended with 5 mg/L concentrations of Lead Nitrate (Pb (NO₃)₂). 16 tolerant colonies were selected and subjected to MIC determination. Various morphological and biochemical identification tests, like Indole, Methyl red, Voges-Proskauer, Citrate, Gelatin, KOH and catalase, were conducted. Results indicated that isolates exhibited high tolerance to Pb (up to 1000 mg/L). Preliminary biochemical characterization revealed the presence of *Bacillus* sp., *Staphylococcus* sp., and *Enterococcus* sp. These findings suggest that indigenous wastewater bacterial isolates possess strong tolerance against Pb under study and might have the potential for heavy-metal bioremediation, which needs further experimentation to be established.

Keywords: Heavy metal, Wastewater, Lead tolerance, Bioremediation.

Green production of xylooligosaccharides through RSM optimized enzymatic hydrolysis of pearl millet straw

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Abstract

Biovalorization of agricultural residues into value-added products, such as prebiotic xylooligosaccharides (XOS), plays a vital role in advancing bioeconomy. Among existing strategies, enzymatic hydrolysis is widely preferred owing its eco-friendly nature, mild operational conditions and controlled polymerization. In this study, optimization of enzymatic hydrolysis of hydrogen peroxide acetic acid (HPAC) pretreated pearl millet straw (PMS) was performed employing response surface methodology (RSM) for enhanced XOS production. Box-Behnken design of RSM was used to investigate the effect of independent variables including xylanase dosage (300-900 U/gds), temperature (40-60 °C) and pH (4-6). Under optimized process conditions (xylanase dosage 545.55 U/gds, temperature 50 °C and pH 5.59), maximum 2.37 g/L of XOS were obtained majorly contained of xylobiose (1.92 g/L) and xylotriose (0.45 g/L). The optimization resulted into 3-fold enhancement of XOS production from unoptimized conditions. Further, XOS were partially purified using activated charcoal column chromatographic technique. Nearly, 86 % recovery of XOS was achieved with corresponding xylobiose and xylotriose yields of 88.54 and 83.50 %, respectively as corroborated by qualitative and quantitative estimation by employing high performance thin layer chromatography and high-performance liquid chromatography. The partially purified XOS display strong antioxidant activity as demonstrated in 2,2-diphenyl-1-picrylhydrazyl (DPPH), 2,2'-azinobis (3-ethylbenzothiazoline-6-sulfonic acid) and ferric reducing antioxidant potential (FRAP) assays with 73.29, 83.71 and 71.60 % activity, respectively. The prebiotic potency of XOS was validated through their efficient utilization as carbon source by probiotic microorganisms. Hence, the results highlight efficient bioprocess strategy for transformation of PMS into prebiotic XOS with promising application as functional food ingredient in prebiotic supplements, nutraceuticals and related health products.

Keywords: Pearl millet straw, Response surface methodology, Enzymatic hydrolysis

Microplastics In The Environment: Integrated Perspectives On Sources, Ecological Risks, Degradation Pathways, And Sustainable Management

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Abstract

Microplastics (MPs), emerging as a ubiquitous pollutant, originate from diverse anthropogenic sources and have raised significant concerns due to their persistence, bioaccumulation potential, and adverse impacts on both ecosystems and human health. This review provides a comprehensive assessment of the literature on the sources and types of MPs, highlighting their prevalence in terrestrial, freshwater, and marine environments. The toxicological consequences of MPs on organisms and humans are explored, emphasizing risks associated with ingestion, bioaccumulation, and disruption of ecological functions. Special focus is given to the degradation mechanisms of MPs, where abiotic processes such as photodegradation, thermodegradation, chemical degradation, and advanced oxidation are evaluated alongside biotic degradation pathways mediated by bacteria, fungi, and microalgae. Furthermore, recent advancements in treatment technologies and current strategies for plastic waste management are discussed within the framework of global regulations and policies. Overall, this article establishes a logical flow of literature from sources and impacts to degradation mechanisms, treatment approaches, and regulatory frameworks, providing an integrated perspective for sustainable solutions to microplastic pollution.

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

Emerging Biotechnological Techniques for the Assessment, Restoration and Conservation of Aquatic and Microbial Biodiversity in Hydropower-Impacted Indian Himalayan River Ecosystems

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Abstract

Rapid hydropower development across the Indian Himalayan Region (IHR) has significantly altered river ecosystems by modifying natural flow regimes, sediment transport, habitat connectivity, and water quality. The present review explores emerging biotechnological techniques that can support ecological restoration and aquatic and microbial biodiversity conservation in hydropower-affected rivers of Indian Himalayan region. This review emphasizes on advanced biotechnological techniques such as environmental DNA (eDNA)-based biodiversity assessment of aquatic and microbial communities, metagenomic analysis of river microbial communities, macroinvertebrate-based bio monitoring indices, periphytic algal biofilm analysis, phytoremediation using aquatic macrophytes, constructed wetlands integrated with microbial processes, and sediment-based microbial fuel cell systems. The findings of this study indicates that these techniques provide efficient and sensitive tools for assessing ecological disturbance and supporting restoration planning in regulated river systems. eDNA and metagenomic approaches enable rapid detection of biodiversity changes and microbial responses to hydropower-induced stress. Macroinvertebrate and algal biofilm-based monitoring techniques act as reliable ecological indicators of river health, while phytoremediation and microbial-assisted treatment systems contribute to pollutant reduction. In addition, constructed wetlands enhance nutrient removal and habitat recovery, while sediment microbial fuel cells offer potential for simultaneous energy recovery. The integration of biotechnological tools for ecological monitoring and restoration of aquatic ecosystems affected by hydropower development, can strengthen conservation strategies in IHR. This review highlights strong alignment with SDG-6 (Clean Water and Sanitation), SDG-13(Climate Action) and SDG-15 (Life on Land) that emphasizes on the need for sustainable hydropower development and river management along with biodiversity conservation in IHR.

Keywords: Environmental DNA, Metagenomics, Aquatic microbial biodiversity

Computational Biology & Bioinformatics

Oral Presentation

Investigation and Comparative Analysis of the Biological Activity of Alpha-Pinene and its Derivatives Using In Silico Models

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Abstract

Terpenes are compounds with high biological activity, exhibiting antioxidant, anti-inflammatory, anticancer, and antimicrobial properties. Alpha-pinene and menthol also clearly demonstrate such activities. This study is dedicated to investigating the biological activity of alpha-pinene and menthol. The research was carried out using the GUSAR Online program to predict antibacterial and antifungal activity, while the PASS Online program was employed to forecast various types of biological activity. The results obtained allowed for the identification of the potential pharmacological properties of the compounds and enabled their comparative analysis.

Keywords: Alpha-pinene, Menthol, *In Silico*, GUSAR Online, AntiBac Pred.

A High-Quality Consensus Genome Assembly of Indian Black Pepper Varieties

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Abstract

Black Pepper (*Piper nigrum* L) is an economically significant spice crop cultivated worldwide. However, the lack of a high-quality reference genome of this species limits our ability to advance genomic studies and develop crops with improved agronomic traits. At present, the only publicly available genome assembly of black pepper is from a Chinese variety *Piper nigrum* cv. Reyin-1, which may not adequately represent the genetic diversity of Indian germplasm. In this study, we aimed to develop a consensus genome assembly representative of Indian varieties of black pepper. A total of 39 black pepper accessions were analyzed to capture population-level genetic variation. Raw sequencing data were processed through a reproducible workflow implemented using Snakemake workflow manager. Cleaned reads were aligned to *Piper nigrum* cv. Reyin-1 genome followed by post-alignment processing steps such as sorting, duplicate marking and indexing to generate high-quality BAM files. The variant file for black pepper was also generated. Base quality score recalibration (BQSR) was then carried out using the Genome Analysis Toolkit (GATK) to improve base call accuracy using the generated known variant file. Variant discovery was performed using GATK HaplotypeCaller in GVCF mode, followed by joint genotyping across all samples. Subsequently, stringent filtering criteria were applied to obtain high-confidence variants, following which each variant position was replaced with major alleles to reconstruct a consensus genome assembly representing Indian germplasm. This approach allowed us to combine the genomic variation from the population into one reference framework that is representative of the Indian varieties of *Piper nigrum*. Furthermore, functional annotation and structural annotation was performed on the newly constructed consensus genome to characterise the gene models and genomic features of black pepper. This genomic resource can support trait studies, GWAS, breeding applications and in addition provides a foundation for future multi-omics integration.

Keywords: Consensus genome assembly, Genome annotation, *Piper nigrum*, Spices, Variant calling.

GrowGen: Stable Property-Conditioned Molecular Generation using a Decoder-Only Transformer and Reinforcement Learning

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Abstract

Generative AI in molecule generation for drug design has gained significant attention due to its potential to create new scaffolds. However, aligning with chemical principles and drug-like properties is still a challenge in stability optimization and property conditioning. Transformer-based methods have the capability to capture these properties that can be incorporated into the model training. This work uses Rotary Position Embedding (RoPE) with property conditioning utilizing descriptor embeddings and policy-gradient reinforcement learning. Physicochemical descriptors were calculated and embedded into the model, which also addresses the global conditioning information. This is achieved using additive embedding. The relationship between structure, properties and SMILES syntax was fed to the supervised pre-training process, followed by reinforcement optimization. Reward scoring was computed using molecular validity, global uniqueness, and QED value. Across several benchmark datasets, including GDB13rand, MOSES, and ZINC, reinforcement learning significantly improves molecular drug-likeness by increasing the average QED while maintaining high levels of chemical validity (above 80%), uniqueness (above 90%), and novelty (above 99%). During generation, temperature-based and nucleus-based sampling strategies are used to find a balance between exploration and chemical validity. Overall, the proposed framework offers a stable and scalable platform for generating molecules based on molecular properties and lays the groundwork for future developments in multi-objective optimization within computational drug discovery.

