4th Annual Conference of Microbiologists Society, India

&

10th Annual International Conference of the Indian Network for Soil Contamination Research (INSCR)

on

"Trends in Biological Sciences 2025 [TIBS-2025]"

ABSTRACT BOOK

8-10 December, 2025

Venue: Convention Center, Jawaharlal Nehru University, New Delhi, India

Organised by
School of Life Sciences, JNU
ICGEB, New Delhi

Programme Schedule	
DAY-1, 8 December 2025	
TIME	**EVENT**
8:00- 9:00 AM	**Tea/Coffee** Venue: Convention Center Foyer & Cafeteria
8:00 AM onwards	**Registration** Venue: Convention Center Gallery
9:45-1AM	**Inaugural Ceremony** Venue: AUDI-I
9:45-9:55 AM	**Welcome of the Guests:** Prof. Atul K. Johri, Convener
9:55-10:00 AM	**Lamp Lighting & Saraswati Vandana**
10:00-10:10 AM	**President MBSI:** Prof. Arvind Madahavrao Deshmukh
10:10-10:20 AM	**President INSCR:** Prof. Rup Lal
10:20-10:30 AM	**Message by Eminent Scientist:** Prof. Robert M. Stroud & Prof. Rakesh Bhatnagar
10:30-10:35 AM	**Dean School of Life Sciences, JNU:** Prof. Supriya Chakraborty
10:35-10:45 AM	**Address by Chief Guest**: Prof. Brajesh Kumar Pandey, Rector-I, JNU
10:45-10:50 AM	**Vote of Thanks:** Prof. Arun S. Kharat
10:50 -11:20 AM	**Inaugural Keynote Talk-1** Venue: AUDI-I **Gut Commensals-Derived Succinate Impels Colonic Inflammation in Ulcerative Colitis** **Prof. Amit Awasthi** **Senior Professor & Head, Center for Immuno-biology and Immunotherapy** **BRIC-THSTI, Faridabad, Haryana, India**
11:20-11:50 AM	**High Tea & Networking** Venue: Convention Center Foyer & Cafeteria

11:50-12:20 PM	**Keynote Talk-2** Venue: AUDI-I
	Catch Me If You Can: Solving the Enduring Challenge of Dormant TB **Prof. Govardhan Das** **Director, IISER Bhopal, Madhya Pradesh, India**
12:20-12:50 PM	**Keynote Talk- 3** Venue: AUDI-I
	Is AI the New Language of Biology? **Prof. Anurag Agarwal** **Trivedi School of Biosciences, Ashoka University, Sonepat, Haryana, India**
12:50-1:20 PM	**Keynote Talk-4** Venue: AUDI-I
	Rethinking Dengue Immunity : A Novel T-Cell Subset That Shapes Antibody Responses **Prof. Nimesh Gupta** **Senior Scientist and Head, Vaccine Immunology Laboratory, National Institute of Immunology, New Delhi, India.**
1:20-1:30 PM	**Industrial Talk-1** Venue: AUDI-I
	CAR-T and Cancer Therapy **Dr. Priya Kapoor G Hingorani** **Miltenyi Biotech, Hyderabad, India**

1:30-1:40 PM	**Industrial Talk-2** Venue: AUDI-I					
	Hi-Media's Advance Cell-Bio Solutions: Advance 3D Bioprinter Technology and It's Applications **Dr. Himanshu Sharma** **Hi-Media, Mumbai, India**					
1:40-2:30 PM	**Lunch** Venue: Convention Center Foyer & Cafeteria					
2:30-4:30 PM	**Concurrent Session –I**					
	Venue					
	Lecture Hall-I		**Committee Room**		**Lecture Hall-II**	
	Session A **Microbial Genetics** **Chairperson:** Prof. Sukanya Lal **Co-Chair**: Dr. Stanzin Dawa		**Session B** **Molecular Microbiology & Host-Microbe Interaction** **Chairperson:** Prof. Supriya Chakraborty **Co-Chair**: Dr. Deeksha Tripathi		**Session C** **Microbial Pathogenesis** **Chairperson:** Prof. Rup Lal **Co-Chair**: Dr. Shailendra K. Verma	
2:30-2:50 PM	**Lead Speaker**	Prof. Sneha Sudha Komath	**Lead Speaker**	Dr. Ved Prakash Dwivedi	**Lead Speaker**	Dr. Suraj Parihar
2:50-3:10 PM	Speaker 1	Prof. Raghuvir Singh Tomar	Speaker 1	Prof. Asish Nandi	Speaker 1	Dr. Mrutyunjay Saur
3:10-3:30 PM	Speaker 2	Dr. H.D. Khade	Speaker 2	Dr. Sudip Mukherjee	Speaker 2	Prof. Ritu Gaur
3:30-3:50 PM	Speaker 3	Prof. Nirala Ramchiary	Speaker 3	Dr. Indranil Chattopadhyay	Speaker 3	Prof. Vaibhav Bhatt
3:50-4:10 PM	Speaker 4	Dr. Vidya Devi Negi	Speaker 4	Dr. Vijay Kumar Prajapati	Speaker 4	Dr. Ravi Tandon

4:10-4:30 PM	Speaker 5	Dr. Nivedita Mishra	Speaker 5	Dr. Chintan V. Kapadia	Speaker 5	Dr. Abhishek Bansal
4:30-5:00 PM	**Tea/Coffee and Networking** Venue: Convention Center Foyer & Cafeteria					
5:00-5:40 PM	**Concurrent Session –II**					
	Venue					
	Lecture Hall-I		**Committee Room**		**Lecture Hall-II**	
	Session A **Clinical Aspects of Dengue Virus** **Chairperson:** Prof. Mrutyunjay Suar **Co-Chair:** Prof. Gaurav Shah		**Session B** **Cancer Biology** **Chairperson:** Prof. Shilpi Dutt **Co-Chair:** Dr. Vikas Yadav		**Session C** **Gut Microbiome** **Chairperson:** Prof. Rajesh Kannan **Co-Chair:** Dr. A. J. Nair	
5:00-5:20 PM	**Lead Speaker**	Dr. Manisha Arora	**Lead Speaker**	Dr. Aparna Anand	**Lead Speaker**	Dr. Anil Kumar
5:20-5:40 PM	Speaker 1	Dr. Supratik Das	Speaker 1	Prof. Vijai Pal Singh Rawat	Speaker 1	Prof. Neelu Jain Gupta
6:00-7:30 PM	**Cultural Program** Venue: AUDI-I					
7:30-9:00 PM	**Gala Dinner** Venue: Convention Center Foyer & Cafeteria					

Programme Schedule	
DAY-2, 9 December 2025	
8:00 – 9:30 AM	**Breakfast** Venue: Convention Center Foyer & Cafeteria
8:00 – 9:30 AM	**Registration** Venue: Convention Center Gallery
9:30-10:00 AM	**Plenary Talk** Venue: AUDI-I
	Marine Bioprospecting: Innovations for a Sustainable Blue Economy **Dr. Debasis Das** **Director, Institute of Life Sciences, Bhubaneswar, Odisha**
10:00-10:30 AM	**Plenary Talk** Venue: AUDI-I
	ATG8 and Sw5: Beleaguer for Virus Infection in Plants **Prof. Manoj Prasad** **Professor & JC Bose National Fellow at Dept. of Genetics, University of Delhi South Campus, New Delhi, India.**
10:30-11:00 AM	**Plenary Talk** Venue: AUDI-I
	Obesity Alters the Metabolic and Immunologic Response of Pulmonary $CD8^+$ T Cells to SARS-CoV-2 Infection **Dr. Shailendra K. Verma** **Center for Vaccine Innovation, La Jolla Institute for Immunology, La Jolla, California, USA**
11:00-11:30 AM	**Tea/Coffee & Networking** Venue: Convention Center Foyer & Cafeteria

11:30-1:30 PM	**Concurrent Session – III**					
	Venue					
	Lecture Hall-I		**Committee Room**		**Lecture Hall-II**	
	Session A **Antimicrobial Resistance** **Chairperson:** Prof. Arun S. Kharat **Co-Chair:** Prof. Sashi Chawla		**Session B** **Immunology and Vaccine Development** **Chairperson:** Dr. Shailendra K. Verma **Co-Chair:** Dr. Deeksha Tripathi		**Session C** **Structure Biology** **Chairperson:** Prof. Rajiv Bhat **Co-Chair:** Dr. Iti Garg	
11:30 -11:50 AM	**Lead Speaker**	Prof. Ramandeep Singh	**Lead Speaker**	Dr. Sunil K. Raghav	**Lead Speaker**	Prof. Deepti Jain
11:50-12:10 PM	Speaker 1	Prof. Hardeep Kaur	Speaker 1	Dr. Niti Puri	Speaker 1	Dr. Bichitra Biswal
12:10-12:30 PM	Speaker 2	Dr. Soma Mondal	Speaker 2	Dr. Prafulla Kumar B. Tailor	Speaker 2	Dr. Gourinath Samudrala
12:30-12:50 PM	Speaker 3	Dr. Ravi Verma	Speaker 3	Dr. Maruthi Krishna Mohan Poluri	Speaker 3	Dr. Apurba Kumar Sau
12:50-1:10 PM	Speaker 4	Prof. Asad Ullah Khan	Speaker 4	Dr. Shailendra Mani	Speaker 4	Dr. Shailendra Asthana
1:10-1:30 PM	Speaker 5	Dr. Tapti Sengupta	Speaker 5	Prof. Amit Dutt	Speaker 5	Dr. Dhaneswar Prusty
1:30-3:00 PM	**Lunch** Venue: Convention Center Foyer & Cafeteria **All Poster Presentation & Evaluation** Venue: Convention Center Gallery					

3:00-5:00 PM	**Concurrent Session-IV**					
	Venue					
	Lecture Hall-I		**Committee Room**		**Lecture Hall-II**	
	Session A **General Environmental Microbiology** **Chairperson:** Prof. Sanjeev Patankar **Co-Chair:** Dr. Meenakshi Dua		**Session B** **Molecular Microbiology** **Chairperson:** Prof. Arvind Deshmukh **Co-Chair:** Dr. Puja Yadav		**Session C** **Microbes for Society** **Chairperson:** Prof. Kiran Babu **Co-Chair:** Dr. Ravi Tandon	
3:00-3:20 PM	**Lead Speaker**	Prof. Prashant Phale	**Lead Speaker**	Prof. Anand Ranganathan	**Lead Speaker**	Prof. Rupesh Chaturvedi
3:20-3:40 PM	Speaker 1	Dr. Iti Garg	Speaker 1	Prof. Shailja Singh	Speaker 1	Dr. Nafisa Patel
3:40-4:00 PM	Speaker 2	Dr. Stanzin Dawa	Speaker 2	Prof. V. Samuel Raj	Speaker 2	Dr. Rajesh Kannan
4:00-4:20 PM	Speaker 3	Dr. Malini Basu	Speaker 3	Dr. Saman Fatima	Speaker 3	Dr. Abhinay Sharma
4:20-4:40 PM	Speaker 4	Dr. Rajendra Singh	Speaker 4	Dr. Amit Kumar Pandey	Speaker 4	Dr. Prasenjit Das
4:40-5:00 PM	Speaker 5	Dr. Shama Afroze	Speaker 5	Dr. Sachin Khurana	Speaker 5	Dr. Sandeepta Burgala
5:00-5:30 PM	**Tea/Coffee and Networking** Venue: Convention Center Foyer & Cafeteria					

5:30-6:00 PM	**Plenary Talk** Venue: Lecture Hall I
	Immunological Correlates Defining Tuberculosis Pathogenesis **Dr. Dhiraj Kumar** **Cellular Immunology Group, ICGEB, New Delhi, India**
6:15-7:45 PM	**Cultural Event** Venue: AUDI-I
8:00-9:30 PM	**Gala Dinner** Venue: Convention Center Foyer & Cafeteria

Programme Schedule	
DAY-3, 10 December 2025	
8:00-9:00 AM	**Breakfast** Venue: Convention Center Foyer & Cafeteria
8:00-9:00 AM	**Registration** Venue: Convention Center Gallery
8:30-9:30 AM	**General Body Meeting MBSI** Venue: AUDI-I
9:30-10:00 AM	**Keynote Talk-5** Venue: AUDI-I
	MAPKs in Action: Orchestrating Plant Growth and Adaptation **Dr. Alok K. Sinha** **National Institute of Plant Genome Research (NIPGR), New Delhi, India**
10:00-10:30 AM	**Keynote Talk-6** Venue: AUDI-I
	Structure and Dynamics of The Essential Endogenous Mycobacterial Polyketide Synthase Pks13 **Prof. Robert Stroud** **Department of Biochemistry and Biophysics, University of California San Francisco, USA**
10:30-11:00 AM	**Plenary Talk** Venue: AUDI-I
	Surviving the Odds: Fungal Survival Under Hostile Host Environment and Mechanism of Overcoming Host Defences to Cause Disease **Prof. Praveen Kumar Verma** **School of Life Sciences, Jawaharlal Nehru University, New Delhi, India**
11:00-11:30 AM	**Tea/Coffee & Networking** Venue: Convention Center Foyer & Cafeteria

11:30-3:10 PM	**Oral Presentation Session**		
	Venue		
	Lecture Hall-I	**Committee Room**	**Lecture Hall-II**
	Session A **Young Women Ph.D./Post-Doc Award**	**Session B** **Young Men & Women Scientist/Faculty Award**	**Session C** **Young Ph.D. Scholar**
11:30-11:40 PM	Dr. Sharmila Chakraborty	Dr. Saurabh Sharma	Prof. Anand Mohan
11:40-11:50 AM	Dr. Pooja Mahajan	Dr. Souvik	Neenu P Raju
11:50-12:00 PM	Aditi Mishra	Dr. Deeksha Tripathi	Kelvin Osei
12:00-12:10 PM	Jyoti Sood	Dr. Sushma Mithina	Nilesh
12:10-12:20 PM	Safura Nisar	Dr. Ditimoni Dutta	Sumedh Pralhad Narwade
12:20-12:30 PM	Harsha	Dr. Narmada S	Ayush Vikram Singh
12:30-12:40 PM	Tanya Bhagat	Dr. Rimpy Kaur Chowhan	K. Geetha Rani
12:40-12:50 PM	Prerna Yadav	Dr. Savita Petwal	Gunjan
12:50-1:00 PM	Gheewala Maitry Kirankumar	Dr. Ganga Jeena	Ramesh
1:00-1:50 PM	**Lunch** Venue: Convention Center Foyer & Cafeteria		
1:50-2:00 PM	Debarati Paul	Dr. Asmabanu Kamruddin Shaikh	Pankaj Kumar Bharti
2:00-2:10 PM	Rhythm Sharma	Pradnya Purushottam Khode	Lovely Singh
2:10-2:20 PM	Sakshi R. Barad	Gayatri Rajesh Chaudhari	Rahul Yadav
2:20-2:30 PM	Ojaswi Singh	Aditi Nanasaheb Deshmukh	Akanksha Verma
2:30-2:40 PM	Mahak Singh	Dr. Nidhi Verma	Dr. Mamta Sharma

2:40-2:50 PM	Anupam Teotia		Dr. Vaishali U. Dange		Dr. Richa Arora	
2:50-2:55 PM	Arpita Ghosh		Hariom Chaudhary		Sneha Shree	
2:55-3:00 PM	Firdous		Asjad Raza		B. Anusha	
3:00-3:05 PM	Veditha Krishna		Om Laxman Dole		Kumkum Dipak Agrawal	
3:10-5:00 PM	**Concurrent Session-V**					
	Venue					
	Lecture Hall-I		**Committee Room**		**Lecture Hall-II**	
	Session A **Molecular Microbiology & Cellular Biology** **Chairperson:** Prof. Ravi Tuteja **Co-Chair:** Dr. Shama Afroze		**Session B** **Crossroads of Environmental Microbiology & Host-Pathogen Interaction** **Chairperson:** Prof. Anand Ranganathan **Co-Chair:** Dr. Alok Singh		**Session C** **Antimicrobial Resistance & Industrial Microbiology** **Chairperson:** Prof. Kashyap Dubey **Co-Chair:** Dr. Ravi Verma	
3:10-3:25 PM	**Lead Speaker**	Dr. Vikas Yadav	**Lead Speaker**	Prof. Anand Sarkar	**Lead Speaker**	Dr. Raj Kumar Haldar
3:25-3:35 PM	Speaker 1	Dr. H. Nanaocha Sharma	Speaker 1	Dr. Swati M. Biswas	Speaker 1	Prof. Kiran Babu
3:35-3:45 PM	Speaker 2	Dr. Iqbal Ahmad	Speaker 2	Dr. Sarfaraz Ahmad	Speaker 2	Dr. Shazia Haider
3:45-3:55 PM	Speaker 3	Prof. Asimul Islam	Speaker 3	Dr. Lakshna	Speaker 3	Dr. Shashikant Ray
3:55-4:05 PM	Speaker 4	Dr. Pushpalata Narayana Rao Jadav	Speaker 4	Dr. Saurav Sagar	Speaker 4	Dr. Puja Yadav
4:05-4:15 PM	Speaker 5	Dr. Swapna Mukherjee	Speaker 5	Dr. Seikh Zarina Moin	Speaker 5	Dr. C.P. Prince
4:15-4:25 PM	Speaker 6	Dr. Digvijay Verma	Speaker 6	Dr. Sunil K. Srivastava	Speaker 6	Dr. Bipransh Kumar Tiwary

4:25-4:35 PM	Speaker 7	Dr. Vijay Wadhai	Speaker 7	Dr. Varsha Sachin Mistry	Speaker 7	Dr. Kirat Kumar Ganguly
4:35-4:45 PM	Speaker 8	Dr. Arunima Biswas	Speaker 8	Dr. Shafaq Rasool	Speaker 8	Dr. Vrushali Wagh
4:45-4:55 PM	Speaker 9	Priya Rai	Speaker 9	Dr. Vivek K. Natarajan	Speaker 9	Dr. Prashant Sridhar Wakte
5:00-6:00 PM	**Valedictory Session** Venue: AUDI-I Award Ceremony, Felicitation & Concluding Remarks					
6:00-7:00 PM	**High Tea/Coffee** Venue: Convention Center Foyer & Cafeteria					
	🙏 **Thank You** 🙏					

Keynote Speakers

Gut Commensals-Derived Succinate Impels Colonic Inflammation in Ulcerative Colitis

Amit Awasthi✉

Center for Immuno-biology and Immunotherapy, Translational Health Science and Technology Institute, Faridabad, Haryana, India

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Abstract:

Gut-microbiota-derived metabolites are critical in modulating inflammatory response in inflammatory bowel disease (IBD). Here, we identify that gut microbiota-derived-succinate triggers an inflammatory response in ulcerative colitis (UC) through succinate-responsive-colitogenic helper T (Th) cells that produce IL-9. We show that the abundance of succinate-producing gut bacteria is increased while succinate-metabolizing gut bacteria is decreased in colitis. Similarly, we show that succinate-producing gut bacteria and levels of succinate are increased in UC patients. Intestinal colonization of succinate-producing gut bacteria or increasing the availability of intestinal succinate promotes colonic inflammation through succinate-responsive colitogenic Th9 cells in UC. On the contrary, Intestinal colonization of succinate-metabolizing gut bacteria or blocking succinate receptor signaling using succinate receptor antagonist or IL-9 using anti-IL-9 neutralizing antibody alleviated intestinal inflammation by decreasing succinate-responsive colitogenic Th9 cells. Our data demonstrated that gut microbiota-derived succinate promotes intestinal inflammation and colitogenic T cells, thus providing the potential to design newer therapeutic interventions for treating IBD.

Catch Me If You Can: Solving the Enduring Challenge of Dormant TB

Gobardhan Das✉

Indian Institute of Science Education and Research (IISER), Bhopal, MP, India

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Abstract:

Mycobacterium tuberculosis (M.tb) is the causative agent of tuberculosis (TB). It causes 1.6 million deaths annually. Approximately, one-third of the global population is latently infected with TB, which a vast reservoir for future pandemic. BCG is the only usable vaccine available for TB, however efficacy of which is unsatisfactory. Available anti-TB therapy consists of multiple antibiotics and lengthy, which incorporates the risks for the emergence of drug-resistant TB variants. Therefore, development of alternative treatments and better vaccines are urgently needed. In our effort to understand the reason as to why TB treatment is lengthy, we discovered that clearance of bacteria upon antibiotic treatment follows a bi-phasic pattern. A majority of the bacteria disappear within 2-3 weeks of treatment, whereas remaining bacilli remain nonresponsive to conventional antibiotics. We found that a small portion of the bacteria infect mesenchymal stem cells (MSCs) and survive in a dormant state. M. tuberculosis can establish dormancy within mesenchymal stem cells (MSCs) by hiding themselves within the host lipid body which renders it nonresponsive to antibiotic therapy. In our efforts to understand the immune responses required for vaccine efficacy against M.tb, we have shown that antigen specific both Th1 and Th17 cells in the lung are essential for optimum vaccine efficacy against TB disease. Furthermore, recently we reported that central memory T cells (Tcm) and Tsm (Stem Cell like memory T cells), dictates longevity of vaccine efficacy. Interestingly, both Tcm and Tsm cells express dramatically less numbers of Potassium channel 1.3 (Kv1.3) than that of effector memory T cells (Tem) cells. Therefore, blocked of Kv1.3 by clofazimine yielded better Tcm and Tsm responses in a murine model of BCG vaccination for TB. These observations suggested that simultaneous modulation of immune responses along with vaccination may provide better vaccine efficacy. In summary, our findings highlight novel TB therapies and strategies to enhance BCG vaccine-induced immunity. Our research paves the way for the development of more effective prevention and treatment strategies for TB.

Is AI The New Language of Biology?

Anurag Agarwal✉

BioSciences and Health Research, Trivedi School of Biosciences, Ashoka University, India

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Abstract:

The rapid convergence of artificial intelligence and biology is revolutionizing our understanding of life at an unprecedented scale. AI tools will be essential for decoding genomic sequences, predicting protein structures, designing new drugs, and even engineering synthetic life. This talk explores how AI is transforming biology, unlocking new possibilities in medicine, biotechnology, and beyond.

Rethinking Dengue Immunity: A Novel T-Cell Subset That Shapes Antibody Responses

Nimesh Gupta✉

Vaccine Immunology Laboratory, National Institute of Immunology, New Delhi, India

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Abstract:

Effective and durable humoral immunity relies on precise and timely crosstalk between T cells and B cells. The threshold, quality, and context of this interaction not only shape protective antibody responses but can also drive pathological outcomes. Dengue virus infection represents a striking example of this dual nature, where humoral immunity may provide protection in some individuals yet contribute to severe disease in others. In our work, we uncovered a previously unappreciated dimension of T cell–B cell collaboration that underlies the development of pathological antibody responses in dengue. By integrating longitudinal clinical cohorts of dengue patients with healthy adults from dengue-endemic regions, we identified a dominant peripheral IL-21producing T-cell subset that expands specifically in severe cases. This subset exhibits potent B-cell help capacity and promotes B-cell differentiation through IL-21mediated signaling. In-depth analyses of human lymphoid tissues revealed that these peripheral helper cells acquire memory and possess the ability to migrate beyond the circulation into lymph nodes and possibly peripheral tissues, positioning them to influence both disease progression and the long-term quality of humoral immunity. Using single-cell transcriptomics and paired TCR profiling, we dissected the dynamics, clonotypic diversity, and transcriptional landscape of this subset, and delineated its relationship to canonical T follicular helper (Tfh) cells. Together, these findings highlight a distinct, $IL21^{+}$ T-cell–driven extrafollicular pathway that fuels heightened antibody production in dengue and may predispose individuals to antibody-mediated immunopathology. By revealing a critical immune axis of antibody responses in dengue, these findings offer key insights to guide the design of next-generation dengue vaccines that elicit protective rather than pathological antibody responses.

MAPKs in Action: Orchestrating Plant Growth and Adaptation

Alok Krishna Sinha✉

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Abstract:

Mitogen-activated protein kinase (MAPK) cascades play a crucial role in transducing environmental and developmental signals from the cell surface to the nucleus, enabling appropriate cellular reprogramming. These cascades consist of three key components: MAPKKKs (MAPK kinase kinases), which activate MAPKKs (MAPK kinases), and finally MAPKs, the terminal kinases in the cascade. In this presentation, the diverse roles of MAPKs in plant adaptation and growth will be explored. Specifically, their role in submergence tolerance in rice and thermomorphogenesis in Arabidopsis will be discussed. Notably, OsMPK3, a MAPK in rice, interacts specifically with the SUB1A1 gene, enabling plants to adapt to submergence. The SUB1A1 gene, found in certain rice varieties, confers short-term submergence tolerance. In Arabidopsis, the MPK4-PIF4-ARP6 module has been identified as a regulator of histone variant H2A.Z deposition, which controls hypocotyl cell elongation and helps plants adapt to elevated temperatures. Additionally, the role of MAPKs in regulating key genes regulating cell cycle in rice will be discussed.

Approaches to Drug Discovery; *Mycobacterium tuberculosis*?

Robert Stroud✉

Department of Biochemistry and Biophysics, University of California, San Francisco, CA, USA

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Abstract:

Seeking new targets in drug discovery against Mtb can come from the structures and mechanisms of new targets among the 625 essential proteins in Mtb. I will describe 2 approaches to circumvent these difficulties. In the first case we focus on the essential last enzyme in cell wall trehalose-meromycolate synthesis, Pks13. In this case endogenous purification from mycobacteria, growing under normal conditions, allows for structure determination, determination of endogenous partnerships with other proteins that feed substrates to Pks13, identification of the endogenous substrates, and critical bottlenecks in the kinetic pathway for this critical activity. This opened the way to new target interactions that interrupt Pks13 (Kim et al., Nature SMB 2023). In the second case drug screening against hypomorphic strains of MTb carried out by the Hung group (Johnson et al., Nature 2019) identified compounds (BRD-8000.3 and BRD-9327) that inhibit the essential efflux pump EfpA. To understand the mechanisms, we determined the structures of EfpA with these inhibitors bound. Our structures define the natural substrates and reveal different mechanisms of inhibition by the two inhibitors. BRD-8000.3 binds in a tunnel competing with the fatty acid chain of a lipid molecule, BRD-9327 binds non-competitively in the outer vestibule suggesting its possible inhibition of the movement necessary for alternate access of the transporter (Khandelwal et al., Nature SMB 2025). Our results show EfpA as a potential lipid floppase, explain the basis of the synergy of these inhibitors and their potential for combination anti-tuberculosis therapy.

Plenary Speakers

Marine Bioprospecting: Innovations for a Sustainable Blue Economy

Debasis Dash✉

BRIC-Institute of Life Sciences, Bhubaneswar, India

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Abstract:

The blue economy emphasizes the sustainable use of marine resources while ensuring the health of our oceans. Currently, 4% of the national GDP comes from the blue economy, primarily from maritime transport and fisheries. India is the second-largest fish producer in the world; however, we face the risk of overexploitation if we do not adopt innovative methods to protect and preserve marine ecosystems. Marine bioprospecting has significant potential for advancing a sustainable blue economy by utilizing the vast biological resources of the ocean. Additionally, marine biotechnology is crucial for facilitating the technological innovations needed to sustainably harness these marine resources. India boasts a coastline of 7,500 km and 1,382 islands, which are home to unique marine living resources. The country's Exclusive Economic Zone (EEZ) spans 2 million square kilometres and is rich in both living and non-living resources. The market for marine-derived pharmaceuticals and industrial products is expected to grow significantly. We aim to utilize advanced biotechnological tools to harness the potential of marine bioresources for developing products and processes that are important for health and nutrition. To achieve this, we will perform multi-OMIC characterization to analyze the genome, metabolome, and proteome of marine microbes. This will create knowledge bases that can be integrated and analyzed through automated AI/ML pipelines. In-silico prospecting of these extensive knowledge bases will enable the identification of gene-metabolome networks, gene clusters, and prospective therapeutic potentials, as well as industrially relevant enzymes. It is essential to inventory and conserve marine biodiversity for the long-term sustainability of fragile marine ecosystems. Adopting the metagenomics and metabarcoding approach we are determining the marine microbial biodiversity, understanding community composition, and studying ecological interactions in the Bay of Bengal and eastern coast of India. The overall goal is to conduct research and development in marine biotechnology to sustainably harness marine resources and promote marine enterprise while maintaining the balance between economic growth and environmental protection.