Keywords: Generative AI, RoPE, QED, Drug Design, Molecule Generation

Exploring Indian Medicinal Plants as ECM Modulators through MMP Inhibition: An *In-Silico* Investigation

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Abstract

The extracellular matrix (ECM) is integral to the maintenance of tissue architecture and the regulation of cellular behaviour. Dysregulation of the ECM, frequently mediated by the excessive activity of matrix metalloproteinases (MMPs), is closely linked to pathological conditions such as fibrosis, cancer progression, and various women's health disorders, including endometriosis and polycystic ovary syndrome. Consequently, targeting MMP-driven ECM remodelling has emerged as a promising therapeutic strategy. In this regard, Indian medicinal plants, which are rich in diverse phytochemicals, represent a valuable and underexplored source of natural MMP inhibitors. This study seeks to explore the potential of selected Indian medicinal plants as extracellular matrix (ECM) modulators through the inhibition of matrix metalloproteinases (MMPs) using an *in-silico* approach. Five plants, *Rosa Rubiginosa* (rose), *Clitoria ternatea* (Aparajita), *Ocimum sanctum* (Tulsi), *Hibiscus rosa-sinensis* (Hibiscus), and *Matricaria chamomilla* (Chamomile) were chosen based on their traditional medicinal applications. Key phytochemicals, including flavonoids, phenolic acids, and alkaloids, were screened for their interactions with major ECM-regulating targets, particularly MMP-2 and MMP-9. Molecular docking analysis was conducted to assess binding affinity, interaction stability, and key amino acid residues involved in ligand protein interactions. The results indicated that several phytochemicals exhibited strong binding affinities and stable interactions within the active sites of MMPs, suggesting their potential inhibitory effects. These findings suggest that plant-derived compounds can modulate ECM remodelling pathways by targeting MMP activity at the molecular level. Overall, this study provides a mechanistic and computational basis for the use of Indian medicinal plants as natural ECM modulators. The integration of traditional knowledge with modern *in-silico* techniques highlights promising avenues for developing plant-based therapeutics.

Keywords: Extracellular Matrix, Matrix Metalloproteinases, Phytochemicals

Design And Implementation of a Modular Software Architecture For Computational Blood Vessel

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Abstract

The latest developments in computational hemodynamics have even allowed us to perform more realistic calculations of blood flow in complicated networks of blood vessels; this is providing important information on physiological mechanisms involved in the genesis of vascular diseases, the diagnosis of vascular diseases and helping in clinical decisions. In this sense reliable simulation of the blood flow under physiological and pathological conditions require good software tools to accomplish it. The paper discusses a new software specifically oriented to computational experiments of blood flow in deformable vascular systems with elastic walls. It provides the complete structure system to solve the mathematical models of hemodynamic processes in arterial and venous structures, and to visualize the result of numerical simulations. It is designed with a modular architecture, to be flexible, scalable and to adapt to different physiological needs. A schematic functional block diagram has been also provided for a better understanding of the correlation among the main features of the system that span from data collection of geometrical and physiological information, solution to the governing equations, data elaboration, data analysis, up to images visualization and results interpretation. The modular nature of the tool should also allow for an easy integration of other computational modules to adapt the tool to a variety of research applications and, hopefully, for clinical applications in the field of vascular medicine.

Keyword: Blood flow computations, Vascular models, Vascular elastic tissues, Simulation of blood flow, Vascular fluids.

Scalable K-Means Clustering for Agricultural Big Data Analytics Using Hadoop Framework.

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The storage, processing, and analysis of agricultural data faces significant difficulties as a result of the rapid growth of ICT-driven agricultural data. Efficient extraction of actionable insights from such large-scale datasets is critical for improving agricultural productivity and decision-making. This study presents a scalable framework for agricultural big data analytics using the K-Means clustering algorithm implemented over the Hadoop distributed environment. The proposed approach integrates heterogeneous data sources, including soil characteristics, weather conditions, and crop yield data, to identify meaningful patterns and cluster similarities. The framework enables efficient data partitioning and supports predictive analysis by leveraging machine learning techniques for estimating future agricultural outcomes. Additionally, time-series forecasting models such as ARIMA and regression techniques are incorporated to enhance yield prediction accuracy. The results demonstrate that clustering-based analytics can significantly assist farmers, researchers, and policymakers in making data-driven decisions related to crop planning, resource optimization, and risk management. The study highlights the potential of combining unsupervised learning with distributed computing platforms to address the complexities of agricultural big data and to support the development of intelligent and sustainable farming systems.

Keywords— Big Data Analytics, K-Means Clustering, Smart Agriculture, Hadoop, Machine

Microbial Diversity and Functional Potential of Plant-Based Fermented Foods: A Comparative Comprehensive Analysis Using 16S rRNA Metagenomic Sequencing Data

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Abstract

Fermented foods have been a part of human civilization for thousands of years and hold significant cultural and nutritional values, especially in India. Consumption of ethnic fermented foods in India and across the world is mostly based on the food preference of the ethnicity, locally available substrates of plant and animal sources, and also the geographical locations. Despite the increasing popularity of plant-based diets in recent times, the functional nutrition and probiotic attributes of plant-based fermented foods remain significantly underexplored. Therefore, we conducted a comparative metagenomic investigation of plant-based fermented foods globally to investigate microbial diversity addressing probiotics, nutritional benefits, and food safety considerations. Comprehensive shotgun metagenomic sequencing of 12 fermented food samples and starter cultures from Himachal Pradesh, India, was conducted, and the 16S rRNA gene was retrieved using in silico methods. This data was analysed alongside the 16S rRNA metagenomic datasets from 688 publicly accessible datasets across 23 more nations. A predominance of diverse microbial taxa within the Lactic Acid Bacteria group, including *Lactobacillus*, *Weissella*, and *Lactiplantibacillus*, was noted in plant-based fermented meals globally, mostly linked to processes such as fermentation and chemoheterotrophy. The presence of pathogenic characteristics in humans was discovered, albeit in limited abundance, highlighting the hazards associated with unregulated fermentation and food safety concerns. Diversity research revealed a statistically significant variation in microbial diversity among countries, various substrate types, fermentation techniques. Moreover, an examination of the V3-V4 region proves to be useful for investigating the microbial diversity of fermented food products.

Keywords: Traditional plant-based fermented foods, Lactic Acid Bacteria, Metagenomic analysis, Food biosafety

Early Detection of Diabetic Retinopathy using Machine Learning

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Abstract

Diabetic Retinopathy (DR) is a leading cause of preventable blindness. Automated screening systems for early detection can improve clinical outcomes and reduce the screening burden on specialists. This paper creates a transfer learning-based deep learning pipeline for multi-class DR severity classification on the APTOS 2019 fundus image dataset. The pre-trained ResNet18 model was fine-tuned with image preprocessing, augmentation, and class-weighted loss to classify five severity levels (No DR, Mild, Moderate, Severe, Proliferative). The model achieved a validation accuracy of 80.2% on a stratified 80-20 split. We also detail how the model performs based on the confusion matrix, precision, recall, and F1-score, while clearly showing high performance for No DR and Moderate classes, while low sensitivity for Severe and Proliferative classes due to dataset imbalance. We highlight practical deployment challenges, limitations, and opportunities for improvement, such as advanced augmentation, ensembling, and using efficient architectures.

Keywords: Diabetic retinopathy, Transfer learning, ResNet, Medical imaging, APTOS

In-Silico Identification of Novel Cholinesterase Inhibitors for Alzheimer's Disease

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Abstract

Alzheimer's Disease (AD) is one of the most prevalent neurological disease, accounting 60 – 70% of all dementia cases worldwide. It is marked by cognitive decline, memory loss and neuronal degeneration. One of the key pathological features of AD is the disruption of cholinergic neurons which leads to reduction in Acetylcholine (ACh) levels in the brain. Acetylcholinesterase (AChE) and Butyrylcholinesterase (BuChE) are the enzymes which deteriorate ACh levels, thereby worsening the disease progression. From recent evidences, we found that mushrooms are the species that have specific metabolites such as ergosterol, ergothioneine, erinacine etc, which are used in the management of AD. Most of the mushrooms contain the neuroprotective properties such as anti-inflammatory and anti-oxidant which are beneficial in maintaining brain's health and its cholinergic activity. The present work focuses on the in – silico screening of the bioactive metabolites from edible mushrooms to determine promising potential novel inhibitors of cholinesterase enzymes. Total 21 metabolites from edible mushrooms were screened for docking analysis. Molecular Docking studies were implemented using AutoDock tool, which targets the AChE enzyme (PDB ID: 7E3H) and Binding interactions were studied using computational tools such as UCSF Chimera and Discovery Studio. Amongst all screened metabolites, ergosterol peroxide from *Inonotus Obliquus* (Chaga) and ergosterol from *Agaricus Bisporus* (Button Mushroom) species showed the strongest binding affinity with docking energies of – 12.75 Kcal/mol and – 11.07 Kcal/mol and low Ki values of 447.95 pM and 7660 pM respectively, with AChE enzyme, signifying their potential as promising therapeutic candidates. This study emphasizes mushroom as a rich source of bioactive metabolites for the treatment and management of AD and provide the groundwork for further in – vitro validation.

Keywords: Alzheimer's disease (AD), Acetylcholine (ACh), Acetylcholinesterase (AChE), Bioinformatics, Docking.

GPU-Accelerated Optimization of Shortest Path Algorithms for Large-Scale Biological Network Analysis

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Abstract

The rapid expansion of biological network data, including protein-protein interaction (PPI) networks, gene regulatory networks, and metabolic pathways, has introduced significant computational challenges for efficient analysis and interpretation. Many critical bioinformatics tasks, such as pathway discovery, disease gene prioritization, and network-based biomarker identification rely heavily on shortest path computations across large and complex graphs. However, traditional CPU-based implementations often struggle to scale with the size and density of modern biological datasets. This study presents a GPU-accelerated framework for optimizing shortest path algorithms tailored for large-scale biological network analysis. The proposed approach focuses on parallelizing graph traversal operations using CUDA-enabled architectures, incorporating techniques such as workload balancing, memory coalescing, and optimized data structures to improve computational efficiency. Variants of Dijkstra's and breadth-first search (BFS) algorithms are redesigned to exploit massive parallelism, significantly reducing execution time for large biological graphs. Experimental evaluation on benchmark biological network datasets demonstrates substantial performance gains in terms of speedup and scalability compared to conventional implementations, without compromising computational accuracy. The proposed framework enables rapid analysis of complex biological systems, facilitating real-time insights in applications such as drug target identification, pathway analysis, and systems biology modelling. By integrating high-performance computing techniques with bioinformatics workflows, this work highlights the critical role of GPU-based algorithm optimization in addressing the computational demands of next-generation biological data analysis and advancing data-driven biotechnology research.