ATG8 And Sw5: Beleaguer for Virus Infection in Plants

Manoj Prasad✉

Department of Genetics, University of Delhi South Campus, New Delhi

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Abstract:

Tomato leaf curl disease (ToLCD), caused by strains of Tomato leaf curl virus (ToLCV), is a major constraint to tomato production. Plants have developed different strategies of defense against viruses which involves: (a) autophagy-mediated resistance mechanism and, (b) identification of viral effectors, avirulence (Avr) genes, by the corresponding resistance (R) genes, and (c) the antiviral RNA silencing mechanism (also called RNA interference; RNAi) (d) instigation of ubiquitin-26S proteasome system (UPS). Our studies focused on the contribution of autophagy-related proteins (ATGs) and resistance genes during geminivirus-plant interactions and the mechanism of plant tolerance against Tomato leaf curl New Delhi virus (ToLCNDV) infection.To understand the molecular mechanism of virus tolerance, we performed a genome-wide study that identified thirty ATG encoding genes in tomato. Further, we functionally characterized (i) SlATG18f gene and (ii) SlATG8f gene, which were differentially expressed after ToLCNDV infection in tolerant cultivar. (i) An increase in viral load upon silencing SlATG18f in cv. H-88-78-1 was observed validating its role in tolerance. Further, a cleaved amplified polymorphic sequence (CAPS) marker was developed which showed a significant association with the tolerance characteristics in the tomato germplasm. (ii) We functionally characterized SlATG8f and found that ATG8f interacts with viral TrAP protein and mediates its degradation by the autophagy pathway. ToLCNDV TrAP is known to possess host RNA silencing suppression (RSS) activity. Degradation of TrAP results in the attenuation of its RSS activity and thus provides defense against ToLCNDV. Apart from autophagy, our studies also focused on the contribution of microRNAs (miRNAs) and R genes in providing resistance against geminivirus infection. Through miRNAome of tomato in response to ToLCNDV infection we found that miR159 is upregulated during infection in susceptible cultivar and the inverse correlation of miR159 abundance with its target, MYB33 suggested their putative involvement in the defense response. Molecular characterization of sly-miR159 and SlMYB33 demonstrated their role in regulating the expression of Sw5a gene. Functional characterization showed that SlSw5a interacts with viral AC4 protein triggering hypersensitive response (HR) and limiting virus spread. Overall, the results obtained from our studies could be employed in developing tolerance in susceptible cultivars of tomato through modern breeding or molecular approaches (Prasad et al. 2022 & 2020; Trends in Plant Science).

Obesity Alters the Metabolic and Immunologic Response of Pulmonary CD8 + T Cells to SARS-CoV-2 Infection

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Abstract:

Obesity is a major risk factor for severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) infection. Although obesity is known to alter the innate and humoral immune response to SARS-CoV-2, the mechanisms by which it affects pulmonary SARS-CoV-2 immunity and worsens disease severity remain unclear. Here, we compared virus–host dynamics in genetically obese Lep ob (ob/ob) mice after intranasal infection with SARS-CoV-2 Beta (B.1.351). Obese mice exhibited delayed viral clearance from the lungs, resulting in worse histopathologic pulmonary injury and clinical outcomes compared with infected lean mice. Eventual viral clearance at day 8 coincided with a heightened SARS-CoV-2-specific adaptive pulmonary CD8 + T cell response in obese mice. Pulmonary CD8 + T cells from obese hosts displayed altered cytokine profiles, a marked shift in transcriptional effector programs and an energy metabolic shift towards preferential fatty acid utilization at the expense of glucose consumption. Depletion of CD8 + T cells in obese mice led to 2-log fold increased viral load. Conversely, complete SARS-CoV-2 clearance from the lungs of obese mice occurred after adoptive transfer of CD8 + T cells from SARS-CoV-2-immunized lean or obese mice. Thus, CD8 + T cells adapt metabolically, transcriptionally and functionally to maintain anti-viral effectiveness in the obese host and are necessary and sufficient for viral protection. This obesity associated cell-autonomous adaptation was specific to pulmonary CD8 + T cells, and did not occur in CD4 + T cells, at other tissue sites, or in the absence of infection. Vaccination strategies that elicit pulmonary SARS-CoV-2 specific CD8 T cell responses therefore are an effective strategy to mediate protection in the high-risk obese population.

Immunological Correlates Defining Tuberculosis Pathogenesis

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Abstract:

Tuberculosis (TB), caused by Mycobacterium tuberculosis (Mtb), is a serious health challenge. The lack of an effective vaccine and the emergence of drug resistance complicates the already challenging TB management program, which requires prolonged treatment with multiple antibiotics. We have been trying to understand the classical innate immune responses during Mtb infection, which could allow us to a) develop novel therapeutics against TB and b) help enhance the efficacy of BCG-mediated protection. One of the areas where we have recently focused is the innate immune cell diversity and its activation mechanisms that could contribute to TB pathogenesis and impact the protective efficacy of vaccines. In this context, we have reported a functionally distinct state of Mtb in diverse cellular niches, such as macrophages, neutrophils, or mesenchymal stem cells (MSCs). They enable us to explore and establish a new set of markers of protection and pathology, the absence of which has significantly impacted vaccine studies. We will discuss the involvement of these less-explored cells in TB pathogenesis and potential avenues for exploring protective immune responses.

Surviving The Odds: Fungal Survival Under Hostile Host Environment and Mechanism of Overcoming Host Defences to Cause Disease

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Abstract:

Fungal phytopathogens pose a serious threat to global crop production. Only a handful of strategies are available to combat these fungal infections, and the increasing incidence of fungicide resistance is making the situation worse. Hence, the molecular understanding of plant–fungus interactions remains a primary focus of plant pathology. One of the hallmarks of host–pathogen interactions is the overproduction of reactive oxygen species (ROS) as a plant defence mechanism, collectively termed the oxidative burst. We hypothesize that the fungus must have an intrinsic mechanism to counter host-generated oxidative stress. Therefore, to survive the oxidative burst and achieve successful host colonization, fungal phytopathogens employ intricate mechanisms for ROS perception, ROS neutralization, and protection from ROS-mediated damage. We have earlier isolated a gene coding for Old Yellow Enzyme (OYE) that showed high expression during oxidative stress conditions. We have revealed the 1.5 Å X-ray structure of a class III member, OYE 6 from necrotrophic fungus Ascochyta rabiei (ArOYE6). We provide the structural and biochemical insights for a fungi- specific class III OYE homologue and dissect the oxidoreductase mechanism. We have isolated a few interacting proteins of ArOYE6 and also performed metabolome analysis in ArOYE6 mutant vs wild type. We identified several metabolites and peptides which may be useful to combat fungal pathogens. Besides ROS, a pathogen must overcome preformed structural barriers and suppress the immune system of the host by evolving tactics to invade and survive inside the host environment. Pathogen-secreted molecules (termed effectors) manipulate the signaling or metabolic machinery of the host to benefit the pathogen. These secreted effectors can act inside (intracellular) or outside (extracellular) the host cells. The legume crop chickpea (Cicer arietinum) is infected by a devastating fungus Ascochyta rabiei, resulting in Ascochyta blight disease. We have isolated an early expressed effector A. rabiei PEXEL-like Effector Candidate 25 (ArPEC25) is essential for fungal virulence on chickpea. ArPEC25 is secreted by fungi and moves to the chickpea nucleus where it physically interacts with LIM transcription factors. The chickpea nuclear localization of ArPEC25 is essential for its virulence activity, since it disrupts the DNA-binding activity of a CaβLIM1a factor, resulting in reduced expression of a phenylalanine ammonia-lyase (PAL) gene. The PAL enzyme is an important protein of the phenylpropanoid pathway that produces various molecules including lignin to provide structural strength to the plant cell. Thus, one mechanism by which ArPEC25 manipulates the host is by suppressing lignin levels in chickpea. These novel finding may pave the way to design new generation antifungal agents for future utilities and strategies to counter fungal phytopathogens.

Invited Speakers

Coordination of GPI Biosynthesis with Filamentation in *Candida albicans*

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Abstract:

Candida albicans, is an opportunistic fungal pathogen whose infection can turn deadly in immunocompromised individuals. A key virulence attribute of the pathogen is its morphological flexibility and ability to transition between yeast, pseudohyphal, and hyphal forms in response to different environmental cues. Crucial to this switching is the transduction of different environmental signals by multiple signaling pathways, including the cAMP-PKA siganling pathway. A second important virulence attribute of this organism is the expression of GPI anchored proteins on the cell surface, many of which are exclusively expressed in the hyphal form. Based on work carried out in my lab for over two decades, this talk will provide a brief description on how hyphal morphogenesis via the cAMP-PKA signaling pathway in *Candida albicans* is regulated in multiple modes, all involving the first step of GPI biosynthesis, and what its implications are for virulence of this pathogen. Despite an apparent overall apparent conservation in pathways, crucial differences exist between the cAMP-PKA signaling pathways in *C. albicans* and *S. cerevisiae*. The former is an opportunistic human pathogen. The latter is a non-pathogenic yeast used in the brewing and baking industry, which serves as the model organism for eukaryotic systems. Both organisms can switch to filamentous growth upon receiving appropriate signals. In *S. cerevisiae*, this pathway is Ras-dependent. In *C. albicans* there are Ras-dependent and Ras-independent arms to this pathway that can function either separately or in concert depending on the cues received. ScRas2 and CaRas1 can complement one another, and it would appear that the Ras-dependent arms of the Cyr1-cAMP-PKA pathways would be similar. Yet, this is not quite the case. There is a second level of control, one that is exerted by the Hsp90 family of heat shock proteins. In *S.cerevisiae* they promote interaction of Ras with Cyr1, in C. albicans they inhibit the interaction. Similarly, at first glance, GPI biosynthesis and the enzymes involved appear to be very similar in the two organisms. Yet differences begin to appear at the very first step. Inter-subunit cross-talk is observed within the C. albicans GPI-N-acetylglucosaminyltransferase (GPI-GnT), the enzyme that catalyzes the first step of the pathway. This inter-subunit regulation is missing in *S.cerevisiae*. As a result, *S. cerevisiae* lowers down GPI biosynthesis while producing filaments and *C. albicans* co-activates filamentous growth with production of GPI-anchored host-recognition and virulence factors for establishing infection.

Interplay between metal ions and metabolites is regulated via epigenetics

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Abstract:

Several of the essential metal ions play key roles in the regulation of fundamental biological processes such as gene expression, mitochondrial functions, autophagy etc. Dysregulation in homeostasis of a few of the metal ions correlates with disease conditions in humans. However, mechanisms involved in the cellular homeostasis of metal ions is not well established. Cellular factors that are involved in maintaining the concentration of the metal ions inside cells are yet to be identified. Import, export and sequestration are the key mechanisms involved in the regulation of metal ions homeostasis. We investigated how metabolic pathways, specifically mitochondrial respiration and autophagy, contribute to copper homeostasis and the translocation of secretory proteins. We show that copper selectively inhibits protein translocation in yeast cells grown in minimal medium but not in rich medium, highlighting a critical role of nutrients in modulating copper toxicity. Supplementation of specific amino acids suppresses the copper-induced defects in protein translocation and cell death, identifying amino acids as suppressors of the copper toxicity. Using a panel of gene deletion mutants affecting mitochondrial functions, autophagy, peroxisomes, and lipid droplets, we demonstrate that metabolic pathways regulate subcellular concentration of copper and translocation of secretory proteins. Further, disruption of redox and pH homeostasis, and pharmacological inhibition of respiration, reveals that correct subcellular concentration of copper is essential to prevent inhibitory effects on protein translocation. My talk will be focused on the identification of cellular that regulate the homeostasis of copper and other essential metal ion.

Understanding the Role of Microbes in Pungency (Capsaicinoids) and Aroma Biosynthesis in *Capsicum* Species

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Abstract:

The biosynthesis of pungency (capsaicinoids) and aroma-associated volatile compounds in *Capsicum* species is a complex process influenced by genetics, environment, and developmental factors. Increasing evidence shows that plant-associated microbes act as crucial modulators of these traits, adding a dynamic ecological dimension to their regulation. A few studies have reported the multifaceted roles of rhizobacteria, endophytes, and surface-associated microbes in shaping the metabolic networks that determine chili heat and aroma. Microbes interact with *Capsicum* plants through diverse mechanisms, including nutrient mobilization, stress mitigation, phytohormone modulation, and metabolic elicitation, each of which can significantly alter secondary-metabolite pathways. Beneficial endophytes have been shown to enhance precursor molecules such as phenylalanine and fatty acids, thereby accelerating capsaicinoids biosynthesis. In our laboratory, we have observed that pungency and aroma levels are lower in plants grown in Delhi compared to those grown in Assam, suggesting that the environmental conditions and microbial communities of the Northeast region are more conducive to high pungency and aroma production in chili fruits. *Capsicum* aroma arising from volatile terpenes, alcohols, aldehydes, and esters is influenced by microbes that modulate plant metabolism or produce complementary volatiles themselves. Microbial communities can also create micro-environmental conditions that affect fruit development, ripening, and ultimately the sensory attributes of aroma. Our laboratory aims to unravel the mechanisms of plant microbe metabolic co-regulation and the biosynthesis of extreme pungency in Ghost chili. In the long term, this knowledge will support the integration of microbiome management through inoculants, agroecological practices, and breeding to enhance flavor, heat intensity, and overall crop quality in *Capsicum* species.

Hidden T Cell Responders: Redefining Immunity in Tuberculosis

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Abstract:

Around one-fourth of the global population is affected by tuberculosis (TB) which is caused by Mycobacterium tuberculosis (Mtb). Mtb infection results in highly heterogeneous immune responses in individuals, ranging from asymptomatic infections to death. Existing literature indicates the protective role of Th1 and Th17 cells during TB, whereas Th2 and Tregs assist in disease progression. Yet, many facets of host immune responses are still understudied during TB. Recently, double-positive $CD4^+$ $CD8^+$ (DP) T cells were reported in Mtb-infected cynomolgus macaques and active TB patients. Though DP T cells are part of T cell development in thymus, these cells are also found in the extra-thymic tissues in healthy individuals whose differential regulation results in a diverse response in various disease settings. However, the origin of DP T cells in extra-thymic tissues is less elucidated and known to be context-specific. We observed expansion of DP T cells in the lungs of infected mice when compared to naïve lungs. Immunophenotyping of these DP T cells revealed their functional behavior similar to CD4+ T cells, yet possessing cytolytic functions like CD8+ cells in the lungs of infected mice. These Mtb-specific DP T cells originate at the site of infection and share a larger central memory pool, which may confer better protection against TB. LC-MS analysis of DP T cells compared to SP T cells exhibited differential regulation of various metabolic processes and morphogenesis. Altogether, we aim to characterize these DP T cells highlighting their potential in Mtb clearance.

Interaction Between Immune Response and Thermotolerance in Plants

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Abstract:

Plants are inherently capable of defending against pathogens through the presence of a very effective immune system. Due to the effectiveness of their immune systems, plants are, by default, resistant to pathogens, and diseases are rare. However, in a congenial environment, pathogens cause havoc in diseases that affect crop plants, especially in susceptible cultivars. Thus, plants, pathogens, and the environment are three interconnected components that collectively determine a plant's performance. Although the effect of the environment on disease susceptibility has been known for years, the mechanism of their interactions is little understood. As an adaptive response, plants that have experienced stress show higher resistance to stresses than naïve plants. A partly infected plants show systemic acquired resistance (SAR) that provides stronger protection during subsequent infections. Similarly, when a plant is exposed to a higher but non-lethal temperature, it develops acquired thermo tolerance (ATT) and can tolerate even a higher temperature that is lethal to naïve plants. Our lab recently uncovered an intriguing interaction between ATT and SAR. Our results show that activation of SAR by pathogens allows plants to tolerate high temperature stress, similar to ATT. The ATT activation is associated with the enhanced expression of heat shock protein (HSPs) and heat shock factors (HSFs). HSPs function as chaperons and protect proteins from getting denatured by heat. HSFs primarily function as transcription factors for the activation of HSP genes. Interestingly, we observed that pathogen inoculation activates HSF and HSP genes, suggesting the presence of a genetic network through which SAR and ATT work in tandem. In contrast to the pathogen-mediated ATT activation, we observed that thermopriming suppresses SAR development. Pathogen-mediated SAR development is associated with the movement of mobile signal from the primary infected tissue to the rest of the plant. Our results show that transient heat exposure significantly suppresses the SAR mobile signal generation and thereby suppresses the activation of ATT.

Development of a Photo-Activated Implantable Chip for Deep-Tissue Treatment of UTI

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Abstract:

Urinary tract infections, primarily caused by uropathogenic *E. coli*, are among the most prevalent bacterial infections globally, affecting over 150 million individuals annually. Deep-tissue UTI is yet another severe form that affects deeper tissues like the kidneys or prostate in addition to the urinary tract's superficial layers. Even after successful antibiotic therapy, 30-50% of patients relapse and develops recurrent UTIs. Moreover, the prevalence of UPECs resistant to last-line antibiotic therapies like carbapenems and colistin is ever-increasing. Nanomaterial-based photo-thermal therapy has gained significant attention recently, owing to its simple application, high antibacterial efficacy and minimal disk of inducing bacterial resistance. Herein, we fabricated an implantable and retrievable chip for photo-thermal inactivation of *E. coli* by NIR exposure. The absorption spectrum demonstrates a broadened spectrum from UV-Vis to NIR-I & II region with a plasmonic peak at around 750 nm wavelength. Deeper tissue penetrative ability was confirmed by significant absorption extending up to 1500 nm. Thermal imaging supported rapid and reversible change in local temperature surrounding the chip leading to optimal and transient hyperthermia. The generation of intracellular ROS led to robust inhibition of bacterial growth, significantly disrupting mature biofilms. Chorioallantoic membrane model revealed biocompatibility supporting vascularization and angiogenesis, signifying its non-toxic nature. Infective wound healing and dermal infection studies demonstrated its efficacy in wound repair and infection control, signifying enhanced healing and bacterial clearance in vivo. Histological analysis indicated rapid tissue repair, with restoration of the epithelial layer, while immunohistochemistry confirmed the expression of key tissue biomarkers involved in tissue regeneration mechanisms. The UTI model revealed the destruction of GFP-tagged *E. coli* using the IVIS Bioimager within 48h of implantation and photo-irradiation. Fluorescence detection by culturing tissue homogenates and body fluids confirmed the therapeutic efficiency of our photo-responsive chip as a promising alternative to achieve targeted eradication of deep-tissue infections.

Post-biotic Impact of *Lactiplantibacillus plantarum* on Transcriptomic Alterations of *Streptococcus mutans* Biofilm

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Abstract:

Streptococcus mutans induces oral squamous cell carcinoma (OSCC) by fostering an immunosuppressive tumor microenvironment via biofilm development and virulence-related metabolic alterations. GC–MS research revealed that the cell-free supernatant (CFS) of *L. plantarum* contains the bioactive metabolite 2, 4-di-tert-butylphenol (DTP), which demonstrates significant antibacterial and anti-tumor activities. The new antimicrobial peptide Plpl_18 also showed substantial biofilm inhibition. Pattern of microbial Biofilm Exopolysaccharides (EPS) secretion showed variation between S. mutans 497 and S. mutans 890 when the cells were exposed to treatments. Treatment with DTP and Plpl_18 was found to increase the accumulation of ROS in the biofilm cells. The accumulation of reactive oxygen species (ROS) induces the disintegration of pre-existing biofilm. The results indicate that the CFS of *L. plantarum*, along with its metabolite DTP and the novel peptide Plpl_18, significantly inhibit biofilm formation. Transcriptomic alterations showed that *S. mutans* 890 treatment with DTP and Plpl_18 down regulated essential biofilm-associated genes (gtfB, gtfC), disturbed carbohydrate metabolism, and initiated a metabolic transition towards lactose utilization. The transcriptomic analysis indicates that treatment with DTP and Plpl_18 induces a metabolic shift in *S. mutans*, activating alternative carbohydrate uptake pathways and inhibiting glucosyltransferase activity, which compromises biofilm integrity. Functional analysis delineates the ten most significantly elevated biological processes, encompassing translation and protein targeting to membranes, whereas down-regulated processes, including signal transduction and DNA repair, underscore potential cellular stress generated by treatment. The molecular docking studies support these findings, demonstrating significant antagonistic interactions between the bacterial virulence factor GtfC and host proteins associated with OSCC progression. This offers insights into potential targeted therapeutic strategies for the management of dental caries and OSCC. Future research on the clinical applications and pharmacological formulations of DTP and Plpl_18 may lead to innovative therapeutic strategies for disrupting pathogenic bacterial biofilms and reducing OSCC progression.

Screening, Knockout, and Apoptosis: Impact on *Leishmania*

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Abstract:

Visceral leishmaniasis, a life-threatening vector-borne illness that disproportionately affects children and elderly immunocompromised people, is a primary tropical neglected disease. No apoptotic partner proteins have yet been reported in *Leishmania donovani*, while their identification could contribute to knowledge on parasite cell death and the establishment of alternative therapeutics. We searched for mammalian Bcl-2 family protein orthologs and found one anti-apoptotic and two pro-apoptotic orthologs in *L. donovani.* A pro-death aquaporin protein, due to its characteristic BH3 domain known to interact with pro-apoptotic proteins in mammalian Bcl-2 family proteins, was also included in this study. Molecular docking and molecular dynamics simulations were conducted to assess protein-protein interactions between the identified apoptotic proteins and mimic mammalian intrinsic apoptotic pathways. The results showed that both pro-apoptotic proteins interacted with the hydrophobic pocket of the anti-apoptotic ortholog, forming a stable complex. This interaction may represent a critical event in an apoptotic pathway in *L. donovani*. To further characterize it, we used CRISPR-Cas9 approaches to target the identified proteins. Pure knocked population mutants, and episomal over-expressing mutant cells were exposed to apoptotic stimuli. Terminal deoxynucleotidyl transferase dUTP nick end labeling (TUNEL) assay and quantitative expression profiling suggested that these proteins are involved in the parasite's apoptosis and could play a role in its survival.

Advancing HIV-1 Therapy with Novel Maturation Inhibitor HRF-10071

Aradhana Singh[1], Yuvraj KC[1], Ronika Singh[1], Soumya Bandopadhyay[1], Vidya Laxmi Jaishi[1] and Ritu Gaur[1]✉

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Abstract:

Maturation Inhibitors (MIs) represent a promising class of antiretrovirals that target the HIV-1 Gag polyprotein at the CA-SP1 junction, preventing the final cleavage event required for viral core condensation and infectivity. First-generation Maturation Inhibitors (MIs) targeting the HIV-1 Gag polyprotein failed mainly due to naturally occurring polymorphisms, particularly within the HIV- Gag SP1 region (SP1: V7A). These polymorphisms are inherently present within the HIV subtype C. The second-generation bevirimat analogues gained activity against both HIV-B and HIV- C. In collaboration with Hetero Pharmaceuticals, Hyderabad, we characterized their lead Maturation Inhibitor HRF-10071 against multiple HIV-1 subtypes. This compound demonstrated very strong potency against wild-type HIV-1 Subtype B and diverse Subtype C clinical isolates (K3016, IndieC1, ZM247), and retained activity against viral strains resistant to Protease and Integrase inhibitors. In vitro resistance selection in MT-4 and MT-2 cells indicated a high genetic barrier; HRF-10071 suppressed viral breakthrough at low multiplicities of infection (MOI), whereas bevirimat selection yielded rapid failure. The fixed-dose (high-MOI) selection revealed a multi-step escape pathway initiated by adaptive mutations, such as V362I, N271I, P356T, and K331M, followed by the definitive resistance substitution, A364V. Site-directed mutagenesis confirmed that mutations, such as V362I, remained largely susceptible, while A364V conferred high-level resistance, mechanically restoring CA-SP1 cleavage in the presence of the inhibitor. The drug combination assays demonstrated that HRF-10071 exhibited significant synergy with Tenofovir alafenamide (TAF), Doravirine (DOR), Emtricitabine (FTC), Cabotegravir, and Lenacapavir. Triple-drug regimens, specifically HRF-10071 combined with TAF and Rilpivirine (RPV), showed significant synergism. These findings underscore the potential of HRF-10071 as a robust candidate for anti-retroviral therapy, with A364V serving as a primary marker for clinical monitoring.

Milk Metagenomics: A Source of More Life Than We Imagine

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Abstract:

This study used metagenomic sequencing to examine the microbial communities in milk from Kankrej, Gir and crossbred cattle with subclinical mastitis. Sequencing generated 63.07, 11.09 and 7.87 Mb of data for the respective breeds, revealing Enterobacteriales as the dominant group, followed by Pseudomonadales, Bacillales and Lactobacillales. Across samples, about 56 species were identified. *E. coli* was most abundant in Kankrej and Gir cattle, while *Staphylococcus aureus* predominated in crossbreds. Functional profiling showed the presence of genes linked to resistance against fluoroquinolones, methicillin and various heavy metals, along with multidrug resistance determinants. Bacteriophages targeting major pathogens such as *S. aureus* and *E. coli* were also detected. These findings provide insights into pathogenic bacteria, resistance patterns and natural defence elements, which may help improve mastitis prevention and treatment strategies in dairy herds.

The Emerging Virome: Shifting Paradigms in HIV Research

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Abstract:

The human virome includes all viruses that inhabit the body, representing a major component of the overall microbiome alongside bacteria, fungi, and other microorganisms. The plasma virome specifically refers to the variety of DNA and RNA viruses, bacteriophages, and giant viruses present in the bloodstream, whether actively replicating or existing in a latent, non-immunogenic form. HIV infection reduces $CD4^+$ T-cell counts and compromises immune function. It can also trigger the activation of human endogenous retroviruses (HERVs), ancient viral sequences embedded in the genome, which may further disrupt immune regulation and influence virome composition. Although alterations in the plasma virome have been well described in untreated HIV infection and in individuals with advanced immunosuppression, far less is known about people on effective antiretroviral therapy (ART) who maintain normal CD4 levels. This study investigated differences in the plasma virome between ART-treated HIV-positive adults and age-matched HIV-negative controls. Plasma viral DNA from both groups was sequenced using the Illumina NextSeq 500 platform and analyzed with the VIROMATCH pipeline to detect and classify viral sequences. Distinct shifts in viral community structure emerged, characterized by a pronounced enrichment of Human gamma herpesvirus 4 (Epstein–Barr virus, EBV) in individuals with HIV undergoing ART. EBV levels correlated positively with markers of T-cell exhaustion, (Tim-3, CTLA-4, and PD-1) and increased TNF-α, indicating that virome alterations may contribute to ongoing inflammation and immune perturbation despite viral suppression. Overall, these findings underscore the potential influence of the plasma virome on immune function in HIV infection.

Loss of Raf Kinase Inhibitor Protein is Compensated by *Plasmodium falciparum* Through Increased Import of Host RKIP

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Abstract:

Raf kinase inhibitor protein (RKIP) plays a key role in regulating critical signaling pathways in higher eukaryotes by modulating protein-protein interactions. The *Plasmodium falciparum* ortholog, PfRKIP, exhibits distinct lipid-binding characteristics driven by conserved residues, such as Pro80 and His92, and unique structural features, including a left-handed α5 helix and the IKK motif. We previously demonstrated that PfRKIP modulates the activity of calcium-dependent protein kinase 1 (PfCDPK1), a key regulator of red blood cell invasion. Here, we have used a pharmacological approach to investigate the function of PfRKIP in the asexual proliferation of the parasite. Treatment of the parasite with a specific inhibitor of mammalian RKIP called locostatin shows a dose-dependent decrease in ring-stage parasites. We have identified a possible mechanism via which locostatin blocks the invasion of RBCs. Locostatin increases the interaction between PfRKIP and PfCDPK1, leading to the sequestration of PfCDPK1 that inhibits the phosphorylation of downstream substrates. However, interestingly, PfRKIP could be knocked out from the parasite without any perceptible growth defect during the asexual proliferation under in vitro conditions. This suggests that either PfRKIP is dispensable for the blood stages or the adoption of compensatory mechanisms by the parasite. Interestingly, the PfRKIP-deficient parasites show an increase in the import of host RKIP. Like the parasite RKIP, the host RKIP interacts with PfCDPK1 and is associated with high-molecular-weight complexes comprising PfCDPK1. Our study reveals a novel host-parasite interaction wherein the parasite co-opts host proteins to maintain critical signaling pathways. These findings highlight the functional interplay between parasite and host RKIP, offering new insights into host-parasite interaction. Targeting the PfRKIP signaling axis, along with the host proteins, represents a potential strategy for anti-malarial drug development. Exploiting host-protein interactions that are less prone to parasite-driven resistance mechanisms could pave the way for novel and effective treatments for malaria.