Keywords: GPU Computing, Shortest Path Algorithms, Bioinformatics, Biological Networks, Parallel Computing, CUDA, Systems Biology

Integrative Network Pharmacology and Transcriptomic Analysis Reveal the Multi-Target Anticancer Potential of *Arnica montana* Essential Oil in Breast Cancer

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Abstract

Arnica montana essential oil is a rich source of bioactive phytochemicals with potential anticancer properties. This study employed an integrative approach combining network pharmacology, transcriptomic validation, molecular docking, and in vitro analysis to investigate its therapeutic potential in breast cancer. Essential Oil Phytochemicals were retrieved from CSIR-CIMAP AromaDB and further screened for their ADMET properties. Target prediction and intersection with breast cancer-associated genes identified 102 common targets. Protein–protein interaction analysis revealed key hub genes, namely, ESR1, AKT1, ALB, GAPDH, MAPK1, IL6, PTGS2, and STAT3. Functional enrichment indicated involvement in inflammatory response, proliferation, and angiogenesis pathways. Transcriptomic validation using GSE42568 confirmed dysregulation of these targets in the breast cancer dataset. Molecular docking analysis demonstrated that NPC2 (thymol) exhibited strong binding affinity across multiple cancer-related targets, with the most favourable interactions observed with PTGS2 (−6.854 kcal/mol) and AKT1 (−6.843 kcal/mol), followed by ESR1 (−6.365 kcal/mol). Notably, thymol exhibited binding energies comparable to or superior to those of methyl thymol (NPC3) and linoleic acid (NPC2), supporting its potential as a promising candidate for further in vitro validation. The MTT assay demonstrated significant anticancer activity, with IC₅₀ values of thymol (50 µg/mL), doxorubicin (2 µM), and essential oil (2 µL/mL). Combination treatments showed enhanced efficacy, reducing IC₅₀ values for doxorubicin (0.5 µM) + thymol (35 µg/mL) and essential oil (1 µL/mL) + doxorubicin (0.5 µM), indicating synergism. Cell migration and Giemsa staining assays further confirmed these effects by revealing decreased cell motility and characteristic anticancer morphological changes. Overall, *Arnica montana* essential oil, particularly NPC2 (thymol), demonstrates multi-target anticancer potential against breast cancer by modulating key oncogenic pathways. These findings provide a basis for further experimental validation.

Keywords: Essential oil, Breast cancer, Network pharmacology, ADMET analysis

LichenBase: An AI-Assisted Static Database Integrating Metagenomic, Ecological, and Ethnopharmacological Data for Lichen Diversity

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Abstract

The symbiotic association between the photobiont(algae) and the mycobiont (fungi) leads to the formation of lichens. More than 20,000 species of lichens have been reported worldwide. These species also consist of diverse microbial communities and together act as vital bioindicators and sources of bioactive secondary metabolites. These organisms, though crucial for both maintaining the ecological balance and a source of unique therapeutic metabolites, remain underexplored. This is largely due to the fragmentation of taxonomic, ecological, metagenomic, and pharmacological information available on these organisms. Therefore, LichenBase was created as a curated, openly accessible static database as a user-friendly platform that can act as a single point source of information for the multifaceted data on lichen. A systematic literature review was conducted, followed by manual curation of lichen species in a standardized spreadsheet. The website for the database was generated by AI-assistance (Claude, Anthropic). The AI-generated code was launched after further manual verification. LichenBase demonstrates a low-cost investment and reproducible method for creating an easily accessible database for niche communities. Presently, the database provides information on 100 different lichen species, including their geographic distribution, NCBI BioProject metagenomes, and their documented therapeutic applications. This database serves as an integrated reference source that can provide detailed information on lichen species, consolidating scattered data on ecological metadata, medicinal applications, and metagenome information, thus saving time and energy and preventing knowledge gaps.

Keywords: Lichens, Biodiversity Database, Metagenomics, Lichen microbiome, Usnic Acid, AI-Assisted Curation

ScGAAC-CL: Enhancing Single-Cell Clustering via Graph Attention and Adaptive Contrastive Learning

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Abstract

Single-cell RNA sequencing (scRNA-seq) has high-resolution capabilities; it also comes with issues such as sparse data, high dimensionality, and noise, which hinder its accuracy in distinguishing various cells. To address these problems, we propose a novel scGAAC_CL model based on a graph neural network that integrates a graph attention autoencoder and contrastive learning methods to perform effective single-cell clustering. The proposed approach uses a deep autoencoder architecture (1024→512→256→64) along with batch normalization to learn low-dimensional latent space embeddings, along with gene selection based on the Seurat method that preserves biologically meaningful genes. Additionally, adaptive contrastive learning is introduced, utilizing data augmentation and entropy minimization in order to improve confidence in the assigned clusters. Furthermore, multi-head graph attention networks and optimization techniques are employed in combination with AdamW and cosine annealing to achieve stable and efficient learning. The results obtained using benchmark single-cell RNA-Seq datasets like Baron and Klein reveal that our model outperforms the baseline scGAAC consistently in terms of clustering accuracy with increases of 3 and 5%, NMI with increases of 2 and 2.5%, and ARI with increases of 4 and 5%, respectively. Our method successfully addresses the issues of dropouts and batches, improving the separability of clusters. The study provides a comprehensive framework for analyzing cell graphs within single cells, which can be used in exploring the diversity of cells.

Keywords: scRNA-seq, single-cell RNA clustering, Adaptive Contrastive learning, Graph Attention Networks

Integrated Evaluation of Processing Methods on Functional and Antidiabetic Properties of Finger Millet Using TOPSIS and In Silico Approaches

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Abstract

Dietary fiber and polyphenol-rich finger millet (*Eleusine coracana*) cereal has a high nutritional value and shows potential for type 2 diabetes management. The impact of processing (milling, soaking, parboiling, and roasting) was assessed on the physicochemical, phytochemical, antioxidant and structural characteristics of finger millet, followed by molecular docking against diabetes-related targets. The objective was to identify the most effective processing method and bioactive compounds with therapeutic relevance to glycemic control. Significant variations were observed: moisture ranged from $0.531 \pm 0.07\%$ (milling) to $11.43 \pm 0.81\%$ (soaking), ash from $2.08 \pm 0.23\%$ (parboiling) to $3.47 \pm 0.42\%$ (roasting), and crude fiber from $16.43 \pm 2.04\%$ (milling) to $68.69 \pm 0.55\%$ (parboiling). Increased fiber in soaked and parboiled millets aids in slowing glucose absorption and controlling blood glucose levels. Tannins (0.363 ± 0.14 – 0.419 ± 0.04 mg GAE/g) and total flavonoids (0.005 ± 0.01 – 0.027 ± 0.006 mg/g) contribute to inhibition of α -amylase and α -glucosidase, lowering postprandial glucose levels. Antioxidant activity (ABTS) was highest in milling ($47.24 \pm 0.004\%$) and roasting ($39.37 \pm 0.003\%$) samples, suggesting high free radical scavenging potential and hence prevention of oxidative stress-induced insulin resistance. Bulk (0.54 ± 0.01 – 0.66 ± 0.01 g/mL) and tapped density (0.62 ± 0.01 – 0.72 ± 0.01 g/mL) influence digestibility and satiety. Soaking was identified as the best method via TOPSIS. Structural characterisations (FTIR, XRD, TGA) revealed changes that might affect bioavailability. LC–MS detected active ingredients (epicatechin, naringenin, catechin, and p-coumaric acid) which were found stable in interactions with targets of diabetes in network pharmacology, molecular docking, RMSF and normal mode analysis. Data were statistically validated (normality, one sample t-test, correlation, PCA). Thus, processing, especially soaking, improves anti-diabetic properties of finger millet, thus justifying its use as functional food.

Keywords: Finger millet, In silico analysis, Type 2 diabetes, TOPSIS, Statistical validation

Repurposing Metabolic Drugs for Breast and Oral Cancer: A Network-Driven and Experimental Study

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Abstract

Drug repurposing has emerged as a cost-effective and time-efficient strategy for identifying novel therapeutic interventions in complex cancers such as Breast Cancer (BC) and Oral Cancer (OC). In the present study, an integrative *in silico* and experimental framework was employed to explore the potential of FDA-approved metabolic drugs targeting both malignancies. Using publicly available databases, such as Reactome, cBioPortal, and KEGG, as well as published literature, a total of 2044 genes associated with BC and 1275 genes associated with OC were systematically retrieved. Following it, Network pharmacology-based analysis, using Cytoscape integrated with the CytoHubba algorithm, was performed to identify critical hub genes. As a result, ACTB, AKT1, ALB, EGFR, GAPDH, HIF1A, IL1B, IL6, INS, STAT3, TGFB1, TNF, and TP53, were identified as the key genes in breast cancer. Interestingly, in the case of OC, a total of 5 hub genes were overlapping with those of BC, including ACTB, AKT1, BCL2, CTNNB1, EGF, EGFR, ESR1, FN1, HRAS, MYC, PIK3CA, PTEN, SRC, STAT3, and TP53. Subsequently, pathway enrichment analysis was conducted by integrating drug-target genes of selected FDA-approved metabolic drugs obtained from SwissTargetPrediction and KEGG. Using Schrödinger Maestro, Molecular docking studies were performed to evaluate binding interactions between selected drugs and key protein targets across both cancer types. This highlights the potential multi-target therapeutic effects of the selected drug. As Most of these identified genes were involved in cell survival and proliferation, the cytotoxic effect of the selected drug was validated on these two different cancer cell line models, including MCF-7 and KB 3-1. Following the MTT assay, the IC₅₀ of the identified drug was observed to be 225 mM on MCF and KB 3-1 cell lines after 24 hours of treatment. Preliminary findings suggest significant anticancer potential, which will be further validated using multiple functional assays. Overall, this study demonstrates a comprehensive pipeline integrating computational and experimental approaches to accelerate drug repurposing for cancer therapeutics.

Keywords: Drug repurposing, Metabolic drugs, *in silico*, *in vitro*

Hybrid ProtBert-CNN Model with Sequence-to-Structure Proxy Learning for Protein–DNA Binding Residue Prediction

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Abstract

Protein-DNA binding residue prediction plays a vital role in the field of gene regulation and protein function; however, the problem remains highly difficult owing to its dependence on context and heavy class imbalance. In this paper, we present a new deep-learning paradigm that uses context-aware protein-language representations with structure-aware learning to predict binding residues. First, we encode protein sequences with ProtBert which is a transformer-based pre-trained protein language model and extracts highly contextual embeddings of proteins. Subsequently, the obtained embeddings are fed into a CNN with multiple layers to learn their local spatial relationships. In order to deal with the issue of long protein sequences, the sliding window technique is used, such that the whole sequence can be considered by the model without any loss of data. Additionally, in order to tackle the problem of high-class imbalance within the binding residue dataset, the Focal Loss function is utilized, resulting in an improvement in the capability of the model to recognize binding residues that belong to the minority class. Lastly, a new learning technique called Sequence-to-Structure Proxy Learning is proposed using the multitask learning approach. The proposed model is developed using the PDNA-543 dataset and tested using the independent dataset PDNA-335. The experimental results show that the proposed method performs well with respect to F1-score, area under the curve (AUC), and Matthew's correlation coefficient (MCC). It outperforms some other techniques currently used. These results suggest the utility of protein language models, combined with CNN-based feature extraction and proxy structure-guided prediction tasks for predicting protein-DNA interaction residues.