From Molecular Mechanisms to Clinical Manifestations: A Clinician's Perspective on Dengue

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Abstract:

Despite significant advances in the molecular characterization of the Dengue virus (DENV), the clinical management of severe dengue remains largely supportive and reactive. While bench science has elucidated mechanisms such as Antibody-Dependent Enhancement (ADE) and NS1-mediated endothelial dysfunction, translating these molecular insights into predictive clinical tools remains a significant challenge. This presentation aims to bridge the gap between basic microbiological research and bedside practice. It will analyze the pathophysiology of DENV infection through the lens of a clinician, highlighting how viral and immunological dynamics manifest as life-threatening clinical phenotypes. We will explore the correlation between viral virulence factors (specifically NS1) and the clinical hallmark of severe dengue: vascular permeability and shock. The discussion will navigate the "cytokine storm," examining why defervescence paradoxically signals the onset of the critical phase. Crucially, the talk will identify major "translational gaps" where current research has yet to solve clinical dilemmas. These include the lack of reliable early prognostic biomarkers for severe disease, the discordance between thrombocytopenia and bleeding manifestations, and the molecular basis of "expanded dengue syndrome" involving cardiac and neurological complications. Moving forward requires a symbiotic relationship between molecular virologists and clinicians. By aligning high-precision microbiological research with the unpredictable realities of human physiology, we can move from reactive fluid management to proactive risk stratification and targeted intervention.

A Host-Directed Therapeutic Approach for the Treatment of Group A Streptococcal Infection

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Abstract:

Group A *Streptococcus* (GAS) is a major human pathogen that is associated with a wide range of infections, including acute pharyngitis, scarlet fever, impetigo, cellulitis and necrotizing fasciitis (NF). Mortality from NF remains high due to non-specific early symptoms, lack of a vaccine, and limited effectiveness of current treatments. Therefore, there is a genuine need for effective treatments against GAS NF. We previously showed that GAS induces endoplasmic reticulum (ER) stress to obtain asparagine from host cells. In this study, we demonstrate that GAS drives asparagine production and release through the PERK-eIF2α-ATF4 arm of the unfolded protein response, and that inhibitors of PERK or the integrated stress response (ISR) block this process-an effect reversed by adding external asparagine. In a murine NF model, these inhibitors reduced mortality, bacterial load, and lesion size, while histopathology revealed improved neutrophil infiltration and reduced damaging inflammation. Notably, treatment remained effective even when initiated 12 hours after infection. These findings suggest that targeting host metabolic responses using PERK/ISR inhibitors represents a promising therapeutic strategy against invasive GAS disease.

From Patients to Functional Models: Translational Lessons Shaping Leukemia Research and Drug Development

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Abstract:

Comprehensive patient sequencing has revealed leukemia as a genetically and epigenetically complex disease, with hundreds of mutated genes, chromosomal translocations, deletions, aberrant gene expression, and widespread epigenetic dysregulation. Translating this complexity into biological understanding requires functional model systems that can test which of these alterations truly drive leukemia initiation and progression and to identify novel drug targets for treatment. Functional murine and human hematopoietic systems have demonstrated that proto-oncogene activation via chromosomal translocation (CT) (e.g., CDX2) can initiate leukemogenesis. Majority of the CT events are not sufficient on their own to induce leukemia. Only upon acquisition of cooperating lesions (such as FLT3-ITD) do models faithfully recapitulate full-blown leukemia. Further, these systems led to the discovery of CDX4 and VENTX as previously unrecognized oncogenic drivers, and enabled the isolation and functional characterization of leukemic stem cells across multiple AML and ALL subtypes. This "patients → functional models" strategy thus refines our understanding of which genetic lesions are "drivers" of disease rather than incidental passengers. Extending beyond genetics, these functional models also uncovered critical epigenetic vulnerabilities. The DNA-modifier TET1 was shown to sustain global 5-hydroxymethylcytosine (5hmC) landscapes and regulate cell-cycle, DNA repair, and oncogenic transcriptional programs particularly in T-ALL. TET3 emerged as a key epigenetic regulator essential for metabolic adaptation and maintenance of leukemic stem cell programs in AML. Crucially, inhibition of TET1 activity by the clinically approved PARP inhibitor Olaparib demonstrated a therapeutically actionable route. These findings, describing CDX2, CDX4, VENTX, TET1, and TET3 as causal drivers and modifiers in leukemia, have been published in leading journals including Blood (IF ≈ 22.1), Leukemia (IF ≈ 13.4), PNAS (IF ≈ 11.2), Journal of Clinical Investigation (IF ≈ 13.6), Journal of Experimental Medicine (IF ≈ 10.4), and Cancer Cell (IF ≈ 31.7). Together, they demonstrate that integrating patient-derived genomics with robust functional modelling and leukemic stem cell assays provides a powerful, translationally relevant framework to identify actionable targets and accelerate development of improved therapies for hematologic malignancies.

Towards Investigating the Anticancer Role of Gut Microbiota-Derived Metabolites

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Abstract:

As per recent research reports, gut microbiota-derived metabolites such as indoxyl sulfate, inosine etc. possess selective anticancer effect on cancer cells. But the majority of gut microbial metabolites have not been screened for their anti-tumor activities nor underlying mechanism have been deciphered for developing therapeutic intervention for cancer management. In the present study, we investigated anti-tumor activity of three gut microbiota-derived metabolites, 4-ethylphenyl sulfate (4EPS), indoxyl sulfate (IndS) and p-Cresyl Sulfate (pCS) on colon cancer cells. Using HCT-116 colon cancer cells, in-vitro cell-based assays were done that demonstrated 4EPS, IndS and pCS can reduce cell proliferation, cell viability and ATP content in dose and time dependent manner. Cell morphology was found to be distorted at concentrations, 2.5 mM, 5 mM and 10mM. HCT-116 cells also showed a decrease in colony formation when exposed to 2.5 mM, 5 mM and 10mM of 4EPS, IndS and pCS. These metabolites enhanced the apoptosis and ROS production as compared to control cells. Cell cycle assay showed the arrest at G2/M phase for 4EPS, IndS and pCS. An animal study was also conducted using balb/c mice to demonstrate the selective deleterious effect of indoxyl sulfate on cancer cells while sparing normal colonic cells. IndS did not cause any harm or inflammation in normal colonic cells of balb/c mice, hence, it can be considered safe for use as an anticancer agent and may have implications in future applications for colon cancer treatment. This warrants further mechanistic investigations in this direction.

Metabolic Resilience is Achieved in Migratory Buntings via Inter-Organ Redox Dynamics and Gut Microbiome Adaptation

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Abstract:

Migration represents the metabolic pinnacle in birds, demanding efficient fuel mobilization and sustained aerobic performance, primarily coordinated by the liver, muscle, and gut. We examined MMP^+, ROS, apoptosis, and expression of genes associated with energy metabolism, and cell survival in liver, pectoralis muscle and intestinal parts of photosensitive nonmigratory (nMig) and photoinduced migratory (Mig) male buntings. Genes assayed included ACADM, PEPCK, GOT, GLUT1, CS (energy); SIRT1 (ROS modulation); SOD1, PRX4, NOS2, GPX1, GPX4 (mitochondrial scavengers); NF-κB (anti-apoptotic) and CASP7 (apoptotic). Histological evaluation assessed tissue-level changes. During migration, both liver and muscle showed reduced MMP^+ and elevated ROS, reflecting heightened metabolic load. Apoptosis increased in liver but declined in muscle, suggesting organ-specific protective strategies in favour of preserving flight musculature. In muscle, elevated SIRT1 and upregulated NF-κB indicate enhanced antioxidant defences and immune-linked protection from oxidative stress. Complementing these systemic changes, gut plasticity played a critical role in sustaining high-energy demands during migration. To evaluate intestinal adaptation, we examined gut morphology, microbiome composition, and expression of immunity- and metabolism-related genes in duodenum and colon of nonmigratory (nMig) and migratory (Mig) buntings. Histological analyses revealed thickening of the submucosa in both intestinal regions during migration, indicating reduced permeability and structural reinforcement. Necrosis in duodenal villi of migratory birds likely reflected temporary gut regression—a known migratory trade-off. Despite semi-captive conditions, subtle yet consistent shifts in microbiome profile were evident. Migratory birds exhibited Firmicutes-dominated communities, particularly Bacillus, whereas nonmigrants harboured Enterobacteriaceae-rich microbiota. Upregulation of immune genes (NF-κB, BCL6) and metabolic regulator SIRT1 further supported enhanced gut defence and energy mobilization during migration. Collectively, these findings reveal an integrated metabolic resilience strategy in migratory redheaded buntings, where organ-specific redox–apoptotic adjustments and gut microbiome remodelling synergistically sustain the immense physiological demands of migration.

Towards Identifying New Druggable Targets and Drugs Against Drug-Sensitive and Resistant *Mycobacterium Tuberculosis*

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Abstract:

To address the growing threat of drug-resistant TB, there is an urgent need to identify small molecules that possess a novel mechanism of action and show synergy with first-line TB drugs. Our group has identified enzymes that are essential for growth in vitro and in vivo. We have performed high-throughput screening against one of these enzymes and identified small molecules that possess activity against intracellular *M. tuberculosis*. We have also performed phenotypic screening to identify small molecules that possess activity against *M. tuberculosis*. We have identified several molecules that possess anti-tubercular activity in the low micromolar range. The pyridine carboxamide-based scaffold identified from phenotypic screening requires AmiC for activation and inhibits *M. tuberculosis* growth in a mouse model of infection. The molecules identified from both target and phenotypic-based screening show activity against drug-resistant strains and synergy with first-line TB drugs. Experiments are in progress to further optimise these lead molecules.

Rising Antimicrobial Resistance-Wake-Up Call to Global Health

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Abstract:

Antimicrobial resistance (AMR) is considered as a global threat that requires comprehensive research to understand the factors that are contributing to this problem, including genetic character of microorganisms, mechanisms of resistance, and clinical or societal implications. AMR mainly arises due to inappropriate use of antimicrobial drugs in agricultural fields, veterinary clinics and human medicine, along with poor sanitation conditions, inadequate and poor infection control measures and several other environmental factors that enables the survival of microorganisms and their proliferation in the presence of drugs, thereby making them drug resistant. Increase in instances of AMR has led to high rate of morbidity and mortality, prolonged period of hospitalization and higher healthcare costs. The data obtained from epidemiological studies indicate that AMR is characterized by evolving parameters that change continuously and impacts human health with a bigger challenge every day. There are many pathways responsible for emergence of AMR that includes horizontal gene transfer, spontaneous mutation, selective pressure from improper use of drugs that results into emergence of new multidrug resistant strains. To combat AMR, effective mitigation and prevention strategies should be adopted such as antibiotic stewardships programs, restrictions on over-the-counter available prescriptions or antibiotics, adoption of strong infection-prevention and control strategies, stringent antimicrobial surveillance in community, One health approach, which emphasizes the interconnectedness of human, animal, and environmental health. Although, the advancements in development of novel therapeutic molecules have helped in slowing down the progression of AMR, but there is still an urgent need to develop new strategies and better drugs to address AMR challenges. Continuous and active collaboration among clinicians, interdisciplinary scientists, researchers, policymakers, and public health professionals is crucial for identifying AMR drivers that could lead to designing impactful interventions. It is imperative to understand that without strong intervention, common infectious diseases might turn untreatable due to the menace of AMR, hence placing enormous pressure on the healthcare systems and medical community and threatening global health security.

Expression and Characterization of Novel GS-LINKED Chimeric Endolysin Chapk-SH3bk Against Biofilm-Forming Methicillin-Resistant *Staphylococcus aureus*

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Abstract:

Methicillin-resistant *Staphylococcus aureus* is one of the major pathogens in hospitals, community and livestock associated infections. The spread of MRSA and its ability to form biofilms impedes antibiotic treatment increasing the risk of mortality in human and animal health sectors. This necessitates the search for novel antimicrobial agents like bacteriophage endolysins which act against peptidoglycan layer of Gram-positive bacterial cell wall effectively when administered from outside of the cell. This study includes expression of novel chimeric endolysin CHAPk-SH3bk composed of enzymatically active domain and cell wall binding domain of phage endolysin LysK and investigate its bacteriolytic and anti-biofilm activity against MRSA. The bacteriolytic activity of the chimeric endolysin CHAPk-SH3bk was analysed through in-vitro antibacterial assays including diffusion lysis assay, CFU reduction assay, and time-kill curve assay. The antibacterial assay results displayed the bactericidal activity of CHAPK-SH3bk against HA-MRSA. The biofilm reduction ability of CHAPk-SH3bk against HA and LA-MRSA was analysed using in-vitro crystal-violet assay, and in-vivo mice skin infection model. The CHAPk-SH3bk displayed effective biofilm reduction activity effective against 24 h and 48 h biofilms of HA-MRSA from plastic, glass and steel surface. The CHAPk-SH3bk displayed significant biofilm reduction activity of 24 h MRSA biofilm from mice skin. The anti-biofilm activity was confirmed on ex-vivo murine skin tissue using IHC, CLSM, and SEM. In addition, the CHAPk-SH3bk was found to inhibit the biofilm formation of hospital and bovine origin MRSA in in-vitro conditions. The in-vitro and in-vivo biofilm reduction activity confirmed that the addition of cell wall binding domain SH3bk to catalytic domain CHAPk enhanced the catalytic activity CHAPk against sessile cells. In conclusion, the research work provides a promising anti-staphylococcal agent CHAPkSH3bk, which works effectively in an antibiotic-exempted environment against MRSA and states that the shuffling of parental endolysin domains may increase the anti-biofilm activity of catalytic domain.

Urbanisation, Mucosal Immunity, and the Gut Microbiota: Integrating Host Defence with Microbial Symbiosis

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Abstract:

Dysregulation of intestinal microflora contributes to inflammatory disorders by impairing the immunosuppressive functions of $Foxp3^+$ regulatory T (Treg) cells. Although commensal microbiota influence Treg generation, the key microbial and dietary factors involved remain unclear. Urbanization marked by reduced microbial exposure and dietary shifts further disrupts these regulatory interactions, increasing susceptibility to intestinal inflammation. We identified Bifidobacterium bifidum as a potent inducer of $Foxp3^+$ Treg cells. Its cell surface β-glucan/galactan (CSGG) polysaccharides were the key molecules driving Treg induction via regulatory dendritic cells (DCs). CSGG-induced Treg cells maintained stable Foxp3 expression, displayed strong suppressive capacity, and alleviated experimental colitis, underscoring the therapeutic potential of CSGG-producing microbes many of which are diminished in urbanized populations. We also show that dietary glucose is essential for establishing retinal dehydrogenase (RALDH) activity in small intestinal $CD103^+CD11b^+$ DCs, enabling retinoic acid dependent iTreg differentiation. Using germ-free mice on antigen-free diets, we found that glucose but not proteins, starch, or minerals is required for optimal DC-mediated iTreg generation, highlighting how urbanization-driven dietary changes may impact this pathway. Together, these findings illustrate how microbial polysaccharides and dietary glucose cooperate to shape intestinal immune tolerance by programming tolerogenic DCs and promoting $Foxp3^+$ Treg differentiation. In an increasingly urbanized world, understanding these interactions offers avenues to restore mucosal homeostasis and counter rising inflammatory diseases.

AMR a Global Concern: Smart Solutions for Resource Challenges

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Abstract:

Antimicrobial resistance (AMR) has become one of the most pressing global health threats, driven by the overuse of antibiotics and the rapid spread of resistance determinants across clinical and environmental boundaries. India, with its dense population and diverse healthcare systems, serves as a major hotspot for the emergence and evolution of multidrug-resistant (MDR) bacteria. Our laboratory investigates environmental reservoirs and molecular mechanisms underlying AMR transmission, focusing particularly on hospital sewage as a key source of resistance gene dissemination. In 2014, we reported the first identification of New Delhi metallo-β-lactamase-4 (NDM-4) from hospital sewage in India, revealing the environmental persistence and potential horizontal transfer of carbapenem resistance. More recently, we detected the mobilized colistin resistance gene mcr-5.1 in hospital sewage samples collected along the West Bengal Bihar border, highlighting the alarming spread of plasmid-mediated colistin resistance the last therapeutic line against Gram-negative pathogens. Parallel investigations in our lab explore innovative countermeasures to mitigate AMR, including vaccine development against resistant pathogens, discovery of novel β-lactamase inhibitors, photodynamic therapy employing photosensitizers, and nanocomposite-based antimicrobial platforms with enhanced bactericidal and antibiofilm activities. Together, these efforts integrate environmental microbiology, molecular genetics, and translational research to advance comprehensive strategies against drug-resistant infections. Our findings emphasize the urgent need for sustained environmental surveillance, rational antibiotic stewardship, and the development of next-generation therapeutics to safeguard global health.

Role of NCOR1 in *Mycobacterium tuberculosis* pathogenesis

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Abstract:

Recently, we identified that nuclear receptor co-repressor NCoR1 plays an important role in fine-tuning host cell energy homeostasis and autophagy flux during Mtb infection by regulating AMPK-mTOR-TFEB axis. Moreover, we found that NCoR1 expression is significantly reduced during active tuberculosis in patients and upon anti-tuberculous therapy of 12 months the NCoR1 levels were restored to normal. Besides, we found that during early infection the alveolar macrophages showed increased NCoR1, and the levels were subdued upon active Mtb infection. Interestingly, the levels of NCoR1 in lung alveolar macrophages negatively correlated with cellular ATP levels during active infection stages. Overall, our initial findings depicted NCoR1 as a potential host factor playing an important role in immune-metabolic switch, which might be controlled by Mtb for taking over host cell defences for its survival. Now, we are trying to understand how the NCoR1 senses the changes in cellular ATP levels and thereby regulates the AMPK-mTOR-TFEB axis during dynamic stages of Mtb infection. Besides, do we observe NCoR1 correlation with tuberculosis disease stages / severity in patients? We are employing integrative single-cell immune-metabolic and genomic approaches to understand the NCoR1 mediated metabolic control of Mtb pathogenesis in mice as well as in patients.

Evasion and Immunity in Leishmaniasis: From Traps to Vaccines

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Abstract:

Leishmaniasis, a neglected and third most fatal vector borne disease, is caused by Leishmania spp. Innate immune cells like mast cells (MCs) and macrophages serve as first responders against Leishmania infection. Their activation followed by recruitment to the site of infection initiates a cascade of immunological events which could either facilitate parasite clearance or contribute to immune evasion. Mast cells (MCs) are found in high amounts in the skin, especially in the superficial dermis where Leishmania parasites invade after a sand fly bite. In our study the interactions of *L. donovani*, causing visceral leishmaniasis, and *L. tropica* and *L. mexicana*, causing cutaneous leishmaniasis with MCs were studied. The primary objective was to assess how MCs contribute to the clearance of Leishmania. Our findings indicated heterogeneity in response of MCs to different species of Leishmania in terms of intracellular clearance by phagocytosis, and extracellular clearance by formation of Mast cell extracellular traps (MCETs). These findings underscored the role of MCs in Leishmania clearance and facilitation of better development of new therapies or vaccines against leishmaniasis. In spite of the availability of antiparasitic drugs, challenges such as drug resistance, toxicity and treatment failure necessitates the development of an effective vaccine. In this study, we employed CRISPR/Cas9 to delete amastigote stage specific genes in Leishmania and tested their potential as live attenuated vaccine candidates against leishmaniasis. One of these mutants having a deletion of Adenosine kinase 2 (ADK2), showed a good potential as a live attenuated vaccine candidate on basis of in vitro and in vivo safety, immune response and challenge studies.

Mining for the Specificity Within Interferon Regulatory Factors Leading to Dendritic Cell Differentiation and Innate Immunity

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Abstract:

The DC subsets are collection of heterogeneous populations that are broadly categorized into plasmacytoid DCs (pDCs) and classical DCs (cDC) represented by the phenotypically diverse cDC subsets (cDC1 and cDC2). IRF family members; Irf8 is essential for pDC and cDC1subtype whereas Irf4 is required for the cDC2 subtype development. A spontaneous IRF8^{R294C} mutation in BXH2 mouse model abolishes the development of cDC1 subtype without impairing pDC development and eliminates production of IL12p40, while retaining that of type I IFNs. BATF3 cooperates with IRF8 towards development of cDC1 while higher expression of Irf8 can compensate for the absence of Batf3 for cDC1 development. In our recent study by employing global gene expression analysis, we revisit the role of Irf8 and Irf4 in defining the DC diversity and innate immune pathways.

Regulating the Chemokine Mediated Leukocyte Trafficking by Small Molecule Inhibitors

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Abstract:

Infections caused by microorganisms such as bacteria, viruses, and fungi etc., are cleared by the host organism using their innate and adaptive immune system. Chemokines are a group of chemotactic cytokines that are involved in regulating leucocyte migration to the infected tissue. They do so by binding to glycosaminoglycans (GAGs) on the endothelial cell surface and thus activating the G-protein coupled receptors (GPCR) present on the leucocytes. The current talk details the structure- function-stability relationships of CXC/CC chemokine orthologs and paralogs. Molecular studies using chemical biology techniques with synthetic GAG molecules and GRO Chemokines suggest that these synthetic sulfated carbohydrate scaffolds and plant derived flavonoids are specific in binding to chemokines and can compete with the natural GAGs/Receptors in resolving inflammations and infections. Further, this study unravelled the molecular specificity of CXC chemokine orthologs and paralogs that are rationally evolved under species specific selection pressure of molecular evolution. Taken together, these molecular partnerships of chemokines can be selectively used to regulate tissue regeneration and wound healing applications.

Structure-Based drug Discovery for mitigation of *Pseudomonas aeruginosa* Biofilms

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Abstract:

Pseudomonas aeruginosa is a polar flagellated opportunistic pathogen that causes severe acute and chronic infections in immunocompromised individuals. It is one of the ESKAPE pathogens known for its multi-drug resistance, primarily due to its ability to form biofilms. Biofilms are structured communities of adherent bacterial cells embedded in a self-produced extracellular matrix composed of exopolysaccharides, proteins and eDNA. This protective matrix enables the bacteria to withstand adverse conditions, leading to persistent and hard to treat infections. Numerous strategies have been explored for combating biofilms but treatment of biofilm mediated infections remains a significant challenge. Therefore, identifying novel molecular targets and elucidating the detailed mechanisms underlying biofilm regulation are of importance. Structure-based drug discovery (SBDD) offers a powerful approach by exploiting atomic-level structural information of target proteins to identify high-affinity ligands. We have utilized transcription factors as targets for SBDD to identify inhibitors of biofilm and validated the hit molecules for anti-biofilm activity. We have also determined the crystal structure of the complex between the target protein and the inhibitor and delineated the detailed mechanism of action of the inhibitors.

Harnessing the Potential of X-Ray and Cryo-EM Studies to Identifying/Designing Anti-Mtb Small Molecules

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Abstract:

Human tuberculosis (TB), caused by *Mycobacterium tuberculosis* (Mtb), still poses a major health issue worldwide despite the availability of several antibiotics and BCG vaccine. To reduce the prolonged current anti-TB treatment duration and furthermore to deal with the pressing drug resistance crisis, exploring new options to limit Mtb escalation is indubitably required. Amino acids are fundamental requirements for any living organism primarily for protein synthesis. Notably, Mtb can biosynthesizes all 20 amino acids de novo; whereas humans do not make nine amino acids-Phe, His, Ile, Lys, Leu, Met, Thr, Val and Trp. These key fundamental differences suggest that chemical annihilation of the function of one or more of these nine amino acids biosynthesis pathways deems a rational strategy for developing novel anti-TB therapeutics. In our view, structure guided drug discovery approach deems an important strategy in this context. Over the years, we have elucidated and analysed high resolution X-ray and Cryo-EM structures of an important enzyme, imidazole glycerol phosphate dehydratase (IGPD; HisB) which catalyses the conversion of imidazole glycerol phosphate to imidazole acetol phosphate, of Mtb His pathway. Both X-ray and Cryo-EM studies demonstrate that the biological functional unit of HisB consists of a multimeric (24-mer) assembly with 24 identical active sites. Each active site pocket is lined with His, Glu, Arg, and Asp residues protruding from three different subunits. The tertiary structure of each subunit forms a funnel-like fold with a four-helix bundle flanked by two anti-parallel beta sheets. Furthermore, in the aspect of the criticality of His pathway, we have demonstrated in mouse model, through genetics and immunological investigations that Mtb employs its de novo His biosynthesis to mount a sustained infection. On the bases of the outcomes of our structural, biochemical and in vivo studies, we have identified/designed a number of triazole- and imidazole scaffold small molecules targeting the active site region of HisB. A couple of such molecules were safe in mice and effectively inhibited the in vitro growth of both free as well as in macrophage-internalized wild-type and drug- resistant Mtb clinical isolates. Notably, one of these also showed a moderate reduction in the bacterial load in organs of mice infected with Mtb.

Unusual GEF, EhFP10 Regulates Myosin-Driven Cytoskeletal Remodeling in *Entamoeba histolytica*

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Abstract:

Entamoeba histolytica has just two myosin isoforms facilitate the organism's motility and phagocytosis. Previous studies have highlighted the involvement of EhMyosin-IB in phagocytosis, with the Rho/PtdIns pathway playing a significant role in actin cytoskeleton remodeling. Specifically, the unique C-terminal domain of EhFP10 interacts directly with the SH3 domain of EhMyosin-IB, inhibiting actin bundle formation (PLoS pathogens, 2019). EhFP10, a multidomain protein exhibiting RhoGEF activity, lipid-binding capabilities, and protein-protein interaction domains, has emerged as a main player in EhMyosin-IB regulation. Crystallographic analysis of the EhFP10 RhoGEF domain has revealed conserved structural features, although the sequence differs significantly from other known proteins. Our studies showed that EhRho2 (RacG) exhibits significant guanine nucleotide exchange factor (GEF) activity when interacting with the EhFP10 RhoGEF-PH domain. Additionally, binding studies revealed that the EhMyosin-IB SH3 domain interacts directly with EhRho2, with variable affinities observed for other Rho GTPases. Lipid-binding assays using PIP strips indicated that the EhFP10 RhoGEF-PH domain specifically interacts with PIP3. Further investigations identified p21-activated kinases (PAK-4) as a downstream effector of EhRho2 within this signaling pathway. Our findings suggest that EhFP10, EhRho2, EhPAK4, and EhMyosin-IB form a complex that modulates cytoskeleton proteins during endocytosis and phagocytosis. This study provides significant insights into the molecular mechanisms underlying actin cytoskeleton remodeling in *Entamoeba histolytica*.

Octamerization of *Helicobacter Pylori* N-Carbamoylputrescine Amidase Reveals a Potential Target for Therapeutic Development

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Abstract:

N-carbamoylputrescine amidase (CPA) is a key enzyme in polyamine biosynthesis and is essential for cell growth and proliferation in plants and many bacteria. Although absent in humans, its presence in *Helicobacter pylori* makes CPA a promising therapeutic target. CPA activity critically depends on the formation of a functional homo-octamer. While most inhibitor discovery efforts focus on active-site targeting, modulating regions outside the catalytic pocket remains a significant challenge. In this study, we identified a conserved aromatic cluster and an adjacent short motif proximal to the active site that are essential for octamer assembly and CPA function. Computational and solution-based analyses revealed that this motif adopts a short helical structure required for generating catalytically competent octamers. We further show that the motif interacts with two residues within the same monomer, forming a non-catalytic triad. Single alanine substitutions at these positions disrupt octamerization, yielding dimers with markedly reduced activity, despite retaining the short helix. This highlights the triad's role in stabilizing the oligomeric architecture. Importantly, we identified a pocket formed by this motif and its surrounding region that can be exploited for inhibitor design. Targeting this site, we developed a small-molecule CPA inhibitor that significantly reduces enzymatic activity. Together, these findings uncover a previously unrecognized regulatory site that controls CPA function through oligomerization, offering new opportunities for the development of potent *H. pylori* therapeutics.