Keywords: Protein-DNA binding site prediction, ProtBert, Sequence-to-structure proxy learning, multi-task learning

Computational Analysis of SLC7A11 in Arsenic-Induced Oxidative Stress and Ferroptosis in Zebrafish

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Abstract

Arsenic pollution is a major environmental and public health concern, known to exert its toxic effects primarily through oxidative stress, leading to disruption of cellular redox balance and biomolecular damage. Iron-dependent lipid peroxidation-mediated regulated cell death, termed ferroptosis, is a recently discovered mechanism of oxidative stress-induced cell damage. SLC7A11, a cystine/glutamate antiporter, is involved in regulating the intracellular concentration of glutathione and protecting cells against oxidative injury, but its involvement in arsenic-induced ferroptosis in aquatic animals is not well studied. The present study aimed to perform an integrated in silico analysis of SLC7A11 to assess its potential role in arsenic-induced oxidative stress and ferroptosis in zebrafish. Sequences were obtained from online databases and subjected to multiple sequence alignment, phylogenetic analysis and domain prediction. The findings showed a high level of conservation of SLC7A11 among vertebrates, including zebrafish, as well as the presence of conserved amino acid transport and redox regulatory domains. Phylogenetic analysis further supported the functional significance and evolutionary stability of the protein. These findings indicate that SLC7A11 may be involved in modulating oxidative stress and ferroptosis under arsenic exposure and provide new computational insights into its role in arsenic toxicity, highlighting it as a promising target for future experimental validation.

Keywords: Arsenic toxicity; Oxidative stress; Ferroptosis; SLC7A11; Zebrafish

RicebeanLncDB: A Comprehensive lncRNA Database for Ricebean (*Vigna umbellata*)

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Abstract

Ricebean (*Vigna umbellata*) is a nutritionally rich legume crop with significant potential to enhance food security because of its adaptability and resistance to biotic stresses. However, genetic improvement has been hindered by limited genomic resources and insufficient molecular characterization. Long non-coding RNAs (lncRNAs) are crucial for gene regulation, stress responses, and development in plants, making their systematic identification in crop species essential. In this study, we present a comprehensive lncRNA database for ricebean that provides detailed information, including sequence length, genomic coordinates, GC content, chromosome location, predicted targets, and miRNA associations. This user-friendly platform facilitates exploration and analysis of ricebean lncRNAs, supporting functional genomics studies and genomics-assisted breeding strategies. By addressing existing knowledge gaps, this resource aims to accelerate research into regulatory mechanisms and contribute to the genetic improvement of ricebean and related legumes.

Keywords: Ricebean, database, lncRNA, gene expression

Multi-class classification of Alzheimer's Disease Stages Using GWAS-Derived Features and Multi-Branch Deep Learning Architectures

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Abstract

Alzheimer's disease (AD) is a progressive neurodegenerative disease that leads to cognitive decline and affects millions globally. Early detection and classification of different stages, like Cognitively Normal (CN), Mild Cognitive Impairment (MCI), and AD, is important for diagnosis and understanding the prognosis of the disease. Genome-Wide Association Studies (GWAS) provide useful information to understand the prognosis of the disease and to identify genetic variants that are associated with AD. Using the high-dimensional GWAS data for multi-class classification remains a significant challenge. In this study, a multi-branch deep learning architecture is proposed that is capable of classifying subjects into CN, MCI, and AD categories by using GWAS data that has been retrieved from the Alzheimer's Disease Neuroimaging Initiative (ADNI) cohort. The dataset contained approximately 620,000 single-nucleotide polymorphisms (SNPs), which were analyzed using GWAS analysis techniques to identify the most important SNPs associated with the disease conditions. The values of different features, such as B-allele frequency (BAF), log R Ratio (LRR), and genotype information, of these selected SNPs were then used to build a predictive model for the classification. These features contain informative signals as they have been derived from the genetic intensity and allelic composition, thus making them ideal for model building. By combining these features with the selected SNPs, a comparative study was performed in which different deep learning algorithms, like one-dimensional Convolutional Neural Networks (1D-CNN), Artificial Neural Networks (ANN), and Transformers, were evaluated to get the best performing model. The multi-branch ANN outperformed with an accuracy of 85%, Micro-average AUC of 0.95, and Macro-average AUC of 0.96, which indicates the good true positive rate (TPR) and generalizability of the model. These results highlight the effectiveness of integrating GWAS-derived features with deep learning architectures for multi-class classification of Alzheimer's disease stages.

Keywords: Alzheimer's Disease, Genome-Wide Association Studies, Deep Learning, Multi-class Classification

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-3 β , cyclin-dependent kinase 5, and NF- κ B, 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.

Keywords: Alzheimer's disease; quercetin; fisetin; synergistic neuroprotection; in-silico studies; molecular docking

Predicting follow-up health status in temporomandibular joint disorder patients using machine learning and radiomic features

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Abstract

Temporomandibular joint (TMJ) disorders involve progressive deterioration of the mandibular condyle and adjacent bony structures, presenting clinically as persistent orofacial pain and restricted jaw movement. Early identification of patients at risk of structural progression remains an unmet need in orofacial medicine, as therapeutic options diminish substantially once significant bone loss has occurred. This study presents a machine learning pipeline that integrates baseline clinical data with radiomic descriptors extracted from the mandibular condyle and articular fossa to predict disease progression at follow-up. A cohort of 66 patients from the University of Michigan Deep Blue Data repository was used, comprising 43 non-progressing and 23 progressing cases. Radiomic features were derived from grey-level co-occurrence matrices and run-length matrices, capturing textural and structural properties of the condylar bone. Three classifiers — Logistic Regression, Random Forest, and XGBoost — were evaluated through stratified 5-fold cross-validation on a synthetically augmented training set of approximately 1,000 instances, while all original patient records were held out exclusively for final evaluation. XGBoost achieved a cross-validation ROC-AUC of 1.000, indicative of augmentation-pattern memorization rather than genuine generalization. Random Forest demonstrated robust performance on real patient data, attaining a ROC-AUC of 0.9666 and 88% accuracy, with a specificity of 95.3% and sensitivity of 73.9%. SHAP-based feature attribution revealed that condylar texture features — including entropy, short-run high grey-level emphasis, and trabecular bone numbers were the most influential predictors, consistent with known mechanisms of early osteoarthritic degeneration. Probability calibration confirmed that model outputs function as clinically interpretable risk estimates. These findings establish the feasibility of radiomic-based TMJ progression forecasting and highlight the methodological importance of separating augmented training data from real-patient evaluation sets.

Keywords: Temporomandibular joint disorders; Radiomics; Machine learning; Random Forest; SHAP interpretability

In Silico Strategies to Develop Therapeutics Against WHO Priority Pathogen *Acinetobacter baumannii*

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Abstract

Antimicrobial resistance emerged as one of the most significant challenges to modern healthcare as it threatens the efficacy of antibiotics that have been used to save millions of lives. *Acinetobacter baumannii* is one of the most treacherously important pathogens on the list of the World Health Organization, which is a multidrug resistant nosocomial pathogen causing severe infections in hospitals since it infects patients around the world, and clinicians have limited treatment options. Its ability to withstand extreme conditions, to persist within medical equipment, and quickly develop resistance determinants makes the organism a model system to study the mechanisms of resistance evolution and transmission. The traditional approach to the discovery of antibiotics has not been able to keep up with the speed of developing resistance, which has led to the need to shift to a more rational and systematic approach. This review summarizes existing information on the ways computation biology and in silico approach therapeutic targets in *Acinetobacter baumannii*. The framework uses these computational approaches in conjunction with mechanistic understanding of bacterial pathogenicity and resistance architecture to determine proteins that are essential in survival during antimicrobial stress. Also, the review discusses the use of natural compounds, especially phytochemicals, as multi-target therapeutic agents that may act as complements to current antibiotics and possibly surmount their resistance. Much emphasis is put on the translation capabilities of computationally identified targets and how they can be used in conjunction with structure-based drug design and virtual screening. The article shows that systems-level analysis combined with stringent validation and natural product discovery can fill the longstanding gap between computational prediction and clinical use. Finally, the review endorses a multifaceted solution to utilize in silico target discovery with experimental validation and phytochemical studies to establish effective antimicrobial solutions to this recalcitrant pathogen and serve as a template to be used in other WHO-priority organisms.

Keywords: Antimicrobial resistance, *Acinetobacter baumannii*, In-silico drug discovery

Artificial Intelligence and Machine Learning-based Antimicrobial Strategies for Combating ESKAPE Pathogens

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Abstract

Antimicrobial resistance (AMR) has emerged as a serious worldwide health concern that has resulted in a notable increase in the rates of morbidity and mortality. Management of nosocomial infections has become increasingly challenging due to the prevalence of multidrug resistance, which leads to prolonged hospitalization. The World Health Organization (WHO) has classified the ESKAPE group (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* spp.) as high-priority pathogens. The reduced effectiveness of traditional antibiotics towards these pathogens has made it necessary to find novel alternatives with lower resistance rates. However, the traditional approach for the discovery and development of antimicrobials involve prolonged development periods and high financial expenditure. Artificial Intelligence (AI) and Machine Learning (ML) based tools could be leveraged to speed up the screening and identification process of potential antimicrobials. These tools can efficiently analyse data from a large number of datasets, and help to predict the associated antibacterial activity, stability, and toxicity within a short duration of time. Furthermore, the models trained on curated datasets can identify hidden molecular patterns, which can support in predicting resistance and prioritize compounds which have a higher probability of success. The virtually selected candidates can be further confirmed using *in vitro* and *in vivo* analysis. Thus, AI and ML methods can be integrated into antimicrobial screening pipelines to identify next-generation antimicrobials that can aid in treating nosocomial infections.