Integrative Computational Approaches to Elucidate PPI Interfaces for Designing Small Molecule Autophagy Inducers

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Abstract:

Protein-protein (PP) complexes orchestrate most of the aspects of cellular biology. Cellular events encompass obligate and transient PP interactions that accurately define the interactome in a time and location dependent manner. Mimicry of the interfacial protein domain of interactome offers a promising strategy to rationally design modulators from the PP interaction interfaces. However, due to the complex nature of PPI it becomes a "tough nut to crack". Here, we are exploring the PP interfaces at atomic and dynamic level to discover small molecules like autophagy inducers, NOSIP inhibitors, etc by applying the non-canonical computational pipeline of existing methods. Autophagy has been found to be dysregulated in many diseases. The interfaces of Beclin-1 and its regulator were underpinned for identification of determinants to generate the autophagy inducers in m-TOR independent manner. The distinct free energy calculations were applied to decipher the most likely binding mode/s of interacting partners from their multiple generated complexes. From many microseconds (μs) molecular dynamics simulations (MD) based 'hot-spot' identification at the interface regions were underscored to design multiple sets of peptides. The computationally active peptides (fulfill the filtering criteria), were evaluated in in vitro assays, binding studies through SPR, followed by in-vivo studies using salmonella and IBD mouse models, indicating a "green signal" for this protocol. Furthermore, we applied this on disordered NOSIP proteins to prevent its binding with iNOS, to increase the endogenous NO level and getting experimental validation, confirm the robustness of the protocol on more complex system as well for peptides and peptide-based small molecules discovery and move towards hit-to-lead direction.

Engineering *Pseudomonas bharatica* CSV86^T to Gain Aromatic Metabolism Diversity

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Abstract:

Pseudomonas bharatica CSV86^T, a novel Indian soil isolate, preferentially degrades aromatics like naphthalene, benzoate, benzyl alcohol over simple carbon sources like glucose or glycerol. Further, availability of genome sequence, well-characterised growth conditions and lack of plasmid make it an ideal chassis for metabolic engineering. Strain CSV86^T was engineered by introducing genes encoding two enzymes and transport proteins at different locations in the CSV86 cells. Engineered strain degrades Carbaryl via 1-naphthol→1,2-dihydroxynaphthalene→→salicylate→catechol route by expressing Carbaryl hydrolase (CH) and 1-naphthol 2-hydroxylase (1NH) under the Pnah promoter. The presence of transmembrane domain and signal peptide at the N-terminus of CH resulted in the compartmentalisation of Carbaryl degradation enzymes by localising CH and 1NH to the periplasm of the engineered strain, thus mitigating the toxicity of 1-naphthol. Enzyme activity, whole-cell oxygen uptake, biotransformation, protein analyses and quantitative-PCR studies suggest that the engineered strain preferentially utilises Carbaryl over glucose and co-metabolizes it with succinate. CSV86 cell were also engineered to gain the metabolic diversity in the lower aromatic degradation pathway by introducing two operons responsible for the metabolism of salicylate via gentisate. Versatile eco-physiological traits with unique preferential utilization of aromatic property make *P. bharatica* CSV86^T a promising chassis/ host for metabolic engineering of aromatic degradation pathways and bioremediation.

High Altitude Illness: Insights from DRDO Research

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Abstract:

High altitude illness (HAI) encompasses a range of hypoxia-related disorders including Acute Mountain Sickness (AMS), High Altitude Pulmonary Edema (HAPE), High Altitude Cerebral Edema (HACE) along with significantly elevated risk of thrombotic complications. These include deep vein thrombosis (DVT), pulmonary embolism (PE), and ischemic stroke, which are emerging as critical health concerns for soldiers deployed to extreme altitudes such as the Siachen Glacier and Eastern Ladakh. Multiple stressors hypobaric hypoxia, dehydration, cold stress, increased blood viscosity, and prolonged immobility synergistically contribute to a hypercoagulable state. Physiological alterations such as hypoxia-induced polycythemia, hemoconcentration, platelet activation, oxidative stress, and endothelial dysfunction further exacerbate the risk of clot formation. While physiological and biochemical responses explain part of this vulnerability, genetic predisposition has emerged as a major determinant of how individuals adapt or fail to adapt to high-altitude stress. Variations in genes regulating coagulation, fibrinolysis, and hypoxia adaptation influence individual vulnerability. These genetic factors partly explain why some soldiers tolerate altitude with minimal symptoms while others rapidly develop severe illness. By addressing thrombosis as a critical but often under-recognized dimension of high-altitude illness, this information will provide actionable insights for both military operations and civilian high-altitude medicine. Comprehensive framework of genetic susceptibility, epigenetic regulation, and environmental stressors would be helpful in prediction, prevention, and management of high-altitude thrombosis and related illnesses. This genetics-driven and systems-biology approach not only strengthens the operational preparedness of Indian soldiers in extreme altitudes but also offers translational benefits for civilian high-altitude travellers, mountaineers, and patients with hypoxia-related conditions.

Inhibiting Protein-Protein Interactions in Pathogens

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Abstract:

Our laboratory had previously developed a method for laboratory-directed evolution of proteins, called 'codon-shuffling'. The potential of this method to create stand-alone de novo protein/peptide libraries, for their eventual use as antibacterial and drug-like entities has since been realised. Because of an inherent property of each of the fourteen dicodons (oligonucleotides 6 bases in length) in the 'dicodon set' to possess a secondary structure imprint, the assembly of such dicodons creates proteins with well-folded characteristics, largely due to the accumulation of so-called secondary structure imprints that form predefined helical and sheet protein folds. The application of codon-shuffling has been the underlying theme of research in our laboratory for more than a decade. Recently, we isolated a peptide that can disrupt the crucial ESAT6:CFP10 protein-protein interaction in M. tuberculosis. Exo- or endogenous presence of this peptide, named HCL2, severely affects mycobacterial growth as well as its cell-wall structure and colony morphology. It was shown that mycobacteria expressing this peptide show a drastic reduction in colony forming units. Efforts are now directed towards exploring the possibility of an HCL2-attenuated M. tuberculosis strain to act as a viable vaccine candidate. More recently, we discovered a codon-shuffled de novo protein M5, of 100 aa length, that was able to disrupt the ICAM-1 dimer formation in vivo. The presence of ICAM-1 (Intercellular adhesion molecule) is crucial for the progression of diseases like tuberculosis, HIV, and Malaria. It was shown that M5, in quantities as little as 25 μM, is able to block the entry of P. falciparum into red blood cells by almost 80%. Not only has this discovery opened avenues to study the role of ICAM-1 or ICAM-like molecules in the invasion process, the drug-like potential of M5, or peptidomimetics based on M5, is also being explored.

Decoding the Multifaceted Role of Erythrocyte PMCA4b in Oxidative Stress Mediated Malaria Protection and Artemisinin Resistance

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Abstract

The ATP2B4 gene, encoding the PMCA4b Ca^{2+}-ATPase in erythrocytes, has been linked to malaria protection via genome-wide association studies, though the proposed dehydration mechanism remains unclear. This study evaluates ATP2B4 genotypes and PMCA4b expression in malaria susceptibility and artemisinin sensitivity. ATP2B4 genotypes were compared across severe malaria, uncomplicated malaria, and healthy controls in Indian population. PMCA4b expression, intra-erythrocytic calcium, oxidative stress markers, Gardos channel activity, and *P. falciparum* growth dynamics were analyzed. Artemisinin sensitivity was assessed using growth inhibition and ring survival assays. ATP2B4 genotypes showed no significant association with malaria protection. Regardless of genotype, low PMCA4b expression correlated with increased intra-erythrocytic calcium, oxidative stress, and reduced in-vitro parasite growth. Gardos channel activity inversely correlated with PMCA4b but did not induce dehydration. Instead, oxidative-stress regulation by PMCA4b emerged as a key factor in malaria protection. Treatment of RBCs with resveratrol, a PMCA inhibitor further validates the functional role of PMCA in regulation of intracellular calcium and oxidative stress. Notably, low PMCA4b expression also reduced P. falciparum artemisinin sensitivity, providing evidence that host genetic variation can influence drug efficacy. These findings suggest PMCA4b's role in oxidative stress and drug response as critical to malaria pathophysiology. We further emphasize that many redox modulating RBC polymorphisms in malaria endemic areas, could also influence artemisinin efficacy and serve as potential biomarkers for predicting therapeutic response.

In Vivo Efficacy and Pharmacokinetics of Rbx 11760 Loaded PLA-PEG Nanoparticles in Mouse Bronchopneumonia and Rat Groin Abscess Caused by *Staphylococcus aureus*

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Abstract:

Staphylococcus aureus is a gram-positive opportunistic pathogen, causes skin infections, respiratory infections such as sinusitis and food poisoning. *S. aureus* is one of the leading pathogens for deaths associated with antimicrobial resistance. Since antibiotic resistant strains are emerging worldwide, there is a need for new antimicrobial agents to tackle the antibiotic-resistant *S. aureus* strains. RBx 11760 is a bi-aryl oxazolidinone antibacterial agent active against *S. aureus* but has poor solubility. Here we have encapsulated RBx 11760 in PLA–PEG Nanoparticles with an aim to improve physicochemical, pharmacokinetics and in vivo efficacy. In vitro antibacterial agar well diffusion assay showed clear zone of inhibition of bacterial growth. RBx 11760 loaded PLA 72K -PEG 4K Nanoparticles as compared to its free form demonstrated an equivalent in vitro activity. In pharmacokinetic study, nanoparticle showed 4.6- fold and 7-fold increase in AUC inf and half-life, respectively, as compared to free drug. RBx11760 nanoparticle significantly reduced bacterial counts in lungs and improved the survival rate of immunocompromised mice as compared to free drugs. RBx 11760 loaded PLA 72K -PEG 4K Nanoparticles exhibited potent in vivo efficacy in mice model of bronchopneumonia and in rat model of groin abscess Thus, RBx 11760 loaded nanoparticles have strong potential to be used as nanomedicine against sensitive and drug-resistant Staphylococcus aureus infections.

Leveraging γ-L-Glutamyl-L-Cysteine Coated HSA Nanoconstructs to Repurpose Ropinirole for Brain-Targeted Therapy in Cerebral Ischemia/Reperfusion Injury

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Abstract:

Treatment of ischemic stroke remains profoundly challenging due to its multifactorial pathophysiology and the significant limitations imposed by the blood-brain barrier (BBB) on therapeutic delivery. Ropinirole hydrochloride (Rp), an FDA-approved drug for Parkinson's disease and restless leg syndrome, offers a triad of neuroprotective mechanisms, i.e., antioxidant, anti-inflammatory, and anti-apoptotic attributes, making it a strong candidate for repurposing in ischemic stroke and reperfusion (I/R) injury. However, its poor brain bioavailability substantially restricts its therapeutic potential. In this study, we developed sub-100 nm γ-L-glutamyl-L-cysteine-coated human serum albumin nanoparticles encapsulating Rp (C-Rp-NPs) to achieve active targeting of the ischemic brain, thereby enhancing therapeutic efficacy and reducing off-target toxicities. Confocal imaging and brain biodistribution studies demonstrated significantly improved targeting efficiency of optimized C-Rp-NPs. Pharmacokinetic evaluation further revealed prolonged systemic retention and markedly increased bioavailability of Rp delivered through C-Rp-NPs compared to free Rp solution (Rp-S). Therapeutic assessment in a transient middle cerebral artery occlusion (tMCAO) model showed that C-Rp-NPs substantially mitigated I/R-induced injury and restored neurological and behavioral functions, achieving a superior therapeutic index at nearly 1000-fold lower dose than Rp-S. Mechanistic investigations confirmed that C-Rp-NPs inhibited mitochondrial permeability transition pore (mtPTP) opening, suppressed apoptotic pathways, reduced oxidative stress and neuroinflammation, and elevated dopamine levels post-tMCAO. Overall, this work highlights the development of a rationally engineered, brain-targeted nanoplatform for repurposing ropinirole with significant translational potential for ischemic stroke therapy.

Ribonuclease Toxin-Mediated Modulation of Host Immunity by *Mycobacterium Tuberculosis*

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Abstract:

Tuberculosis eradication efforts are severely hampered by antimicrobial resistance (AMR). Our research explores the host-pathogen network driving antibiotic and disease persistence in *Mycobacterium tuberculosis* (*M. tuberculosis*). We investigated the VapBC12 Toxin-Antitoxin system and demonstrated its role in modulating bacterial growth and antibiotic susceptibility during infection. Structurally, we identified a unique Cholesterol Recognition Amino acid Consensus (CRAC) motif in VapC12 ribonuclease toxin and confirmed its toxicity in *M. smegmatis*. We solved the crystal structure of VapB12 and identified specific residues critical for the assembly and activity of the VapBC12 TA system. Mechanistically, our data suggests that cholesterol activates the ribonuclease toxin by competitively displacing its cognate antitoxin at the CRAC motif which consequently restricts the growth of *M. tuberculosis*. In-vivo studies using a VapC12 deletion mutant (ΔvapC12) in mice revealed a complex role in pathogenesis. The absence of VapC12 led to an increases pathogen load, induced a pro-inflammation response, and resulted in an enhanced susceptibility to anti-TB treatment. Interestingly, in a high-dose infection model, all the mice infected with ΔvapC12 succumbed early to the disease. The above VapC12 -mediated phenotype was found to be dependent on the presence of TLR4. We conclude that the inability of ΔvapC12 to resolve neutrophil-mediated inflammation impaired bacterial killing by altering the host T-cell response. Overall, our findings suggests that the VapC12 ribonuclease toxin modulates growth that favors long-term survival of the pathogen within the host and that the chemical inhibition of VapC12 prevents growth restriction and potentiates the activity of anti-TB drugs.

The Multi-subunit GID/CTLH E3 Ubiquitin Ligase Regulates Stage Differentiation in *Toxoplasma gondii*

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Abstract:

It is estimated that a third of the world's population is infected by *Toxoplasma gondii*, an obligate intracellular parasite that causes severe disease in immunocompromised individuals and can persist for life. Toxoplasma can alternate between distinct biological stages, reproducing sexually only in felines and can reproduce asexually in any warm- blooded animal. During asexual reproduction, very little is known about how the parasite alternates between the acute tachyzoite stage and the chronic bradyzoite stage when it reaches the brain/muscle tissues. We performed a whole genome CRISPR screen to identify genes required for growth in the presence of different carbon sources and identified genes that are responsible for stage conversion to latent forms. The screen identified over 60 genes that potentially regulate parasite differentiation and included several genes involved in protein ubiquitination. We identified the Toxoplasma orthologue of the yeast/human glucose induced degradation deficient (GID)/ C-terminal to LisH (CTLH) multi-subunit E3 ubiquitin ligase complex. Immunoprecipitation and mass spectrometry confirmed the composition of this complex and its genetic removal significantly reduced cyst formation in vitro and resulted in decreased cyst burden in the brain in vivo. This work highlights the importance of parasite ubiquitination in regulating stage conversion in apicomplexan parasites.