Keywords: Antimicrobials, Antimicrobial resistance, Machine Learning, Artificial Intelligence

Computational Design of Potent siRNAs Targeting SIRT7 in Gynaecological Cancers with Optimized Intracellular Delivery Strategies

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Abstract

SIRT7 is a multifunctional epigenetic regulator and is significantly overexpressed in three major gynaecological cancers i.e., ovarian, cervical, and endometrial cancers, contributing to the proliferation and progression of tumors. This study focused on computationally designing and evaluating small interfering RNAs (siRNAs) as potential therapeutic candidates targeting SIRT7. In silico expression analysis has confirmed overexpression of SIRT7 in tumor tissues as compared to normal samples. siRNAs (S1-S6) were designed using in silico approaches which were then screened for target specificity. Molecular docking and simulation studies revealed interactions of siRNA candidates with human Argonaute 2 (Ago2) protein, maintaining strong post-simulation hydrogen bonds and salt bridges. Both S1 and S6 showed stable interactions with key domains of Ago2 protein, highlighting incorporation into RNA induced silencing complex (RISC). Overall, S1 and S6 emerge as promising siRNA candidates for targeting SIRT7.

Keywords: SIRT7, siRNA, in silico, Argonaute2, gynaecological cancers

SmartABCPeptide: Anti-breast cancer peptide Designing and Prediction Tool

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Abstract

Breast cancer remains one of the most prevalent and life-threatening malignancies among women worldwide, and existing therapeutic strategies such as chemotherapy, radiotherapy, endocrine therapy, and targeted therapy are often associated with severe side effects, drug resistance, recurrence, and limited specificity. Anti-cancer peptides (ACPs), particularly anti-breast cancer peptides (ABCPs), have emerged as promising therapeutic candidates due to their high specificity, low toxicity, and ability to selectively target cancer cells while sparing normal tissues. However, the experimental identification and validation of novel ABCPs are time-consuming, costly, and labor-intensive. To address this challenge, we developed SmartABCPeptide, a machine learning-based prediction and peptide designing tool for accurate classification of peptides as ABCPs or non-ABCPs. Experimentally validated peptide datasets were curated from CancerPPD, UniProt, TumorHope, and ApInAPDB, followed by preprocessing using SeqKit and redundancy reduction using CD-HIT. Multi-source feature extraction was performed using sequence-based descriptors, physicochemical properties from ProtParam, and 210 structural descriptors from RDKit, generating a comprehensive biochemical representation of peptides. To handle class imbalance, novelty-based under sampling using Isolation Forest and SMOTE oversampling were applied, resulting in a balanced dataset of 500 ABCPs and 500 non-ABCPs. Feature selection was performed using mRMR followed by Recursive Feature Elimination, reducing 920 features to the 150 most informative descriptors. Four classifiers: Artificial Neural Network, Random Forest, Support Vector Machine, and AdaBoost were trained and integrated using a soft-voting ensemble strategy. The ensemble model achieved outstanding performance with 98.9% accuracy, 0.98 precision, 0.99 recall, 0.98 F1-score, and 0.99 ROC-AUC, outperforming individual models.

Keywords: Anti-cancer peptides, breast cancer, peptide designing, machine learning, drug discovery

Bioinformatic identification of molecular targets of *Ziziphus jujuba* (Mill.) leaf phytochemicals in endocrine metabolic disorders

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Abstract

Endocrine metabolic disorders, including obesity and type 2 diabetes, represent major global health challenges characterized by complex molecular interactions affecting glucose homeostasis, insulin signaling, and oxidative stress pathways. Natural products have gained increasing attention as potential sources of bioactive compounds capable of modulating these pathways. *Ziziphus jujuba* (Mill.), a medicinal plant widely used in traditional medicine, contains a variety of phytochemicals such as flavonoids, saponins, and phenolic compounds with potential metabolic regulatory effects. The present study aimed to identify potential molecular targets of bioactive compounds derived from *Ziziphus jujuba* leaves using bioinformatic approaches. Major phytochemicals reported in the leaves were first retrieved from phytochemical databases and literature sources. Subsequently, computational target prediction and pathway enrichment analyses were conducted using publicly available bioinformatics tools and databases. The predicted targets were further analyzed to identify their involvement in metabolic and endocrine-related signaling pathways, including insulin resistance, glucose metabolism, lipid regulation, and oxidative stress responses. Network analysis highlighted several key molecular targets potentially involved in the regulation of endocrine metabolic dysfunction, suggesting possible mechanisms through which *Ziziphus jujuba* leaf compounds may exert therapeutic effects. The findings provide preliminary computational evidence supporting the pharmacological relevance of this plant and highlight promising molecular targets for further experimental validation. This integrative bioinformatic approach contributes to the understanding of plant-derived compounds in metabolic disease modulation and may support the development of novel phytotherapeutic strategies targeting endocrine metabolic disorders.

Keywords: *Ziziphus jujube* (Mill.), Bioinformatics, Molecular targets, Phytochemicals.

Computational Biology & Bioinformatics

Posters

The role of conformational dynamics of Htt in Huntington's disorder-like protein aggregation

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Abstract

The Htt (huntingtin) protein associated with HD (Huntington's disorder) is among the leading neurodegenerative diseases, is caused by a gain-of-function mutation in the N-terminal polyQ region of the Htt. Htt consists of 3138 (17 polyQ) amino acids and is further divided into three sub-parts. HD affects the cognitive, motor, and psychiatric functions. In disease cells, inclusion bodies are enriched in Htt fragments containing polyQ. The expansion of the polyQ correlates with aggregate size and the onset of HD. However, the exact role of full-length Htt in aggregate formation remains unclear. Using coarse-grained molecular dynamics simulations, our study indicates the conformational dynamics of Htt and the effects of sub proteins on the structural facade. The intra- and inter-contact analyses suggest that the polyQ region can loop like a structure similar to a beta sheet with a higher probability for a larger polyQ length. However, HAP40 reduces the looping probability by increasing contacts between polyQ and other regions of Htt. Thus, our findings indicate that polyQ has a significant role in the disease's pathogenesis; altered functional activity and structural modifications lead to inclusion body formation, and these effects can be overcome with the help of HAP40.

Keywords: HD, Coarse-graining, HAP40, HAP1, polyQ.

In silico-based screening and molecular dynamic simulation of natural products as potential inhibitors of lumpy skin disease in cattle

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Abstract

This study explores the potential of natural products as inhibitors against lumpy skin disease (LSD) in cattle through an integrative in silico approach. Lumpy skin disease, a viral infection causing severe economic losses in livestock, lacks highly effective antiviral therapeutics, prompting the need for alternative strategies. Here, a curated library of plant-derived bioactive compounds was screened against a key viral target protein using molecular docking to identify promising inhibitory candidates. Top-ranked compounds were further evaluated based on binding affinity, interaction stability, and pharmacokinetic properties, including ADMET profiling. To validate the stability of ligand–protein complexes under physiological conditions, molecular dynamics simulations were performed over an extended timescale, assessing parameters such as root mean square deviation (RMSD), root mean square fluctuation (RMSF), and hydrogen bonding patterns. The results revealed several natural compounds exhibiting strong binding affinity and stable interactions within the active site of the viral protein, suggesting their potential as effective inhibitors. Notably, these compounds demonstrated favorable drug-like properties and minimal predicted toxicity, highlighting their suitability for further development. This study provides a computational framework for accelerating antiviral drug discovery and underscores the value of natural products as a rich source of bioactive molecules. The findings offer a foundation for future experimental validation and contribute to the development of sustainable and cost-effective therapeutic strategies against LSD in cattle.

Keywords: Lumpy skin disease, natural products, molecular docking, molecular dynamics simulation, antiviral drug discovery

Explore complex interactions between genes and proteins to understand the regulatory mechanisms of Parkinson's disease (PD)

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Abstract

Parkinson's disease (PD) is a progressive neurodegenerative disorder marked by motor dysfunction and underlying molecular complexity involving gene–protein interactions. This study aims to systematically explore the intricate regulatory networks connecting genes and proteins to better understand PD pathogenesis. We employed an integrative bioinformatics framework combining gene expression profiling, protein–protein interaction (PPI) network construction, pathway enrichment analysis, and systems biology approaches. Publicly available transcriptomic datasets were analyzed to identify differentially expressed genes, followed by network modeling using STRING and Cytoscape to uncover key regulatory hubs. Our findings reveal critical gene clusters and protein modules associated with dopaminergic neuron degeneration, oxidative stress, and mitochondrial dysfunction. Notably, several hub proteins demonstrated strong connectivity, suggesting their central role in regulatory signaling pathways linked to disease progression. Functional enrichment highlighted significant pathways, including neuroinflammation and metabolic dysregulation, emphasizing the multifactorial nature of PD. These results provide deeper insight into the molecular circuitry governing PD and identify potential biomarkers and therapeutic targets. Overall, this study underscores the importance of integrative omics approaches in unraveling complex biological systems and contributes to advancing precision medicine strategies for neurodegenerative diseases.

Keywords: Parkinson's disease, Gene–protein interaction, Bioinformatics, Regulatory networks, Neurodegeneration

In-Silico Appraisal of Phytochemical's Efficacy as Protein Inhibitors for Neurodegenerative Disease

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Abstract

Neurodegenerative diseases (NDs), particularly Alzheimer's disease (AD), are progressive disorders characterized by cognitive decline and neuronal dysfunction. Current therapeutic agents, such as Donepezil, primarily provide symptomatic relief and are often associated with adverse side effects, highlighting the urgent need for safer and more effective alternatives. In this study, a comprehensive in-silico approach was employed to evaluate the inhibitory potential of phytochemicals against human acetylcholinesterase (AChE), a critical therapeutic target in AD. A total of 93 phytochemicals derived from 22 medicinal plants were screened using molecular docking techniques. The results identified several compounds, including Withaferin A, Asparagoside A, Rauwolscline, Arjunetin, and Tinocordiside, exhibiting binding affinities superior to the reference drug Donepezil (−11.08 kcal/mol). Among these, Withaferin A demonstrated the highest binding affinity (−11.99 kcal/mol), indicating strong interaction with the active site of AChE. Top-performing compounds were further subjected to ADMET profiling and toxicity prediction to assess their drug-likeness and safety. Molecular dynamics simulations over 100 ns revealed that Tinocordiside and Arjunetin formed stable protein–ligand complexes, supported by consistent root mean square deviation (RMSD), radius of gyration (Rg), and solvent-accessible surface area (SASA) profiles. Binding free energy calculations using MM-PBSA further validated the stability and favorable interaction energies of these complexes. Additionally, principal component analysis (PCA) confirmed their conformational stability under simulated physiological conditions. Overall, this study highlights the potential of plant-derived phytochemicals as promising AChE inhibitors and demonstrates the effectiveness of bioinformatics-driven strategies in early-stage drug discovery. These findings provide a strong foundation for further experimental validation and the development of novel therapeutic candidates for Alzheimer's disease and related neurodegenerative disorders.

Keywords: Acetylcholinesterase (AChE), Alzheimer's disease, Bioinformatics, Molecular dynamics simulation, Neurodegenerative disorders

Multi-Target Analysis of Bioactive Compounds in Cardiovascular Disease Using a Computational Pipeline

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Abstract

Cardiovascular diseases (CVDs) involve interconnected pathological mechanisms, including dyslipidemia, chronic inflammation, oxidative stress, and endothelial dysfunction, making single-target therapeutic strategies insufficient for effective management. This study proposes a computational pipeline to evaluate the multi-target potential of natural bioactive compounds in addressing complex CVD pathways. Four compounds—resveratrol, epigallocatechin gallate (EGCG), lycopene, and omega-3 fatty acids—were selected based on established pharmacological evidence, bioavailability, and structural data availability in public databases. A panel of ten protein targets was curated, including established markers like LDLR, APOB, NOS3, CRP, and ACE, as well as emerging regulators such as SIRT1, NRF2, KEAP1, NLRP3, and PCSK9, which are key players in lipid metabolism, oxidative stress response, and inflammatory signaling. Protein–protein interaction (PPI) analysis was conducted using the STRING database with high-confidence interaction thresholds to map functional connectivity among selected targets. Network visualization and clustering revealed strong associations within lipid regulation, redox homeostasis, and inflammatory modules, highlighting key hubs and pathway interdependencies. These findings support a systems-level understanding of CVD progression and emphasize the importance of multi-target modulation. The proposed workflow integrates compound selection, target identification, structural data retrieval, and interaction network analysis in a stepwise manner, ensuring reproducibility and scalability. Furthermore, this framework enables prioritization of bioactive compounds based on their potential to influence multiple interconnected targets simultaneously. Docking-based validation and binding affinity ranking are proposed as subsequent steps to refine candidate selection. Overall, this study provides a robust computational strategy for accelerating the identification of multi-target therapeutics.

Keywords: Cardiovascular disease, Bioactive compounds, Protein–protein interaction, STRING, in silico pipeline

Modelling Cyber Trust and User Behaviour in Digital Health Platforms Using PLS-SEM

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Abstract

The user interactions have revolutionized, with the rise of digital health and bioinformatics systems, which present significant challenges in terms of privacy, security, and reliability. In such a landscape, cyber trust is an important factor in shaping user behaviour and brand engagement. The purpose of this research is to explore the interconnections between cyber trust and brand loyalty in the health domain. The study builds upon existing theories; the research introduces a structural model whereby cyber trust has a direct and indirect effect on brand loyalty via brand commitment as well as indirectly via brand commitment. The proposed model is based on a network approach, similar to systems-based approaches, in which relationships between constructs are examined in a complex ecosystem. Quantitative research is undertaken using a cross-sectional survey, gathering information from social media users. The model will be tested using Partial Least Squares Structural Equation Modelling (PLS SEM) using SmartPLS. The results will show that cyber trust plays a critical role in improving user experience and continued use, especially for digital health and data analytics platforms. The study contributes by offering a behavioural modelling approach that explains the role of adoption, use, and continued use. What's more, this research is in line with cloud-based platforms and computational and network analysis techniques, thus offering interdisciplinary value to computational modelling and providing cross-disciplinary value to it.

Keywords: Cyber trust, Digital Health platforms, User Behaviour, PLS-SEM, Network modelling

In-Silico Screening of Therapeutic Bioactive Peptides from Pearl Millet Using a Comparative Similarity Strategy

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Abstract

Pearl millet (*Pennisetum glaucum*) is a nutritionally rich cereal crop and a potential source of therapeutic bioactive peptides with applications in functional foods and pharmaceuticals. The present study aimed to identify putative therapeutic bioactive peptides from pearl millet using a comparative similarity-based *in-silico* strategy. A curated dataset of 20 experimentally validated therapeutic peptides (14 peptides mined from medicinal plants and 6 antimicrobial peptides from public databases) was compiled from literature and peptide repositories. These peptides were associated with antimicrobial, antioxidant, anti-inflammatory, antihypertensive, anticancer, and immunomodulatory properties; were retrieved in FASTA format; and were used as query sequences for similarity screening against the pearl millet genome/proteome using BLAST. The comparative analysis found 48 important homologous hits, and 16 of these pearl millet-derived bioactive peptides met the selection criteria ($\geq 70\%$ identity, $\geq 60\%$ query coverage, and $E\text{-value} \leq 1e^{-5}$). The shortlisted peptides ranged from 8 to 32 amino acids, with several enriched in cationic and hydrophobic residues linked to therapeutic activity. Physicochemical characterization predicted 11 peptides with favorable stability profiles, while toxicity and allergenicity assessment indicated 14 peptides to be non-toxic and non-allergenic. Functional annotation suggested 7 antimicrobial, 5 antioxidant, 4 anti-inflammatory, and 3 multifunctional peptides. Conserved motif analysis revealed similarity with known plant-derived therapeutic peptide families, supporting their potential bioactivity. These findings highlighted pearl millet as a promising reservoir of novel therapeutic peptides and suggested that comparative *in-silico* screening provides a rapid and cost-effective strategy for peptide discovery. The identified candidate peptides provide a foundation for future experimental validation and development of peptide-based nutraceutical and therapeutic applications

Keywords: Pearl millet, Bioactive peptides, In-silico screening, Comparative similarity, BLAST

In Silico Phylogenetic and Motif Analysis of ACE2 Gene Across Eukaryotes

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Abstract

The Angiotensin-Converting Enzyme 2 (ACE2) gene encodes a type I transmembrane glycoprotein that occupies a central position in eukaryotic physiology, serving both as a carboxypeptidase within the Renin-Angiotensin System and as the primary cellular entry receptor for SARS-CoV and SARS-CoV-2. Despite its well-established biomedical relevance, the evolutionary conservation of ACE2 across eukaryotes and the breadth of its functional motif repertoire beyond the viral receptor-binding interface remain poorly characterized. This study presents a comprehensive in silico phylogenetic and motif analysis of the ACE2 gene across 67 taxonomically diverse eukaryotic species encompassing Mammalia (n = 34), Fungi (n = 12), Pisces (n = 9), Aves (n = 5), Reptilia (n = 3), Amphibia (n = 2), and viral-associated sequences (n = 2). Nucleotide sequences retrieved from NCBI GenBank were subjected to MSA using ClustalW algorithms, yielding a curated alignment of 1,000 base pairs with 784 informative columns after gap masking. Phylogenetic reconstruction using the Neighbour-Joining method under the Jukes-Cantor substitution model with 1,000 bootstrap replicates resolved distinct vertebrate-specific clades, confirming progressive divergence from mammals through fish and fungi. Shannon entropy-based conservation scoring coupled with sliding-window peak detection identified 17 statistically significant conserved motifs (M1–M17), with conservation scores ranging from 0.279 to 0.462 bits. Motif 5 (positions 298–317) exhibited the highest conservation across all taxa, while Motif 14 (positions 771–790) demonstrated the broadest cross-species coverage at 67.8%. GC content across motifs ranged from 37.5% to 49.8%, suggesting lineage-specific nucleotide compositional shifts. Differential motif retention across taxonomic groups indicated pronounced conservation in mammals and notable divergence in fungal and piscine lineages. These findings delineate a dual evolutionary trajectory for ACE2 strict conservation of catalytically and structurally essential motifs alongside lineage-specific divergence in regulatory regions providing a molecular reference framework.

Keywords: ACE2, Phylogenetic analysis, Conserved motifs, Eukaryote evolution

Genome Characterization and Molecular Detection of Indian Isolates of Hibiscus Chlorotic Ringspot Virus Using High-Throughput Sequencing and Bioinformatics Analysis

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Abstract

Hibiscus chlorotic ringspot virus (HCRSV) is an important pathogen of *Hibiscus rosa-sinensis*, affecting its ornamental and medicinal value. In this study, we characterized Indian isolates of HCRSV using high-throughput sequencing (HTS) and bioinformatics analysis. Infected leaf samples were subjected to HTS, followed by genome assembly and analysis using standard bioinformatics tools, including mutation profiling, sequence identity (SDT), phylogenetic analysis, and recombination detection. Two genome sequences, HRS1 (3.888 kb) and HRS2 (3.913 kb), were obtained. Both isolates showed more than 92% nucleotide identity with the reference genome. Mutation analysis identified 264 variations in HRS1 and 233 in HRS2, including transitions, transversions, insertions, and deletions, indicating genetic diversity. Phylogenetic analysis grouped the Indian isolates with strains from South Africa and China, forming a closely related cluster. Recombination analysis detected four events involving isolates from Singapore, Colombia, and Brazil, suggesting possible genetic exchange across regions. The presence of sequence variation between the two assemblies indicates heterogeneity within the viral population. Overall, this study provides the first complete genome information of HCRSV from India and highlights the role of bioinformatics approaches in understanding viral diversity and evolution. The results were further validated through one-step, two-step RT-PCR assays and mechanical inoculation.

Keywords: *Hibiscus rosa-sinensis*, NGS, Phylogeny, RT-PCR assay, SNP analysis

Drug Repurposing for Polycystic Ovary Syndrome

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Abstract

Polycystic ovary syndrome is one of the most frequent and heterogeneous endocrinometabolic disorders in reproductively active human females. It is usually characterized by an excess of androgen, anovulation, polycystic ovarian appearance, and increased incidence of insulin resistance. Since metabolic dysfunction and female reproductive dysregulation mutually affect each other, PCOS is hard to control, and conventional treatment methods based only on alleviating symptoms have relatively little effect in the long run. Effective management of PCOS requires multifunctional agents that simultaneously target insulin resistance, hyperandrogenism, ovulatory dysfunction, and hormonal imbalance. In this study, a virtual screening method based on structural similarity was used to assess the potential of approved anti-diabetic drugs to be repurposed for PCOS treatment. These drug targets play an important role in follicular development, ovulation, granulosa cells' functions, and hormonal homeostasis, which are compromised in PCOS patients. In this syndrome, insulin signalling abnormalities are closely linked to alterations in steroid hormone levels. The dataset was created by selecting antidiabetic compounds from PubChem. Receptor preparation, ligand energy minimization, generation of the active-site grid, and molecular docking were performed using AutoDock Vina. For binding analysis, we evaluated docking scores, ligand conformation, hydrogen-bonding patterns, hydrophobic interactions, and the occupation of key amino acid residues within the classical ligand-binding pocket. Some anti-diabetic compounds demonstrated potent binding conformations similar to those of known ER α agonists, suggesting potential compatibility with the protein. These findings suggest that certain anti-diabetic drugs may have dual effects on PCOS, as they can not only ameliorate insulin resistance but also regulate ovarian function by modulating the ER α pathway. This research demonstrates that repurposing strategies can uncover connections between pharmacology and metabolic-reproductive mechanisms in multifactorial endocrinopathies.

Keywords: Drug repurposing, PCOS, Virtual screening, ER α pathway

Comparative Transcriptomic Analysis of Preimplantation Embryogenesis Reveals Conserved and Species-Specific Regulatory Mechanisms in Mammals

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Abstract

Preimplantation embryogenesis is an essential stage in the developmental process in mammals and offers significant insights into reproductive biology and assisted reproductive technologies. This study was conducted to compare the dynamics of transcriptomic changes between *Homo sapiens* and *Bos taurus* at the onset of embryogenesis, particularly during the morula to blastocyst transition. RNA-seq data were used to analyze the differentially expressed genes (DEGs) in both organisms, followed by DEGs' prediction using machine learning approaches with LSTM and FNN networks and enrichment pathway analysis. The findings of this study indicated significant transcriptomic reprogramming in humans, as evident from >9,500 genes being differentially expressed during various stages. On the other hand, *B. taurus* had fewer genes (100-150 genes) being differentially expressed, implying that it follows a simple transcriptional pattern compared to *H. sapiens*. The PCA plot showed distinct separation among different stages in *H. sapiens* with the first PC explaining most of the variance, indicating accurate identification of developmental progress. LSTM networks outperformed FNN networks, giving almost perfect prediction of gene expression (AUC approaching 1.0). The analysis highlighted a few conserved key genes and a unique novel candidate in *B. taurus*, LOC783399. The enrichment analysis indicated differences in biological significance between the two organisms: while human embryos were enriched for stress response, nucleic acid binding, and implantation primed biological processes, *B. taurus* was characterized by enrichment of lipid metabolism and fast development. This information indicates that there is an evolutionary compromise between biological complexity and metabolic simplicity in early stages of embryo development. This research contributes significantly to our knowledge of the processes involved in the development process in a variety of organisms.

Keywords: Preimplantation embryogenesis, Machine learning, Comparative genomics

Artificial Intelligence and Machine Learning–Enabled Drug Discovery, Biomarker Identification, and Biotechnological Interventions in Schizophrenia

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Abstract

Medical advancements in the current era have set out new medical practices that eliminate the need for hospital-based medical diagnosis techniques while employing modified systems for medical decision-making based on data generated to improve medical practices. Medical sensor technology has been developed in terms of progressing analog techniques to nanotechnology-based complex systems for providing on-demand, perpetual observation of physiological and biochemical inputs. This analysis attempts to estimate the utilization of nanotechnology and artificial intelligence together, which has the potential to provide innovative medical sensors. The unique physicochemical properties offered by the high surface-to-volume ratios of nanomaterials, such as the presence of nanometals, nanometal oxides, carbon nanomaterials, and nanohybrids of polymeric nanomaterials, provide an exceptional sensing ability together with excellent biological compatibility. These nanomaterials are known to provide the detection of even trace amounts of biomarkers. This metabolic information is dealt with complex nano-sensing inputs, including inputs with varied dimensions, noise, and non-linear patterns, requiring smart analytical systems for efficient sensing analysis. These systems integrate artificial intelligence concepts, including machine learning, deep, and reinforcement learning for effective signal analysis, feature extraction, dimensionality, and intelligent adaptive analysis. The chapter offers the classification of diagnosis based on supervised, also known as conventional, deep learning approaches for the analysis of continuous sensor readings, as well as reinforcement learning for the calibration of sensors in a real-time, stable fashion. There are also details on the advancement in surface engineering, plasmonic sensing, quantum sensing, and nanofabrication, which are significant enablers for high-quality, label-free sensing. Precision medicine, ongoing surveillance, and self-management are made possible by the scalable platform provided by the combination of AI approaches with nanotechnology for medical devices and sensors.

Keywords: Artificial Intelligence, Biosensing, Digital healthcare, Medical sensors

EEG-Based Epileptic Seizure Detection Using Hybrid 1D-CNN and Liquid Neural Networks

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Abstract

Epilepsy is a chronic neurological disorder characterized by a predisposition to recurrent, unprovoked seizures. It affects more than 50 million people worldwide, and it is caused by sudden, excessive electrical discharge in the brain. These electrical discharge signals can be captured by electroencephalogram (EEG) signals through scalp electrodes. The detection of epileptic seizure (ES) becomes clinically challenging as signals exhibit abnormal and sharp waves that are more complex and non-stationary in nature. Traditional analysis of EEG signals is time-consuming and heavily dependent on expert interpretation, creating the need for robust automated machine learning-based models. In this study, several deep learning algorithms were implemented for early detection and classification of ES by analysing EEG signals, as these models are capable of decoding the complexity of these signals. A comparative analysis was conducted to identify the best hybrid model with high accuracy and good performance. The hybrid approach used a backbone of one-dimensional Convolutional Neural Networks (1D CNN) for feature extraction and was integrated with different deep learning architectures, such as Closed-form Continuous-depth Networks (CfC), Liquid Time-Constant Networks (LTC), Long Short-Term Memory (LSTM), and Multilayer Perceptron (MLP). These architectures were trained and evaluated on a publicly available benchmark EEG dataset, the Bonn University EEG dataset, encompassing both multi-class and binary classification tasks. The CfC model shows superior performance, achieving an average accuracy of 86% and an AUC score of 0.95 on the Bonn dataset. These results highlight the potential of liquid neural network-based architectures, particularly continuous-depth models, as promising tools for epileptic seizure diagnostics. The deployment of Liquid Neural Networks offers a more adaptive and flexible approach compared to conventional deep learning methods, making them better equipped to handle the complex and unpredictable nature of epileptic brain signals.

Keywords: Epileptic seizure detection, Electroencephalogram, Liquid Neural Networks

The Role of Fermented *Picrorhiza kurroa* Extract in Mitigating Palmitic Acid-Induced Lipotoxicity

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Abstract

Medicinal plant-derived bioactives have emerged as promising therapeutic agents due to their multi-targeted mechanisms and safety profiles. However, limited studies have explored the enhanced efficacy of fermented medicinal plants in modulating metabolic and immune dysfunction. The present study investigates the therapeutic potential of fermented *Picrorhiza kurroa* (FPK) in mitigating lipid toxicity and inflammatory responses in *in vitro* models. Palmitic acid is induced in HepG2 and C2C12 cell lines. Cells were treated with different concentrations of FPK, followed by assessment of lipid accumulation through Oil Red O staining. Gene expression qRT-PCR was performed for key markers involved in lipid metabolism (PPAR α , SREBP-1c), glucose metabolism (GLUT4) and inflammation (TNF α , IL-6, NF-kB). FPK treatment significantly reduces intracellular lipid toxicity compared to untreated controls. Gene expression analysis revealed a regulation of lipid oxidation and glucose metabolism genes, along with downregulation of lipogenic and pro-inflammatory markers. These findings suggest that FPK exerts its effect by modulating metabolic inflammatory pathways. Furthermore, fermentation is hypothesized to enhance the bioavailability and efficacy of active phytoconstituents, thereby amplifying positive therapeutic outcomes. This study also proposes future validation of *in vivo* model to confirm systemic effects and translational relevance. In conclusion, FPK demonstrates significant potential as an anti-steatotic and anti-inflammatory activity *in vitro* model. A natural therapeutic candidate for lipotoxicity management. This study provides a mechanistic basis for further *in vivo* investigation and supports the development of plant-based interventions for metabolic disorders.

Keywords: Lipotoxicity; Inflammation; *Picrorhiza kurroa*; Fermentation; Palmitic Acid

Network Pharmacology and Molecular Dynamics Highlight Oncogenic Nodes Along the Gut–Brain Axis Modulated by Bioactive Compounds of *S. boulardii*

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Abstract

Saccharomyces boulardii, a probiotic yeast, is known for its beneficial effects on gut health and promoting overall human well-being. Thus, the present study examined the role of bioactive compounds from *S. boulardii* in the context of interconnected gastrointestinal, neurological disorders, and associated cancers via the gut-brain axis using network pharmacology. Out of 116 compounds identified through literature mining, 10 were shortlisted based on ADMET analysis. Target prediction through SwissTargetPrediction and SuperPred identified 682 unique human targets associated with these compounds. Gene–disease association analysis revealed 1,390 genes common to targeted disorders, obtained from GeneCards and DisGeNET databases, resulting in 115 overlapping genes between predicted targets and disease sets. STRING and Cytoscape were used for protein–protein and protein-target interaction analyses, showing 1,174 interactions, indicating strong connectivity. Integration with *S. boulardii* compounds formed a network of 127 nodes and 1,509 edges. Key bioactive compounds included phenyllactic acid, tyrosol, 4-hydroxymandelonitrile, and 2-propylpiperidine. Function enrichment via GO, KEGG, and Reactome revealed associations with the regulation of signal transduction, cell death, and cancer-related pathways. Twenty-two top targets with four selected bioactive compounds were subjected to binding affinity evaluation. The top four sets were analysed for molecular interactions via MD simulations, and free energy calculations showed strong 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) complexes. The results demonstrate that bioactive compounds from *S. boulardii* interact with human proteins, including ABL1, PTPN11, EGFR, and CXCR4, highlighting their potential in anticancer therapy.

Keywords: Free energy calculations, Gut-brain axis, Molecular dynamics simulations,

In Silico Analysis of Neuroactive Compound Biosynthesis *Streptomyces rimosus* via Protein Association Networks: Implications for the Gut-Brain Axis and Novel Psychobiotic Applications

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Abstract

The genus *Streptomyces* is widely recognized for its ability to synthesize diverse bioactive secondary metabolites with important pharmaceutical applications. Recently, increasing attention has been directed toward microbial metabolites capable of influencing the gut–brain axis. In this study, *Streptomyces rimosus* ATCC 10970, a well-known industrial producer of oxytetracycline, was used as a model organism to investigate the biosynthetic potential for four neuroactive or neuromodulatory compounds: L-histidine, L-tryptophan, γ -aminobutyric acid (GABA), and geosmin. Protein–protein interaction (PPI) networks were constructed for key biosynthetic enzymes, including histidinol dehydrogenase (HisD), tryptophan synthase subunit beta (TrpB), glutamate decarboxylase (GadB), and germacradienol/geosmin synthase (GeoA). K-means clustering (K = 4) identified distinct functional modules within these biosynthetic pathways. HisD, TrpB, and GeoA exhibited strong associations with curated KEGG metabolic pathways, corresponding to L-histidine biosynthesis (map00340), L-tryptophan biosynthesis (map00400), and terpenoid backbone biosynthesis (map00900), respectively. In contrast, GadB showed indirect connectivity with glutamate metabolism and broader nitrogen metabolic networks. Homology analysis using BLASTP (bit score > 500) revealed conserved orthologs in *Streptomyces coelicolor*, *Streptomyces avermitilis*, and *Streptomyces venezuelae*. Comparative co-expression analysis further identified evolutionarily conserved functional gene pairs, including hisD–hisF, trpB–trpC, and geoA–ispA, across representative bacterial and eukaryotic systems such as *Escherichia coli* K-12 and *Saccharomyces cerevisiae*. Notably, geosmin synthase (GeoA) displayed high sequence conservation and strong predicted interactions with isoprenoid biosynthetic enzymes, including IspA and HmgS, suggesting the presence of a specialized terpenoid biosynthetic module.

Keywords: *Streptomyces*, Secondary metabolism, Psychobiotics, Gut–brain axis.

Global Resistance Mapping and Eco-Evolutionary Trends of Uropathogens: Integrating AMR, Climate, and Lifestyle Data

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Abstract

Antimicrobial resistance (AMR) among uropathogens is an increasing global health issue that hampers the successful treatment of urinary tract infections (UTIs), one of the most common bacterial diseases worldwide. In addition to traditional clinical surveillance, AMR is increasingly understood as a consequence of complex eco-evolutionary dynamics shaped by environmental, climatic, and lifestyle factors. Key uropathogens, such as *Escherichia coli*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa*, are increasingly showing multidrug resistance, driven not only by antibiotic misuse but also by environmental reservoirs, horizontal gene transfer, and adaptive genomic plasticity. Emerging evidence suggests that climatic stressors and anthropogenic activities synergistically accelerate selection and transmission of resistance across environmental and clinical interfaces. But there are still big gaps in how we bring together One Health data streams and turn computational insights into actionable surveillance strategies. This review proposes an integrative framework for global resistance mapping by integrating epidemiological datasets with climate variables (e.g. temperature gradients, extreme weather events), ecological drivers (antimicrobial pollution and environmental resistomes), and lifestyle determinants (urbanization, sanitation, and healthcare access). We further integrate advanced in silico pipelines, including comparative genomics, resistome profiling, genome-wide association studies, and phylogeographic modelling to decode the evolution and dissemination of resistance traits. Models and networks utilizing machine learning algorithms, which can be used to predict resistance hotspots, anticipate the trends of AMR, and discover unknown relationships within multi-dimensional data sets, are mentioned here too. This theoretical framework offers the basis for precision surveillance, intervention methods, and preparedness of antimicrobial stewardship under environmental conditions that are changing globally.

Keywords: Comparative genomics, Phylogeographic Modelling, machine learning

Exploration of Protein Biomarker Compound in *Morchella Esculenta* via Phytochemical Analysis vis-à-vis In-Silico Studies

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Abstract

The main characteristic of *Morchella esculenta*, a plant of medicinal value, is antioxidants and anti-inflammatory properties, and their alkaloids component, which additionally exhibit immune-regulating, anti-cancer, anti-diabetic, and antimicrobial activities. The plant, frequently referred to as morel mushrooms, develops on well-drained soil that is packed with organic material. It blooms during the spring season. *Morchella esculenta*, commonly referred to as Morel Mushrooms, is the costliest fungus in the Morchellaceae family and is significant for nutrition and medicine. It is frequently found as a mycorrhiza or saprobic. The mycelium is the primary component of the morel. The thread-like underground network that gives it a comparably large surface area is made up of individual fungal hyphae that spread out below and develop in mass, and this helps to grow mushrooms even after two decades in suitable conditions. It is an important mushroom belonging to the family of Helvellaceae and is locally known as Guchhi, and is locally sold to the traders at Rs 10,000 to Rs 30,000 per kg. The extract preparation was carried out in different ways from the raw morels, as they were washed properly in boiling water, then clean and dried and the extract was prepared by grinding them in mortar and pestle by liquid nitrogen and dissolving in the chaps solution the filtrate – Chaps Solution of Guchhi (CSG) as well as residue – Aqueous Paste of Guchhi (APG) both were used for the phytochemical screening, it indicates that the protein content is approximately 12.62 mg/ml in CSG and 20.17 mg/ml in APG. Therefore, the present study evaluates that the Biomarker Compound of Protein EF1- α to be detected in the protein extracted from guchhi as protein was in high amount in APG there is there EF1- α present in the samples by in-silico studies by KEGG pathway analysis.

Keywords: Protein biomarker compound; In-silico studies; *Morchella esculenta*; APG, CSG; KEGG Pathway Analysis.

GDSL Lipases as Regulators of Lipid Rancidity in millet

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Abstract

Millet is a climate-resilient crop with high nutritional value, but its storage quality is often affected by rancidity. Rancidity mainly occurs due to lipid hydrolysis and oxidation, leading to off-flavors, unpleasant odor, nutrient loss, and reduced shelf life. Since millets contain lipid-rich germ fractions, they are more prone to rancidity during processing and storage, especially under high temperature, moisture, and oxidative stress. Plant GDSL esterases/lipases are a diverse family of SGNH hydrolases involved in lipid metabolism, membrane remodeling, and stress responses. In millets, these enzymes may play an important role in rancidity by hydrolyzing storage lipids and membrane lipids, releasing free fatty acids that can accelerate hydrolytic rancidity. These free fatty acids may further undergo oxidation, producing compounds responsible for poor taste and odor. Studies in other crops show that GDSL lipases are regulated by stress-, hormone-, and light-responsive elements and can influence reactive oxygen species levels, antioxidant activity, membrane stability, and lipid remodeling. These processes are closely linked to rancidity because oxidative stress and membrane damage promote lipid oxidation. Therefore, some GDSL lipases in millets may increase rancidity, while others may help protect lipids by supporting antioxidant defense and membrane stability. However, the specific role of GDSL lipases in millet rancidity is still poorly understood. Focused biochemical, structural, and multi-omics studies could help identify millet GDSL genes involved in lipid breakdown and oxidation. This knowledge may support the development of millet varieties with improved shelf life, better storage stability, and reduced rancidity.

Keywords: GDSL lipase, Millet rancidity, Lipid hydrolysis, Lipid oxidation.

Population Genetic Data of 23 Autosomal Str Loci in the Population of Uzbekistan

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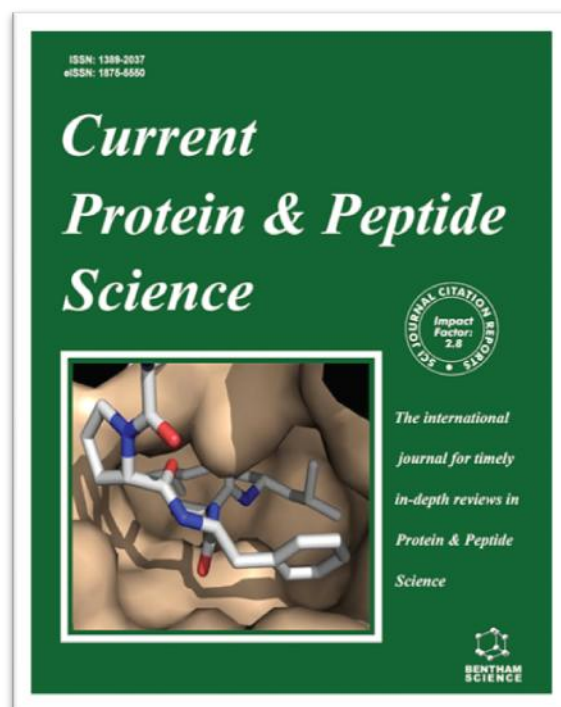
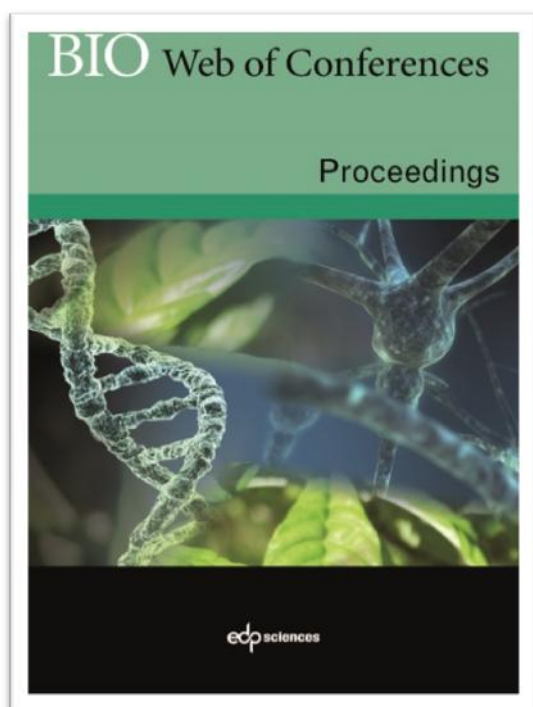
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Abstract

Autosomal short tandem repeat (STR) markers are widely used in forensic genetics for personal identification and kinship analysis. However, comprehensive population data for Central Asian populations, including Uzbekistan, remains limited. This study presents population genetic data for 23 autosomal STR loci based on a substantial sample of 1,538 unrelated individuals from Uzbekistan. DNA extracted from buccal swabs and blood samples was genotyped using the VersaPlex™ 27 PY System Kit and analyzed on the ABI 3500xl Genetic Analyzer. A total of 333 alleles were detected, with a mean of 14.47 alleles per locus. The average expected heterozygosity was 0.8092, indicating high genetic diversity. All loci conformed to the Hardy–Weinberg equilibrium and showed no significant linkage disequilibrium after Bonferroni correction. The cumulative power of discrimination approached unity (CPD >1 - 10⁻³⁶), with a combined random match probability (CMP) of 1 in 2.13 x 10⁻³⁷. The study highlights exceptional forensic utility for kinship analysis: the combined probability of paternity exclusion (CPE) reached 0.9999999968, while the combined paternity index (CPI) was estimated at 1.262 10¹⁷, corresponding to a probability of paternity of 0.9999999999999999207. Eight loci were reported for the first time in the Uzbek population. Several markers (D1S1656, Penta E, D18S51, D2S1338, D21S11, D12S391, D6S1043, and FGA) showed particularly high discriminatory power (PIC > 0.8). These findings demonstrate the high forensic efficiency of the analyzed STR loci and provide a robust, high-precision scientific basis for forensic DNA identification, paternity testing, and population genetic studies in Uzbekistan and the broader Central Asian region.

Keywords: Genotype, Loci, Allele, Frequency, Population.

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