Spatial Genomics of *M. tuberculosis*: Architectural Signatures of Virulence

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Abstract:

Three-dimensional (3D) genome architecture has emerged as a key regulator of gene expression in bacteria, yet the spatial chromatin organization of *Mycobacterium tuberculosis* (Mtb) remains largely unexplored. Understanding this structural landscape is particularly important for deciphering why the attenuated strain H37Ra displays reduced virulence compared to the virulent H37Rv, despite high sequence similarity. In this study, we present the first genome-wide Hi-C based contact maps of Mtb H37Rv and H37Ra, providing new insights into how large-scale chromosomal organization may influence pathogenic potential. Our analysis reveals clear differences in chromosome interaction domain (CID) patterns between the two strains, including an overall increase in CID size in H37Ra. CID boundaries in H37Rv were enriched for highly expressed genes and operon-dense regions, suggesting a structural basis for transcriptional activity. Notably, differentially expressed PE/PPE family genes important contributors to virulence were preferentially located near CID boundaries in H37Rv but not in H37Ra. Exposure to hypoxia triggered systematic CID reorganization in both strains, indicating that environmental stress shapes higher-order chromatin structure. Together, these findings provide the first evidence that differential 3D genome topology may contribute to virulence attenuation in H37Ra and highlight the value of chromosome conformation approaches for understanding the molecular basis of Mtb pathogenicity.

Exploitation of Host Metabolic Stress by Group A *Streptococcus* for its Own Proliferation

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Abstract:

Streptococcus pyogenes (Group A *Streptococcus*; GAS) is a strictly human pathogen responsible for a broad spectrum of diseases, ranging from asymptomatic colonization and superficial infections such as pharyngitis and impetigo to severe, life-threatening, highly invasive conditions, including necrotizing fasciitis (NF) and streptococcal toxic shock syndrome (STSS). Globally, GAS imposes a substantial health burden. Each year, GAS is estimated to cause 616 million cases of pharyngitis and 1.78 million cases of invasive disease, resulting in more than 500,000 deaths worldwide. Despite decades of research, the mechanisms by which GAS adapts to distinct host niches and dynamically regulates its virulence remain incompletely understood. GAS exploits host metabolic stress to transition from asymptomatic colonization to invasive disease. During infection, GAS streptolysins trigger endoplasmic reticulum stress in host cells, activating the PERK-eIF2α-ATF4 arm of the unfolded protein response and increasing host asparagine (Asn) production. GAS imports this Asn to enhance its metabolic activity and proliferation. Elevated intracellular Asn increases the ADP/ATP ratio, thereby reducing the phosphorylation of CovR, the central regulator of the two-component system CovR/S, and thus derepressing the expression of virulence genes. The Asn-dependent regulatory mechanism mirrors ATF4-driven metabolic adaptation in cancer cells. Overall, these findings establish Asn as a key metabolic signal that couples host stress responses to the control of GAS pathogenicity.

Novel Application of an Indigenous Cysteine Protease in the Generation of Anti-Hypertensive Peptides from Anchovy Fish

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Abstract:

In this study, a protease-producing Bacillus subtilis A4 strain was identified from a local soil sample in Hyderabad, India. The strain was observed to show the highest protease specific activity at 76,153.84 U/mg. The enzyme was identified to have 71% sequence similarity with Bacillus subtilis cysteine protease. To test the applications of the cysteine protease in generating bioactive peptides, anchovy fish (*Stolephorus indicus*) meat was utilized as a substrate and the generated peptides were identified by LC-MS/MS analysis. in silico analysis of the peptides using CASTp server and GOLD software revealed peptide-10 to have binding score of 74.99 for binding ACE2 enzyme active sites, mainly by hydrogen bonding. The peptide showed least cytotoxicity against HEK-293T and 85-100 % of cell viability was observed even at high concentrations of 100 µg/mL with cancerous and non-cancerous cell lines. During in-vivo studies in Dexamethasone mediated hypersensitivity induced male Wistar rat model, it was observed that, peptide-10 resulted in restoring systolic and diastolic blood pressure to normal levels within 10 min of IV mode administration, similar to a synthetic generic drug (Lisinopril). Biochemical and hematological parameters revealed no significant difference among all the groups of treatments. Upon histopathological analysis, major organs like the heart, kidney, liver and adrenals in the rats associated with Hypertension were revealed to have abnormalities upon lisinopril treatment, whereas treatment with peptide-10 showed no abnormalities indicating its potential safety and efficacy in treatment of hypertension. Further studies involving peptide-10 will be useful in devising alternative treatments for hypertension.

Nuclear Receptor Expression Profiling and Transcriptional Modulation of Endothelium Inflammation by Orphan Nuclear Receptor NR4A2

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Abstract:

Endothelial cells are a critical component of the inflammatory response in the vasculature. While nuclear receptors are widely described to play a role in immunity, their expression profile and role in inflammatory response in endothelial cells remain under-explored. By profiling basal and TNFa-activated endothelial cells, we have classified the nuclear receptors into high (e.g. COUP-TF I/II, PPARβ/δ, NR2F6), intermediate (e.g. ERRα, REV-ERBα/β) and low (e.g. HNF4α, PGR) expressing, as well as highly inducible (e.g. NR4A1, NR4A2, NR4A3) categories. We further investigated the role of NR4A2 in the endothelial inflammatory response. NR2A2 is robustly induced in endothelial cells within 1 hr of TNFa and LPS stimulation. The cytokine-mediated induction of NR2A2 is dependent on NFkB activation and involves the recruitment of the p65 subunit to a conserved NFkB response element (NBRE) within the NR4A2 gene promoter. Using lentiviral overexpression, pharmacological activation and CRISPR/Cas9-mediated knockout in endothelial cells, we show that NR4A2 represses basal and LPS/TNFa-stimulated pro-inflammatory genes, while inducing anti-inflammatory genes. As a result, NR4A2 overexpression or activation blocks, and NR4A2 knockout promotes LPS or TNF alpha-stimulated macrophage adhesion to the endothelial cells. In summary, we have defined the nuclear receptor expression atlas and the anti-inflammatory role of NR4A2 in endothelial cells. Our finding can be further explored for the therapeutics for diseases related to endothelial inflammations ie. atherosclerosis.

Paris polyphylla sm. Extract Enriched with Diosgenin as an Antidiabetic Agent: In Vitro and In Vivo Study

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Abstract:

The global epidemic of diabetes mellitus (DM) has become a severe metabolic disorder and a threat to public health. Medicinal plants as a remedy for managing diabetes is accepted worldwide due to their long- term effectiveness and fewer side effects, mainly attributed to the phytochemicals. *Paris polyphylla* is a valuable medicinal herb endowed with steroidal saponins of therapeutic importance. The plant is popularly used as an anticancer agent. However, the antidiabetic potential of *P. polyphylla* has not been explored. So, the present study was undertaken to investigate the antidiabetic potential of *P. polyphylla* extract enriched with diosgenin (PPED) in vitro and in vivo in streptozotocin (STZ) induced diabetic rats. The in vitro antidiabetic efficacy of PPED was determined by α-glucosidase and α-amylase enzyme inhibitory activity. And, it was confirmed by in vivo study. PPED 1 and PPED 2 were orally dosed for 28 days daily in STZ-induced diabetic rats, and the fasting blood glucose level and body weight were monitored every 7 days. Furthermore, the antioxidant, serum biochemical parameters, and pancreatic histopathology were studied. PPED exhibited a concentration-dependent inhibition of α-glucosidase enzymes with IC 50 275.7 ± 0.59 µ g/mL and 121.9 ± 1.21 µ g/mL. Daily oral dosage of PPED 1 and PPED 2 for 28 days leads to a significant decrease in fasting blood glucose level and recovery of body weight compared to the diabetic control. The liver and kidney antioxidant parameters also improved with PPED dosage. According to the study, the PPED 1 and PPED 2 treated groups showed a decrease in glycated hemoglobin (HbA1c) and hyperlipidemia, as well as an improvement in protein, liver, and kidney function parameters. Moreover, PPED administration also ameliorates the pancreatic islets' size and β-cell granularity compared to the diabetic control group. It is, therefore, possible to conclude that PPED has the potential as an antidiabetic agent. Conclusion: This is the first report of *P. polyphylla* extract enriched with diosgenin as a potent antidiabetic agent.

Pharmaceutical Wastewater in Himachal Pradesh, India: A Reservoir of Potentially Pathogenic MDR Bacteria

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Abstract:

Wastewater is a potential reservoir of pathogenic, multi-drug-resistant (MDR) bacteria and their associated resistance genes (ARGs). Numerous studies have confirmed high levels of antibiotic residues and the presence of MDR pathogens in Indian Rivers and some hospital wastewater and sewage. However, the contribution of pharmaceutical wastewater to the emergence and evolution of antibiotic resistance is poorly explored in the Indian context. The emergence of antimicrobial resistance (AMR) in environmental isolates, particularly in regions with significant industrial activity, poses a substantial public health risk. In an ongoing collaborative study, the prevalence of multidrug-resistant (MDR) bacteria and their biofilm-forming abilities in the Baddi (Industrial) area) and the Kangra region (non- industrial area), was investigated. This study aims to fill the gap by providing a comprehensive analysis of the antibiotic-resistant bacteria, resistance profiles and biofilm-forming capabilities of environmental isolates from these two distinct regions. The total heterotrophic count of bacteria was determined on antibiotic-amended (cefotaxime, cotrimoxazole, ciprofloxacin, and meropenem) and non-amended nutrient agar (NA) and eosine methylene blue (EMB) agar plates. The study employed antimicrobial susceptibility testing (AST), MPN analysis, carbapenemase production using the mCIM/ eCIM method and quantitative assessment of biofilm formers using standard methods. The total heterotrophic count in non-amended media revealed higher bacterial counts in Baddi samples, with maximum values reaching 5.95 log10 CFU/mL, followed by Kangra (4.93 log10 CFU/mL). A total of 235 bacterial isolates were collected from 29 environmental samples of Baddi and Kangra. The MPN value of collected samples of Baddi and the Kangra ranged from 23 to >1800 MPN/100ml. There was a high prevalence of MDR bacteria, particularly in Baddi. A total of 141 (60%) of isolates produced extended-spectrum β-lactamases (ESBLs). Carbapenemase production was higher in Baddi isolates (40.69% in Batch II and 31.57% in Batch III) compared to Kangra (36.53% and 22.5%, respectively). The biofilm formation was high in Baddi (61.40% moderate to strong biofilm formers) compared to Kangra (55%). Varying MIC values indicate diverse resistance levels. Among characterized isolates, major ARB include *Escherichia coli, Klebsiella aerogenes, Klebsiella sp., Klebsiella pneumoniae, Pseudomonas aeruginosa, Salmonella sp, Shigella sp, and Proteus sp.* Some of the strains were identified as partial 16S rRNA sequencing and confirmed as 1 *Escherichia coli* (IND_446), 2 *Klebsiella pneumoniae* (IND_446 & IND_380), 1 *Pseudomonas aeruginosa* (IND_441), *Shigella sp* (IND_376) and 1 *Acinetobacter sp* (IND_421). The findings also highlight the role of biofilms in bacterial survival and persistence in the wastewater. The study highlights the critical environmental and public health risks posed by contamination from pharmaceutical activities, highlighting the urgent need for improved wastewater management and stricter regulatory controls in these regions.

Mitigation of α-Synuclein Aggregation by Brain Osmolytes to Modulate Parkinson's Disease

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Abstract:

The pathological accumulation of α-synuclein (α-syn) into amyloid fibrils is a defining hallmark of Parkinson's disease, driven by aberrant protein aggregation that ultimately leads to neuronal dysfunction. Modulating α-syn aggregation therefore represents a promising therapeutic strategy. In this study, we explored the protective role of naturally occurring brain osmolytes, specifically N-acetylaspartate and taurine, against α-syn aggregation. These molecular chaperone-like metabolites accumulate under stress conditions and possess the ability to cross the blood-brain barrier. Computational analyses revealed that these osmolytes interact with aggregation-prone regions of α-syn monomers. Complementary wet-lab experiments demonstrated a concentration-dependent effect: at low concentrations, the osmolytes inhibited fibrillation, whereas at higher concentrations they paradoxically accelerated aggregation. This biphasic behavior suggests that the brain maintains an optimally balanced osmolyte concentration for natural protection against protein misfolding. Our findings highlight that nature has endowed the brain with intrinsic molecular chaperones in the form of osmolytes. Additionally, five sugar-based nanoparticles (derived from glucose, fructose, maltose, sucrose, and trehalose) were synthesized via carbonization, thoroughly characterized, and evaluated for their anti-aggregation potential. These nano-osmolytes effectively suppressed α-syn fibrillation even at low concentrations, offering a complementary strategy to conventional osmolyte-mediated modulation. Collectively, our results demonstrate that both native osmolytes and sugar-derived nano-osmolytes exhibit strong anti-aggregation properties, underscoring their potential as therapeutic candidates for α-synucleinopathy-related disorders.

PGPR Bacteria from Distinct Niches Regulate Root Development and Plant Growth Through Variable Modulation of Auxin Pathway

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Abstract:

Both sewage and rhizosphere are home to a large number of various bacteria with diverse potential. Many of these bacteria can mitigate water pollutants or cohabitate with the plant rhizosphere to secure and expand their ecological niche. Due to the diverse nature of the environment and microbial population, their mechanism to remediate the environment or promote plant growth is likely to differ. However, the molecular mechanisms related to these remains poorly understood. Here, through targeted enrichment and screening, we identified a methanol-tolerant ASBT-KP1 bacterial isolate, which could mitigate the effect of environmentally harmful lanthanide and promote plant growth. We found that methylotroph ASBT-KP1 also produced exogenous phytohormone IAA (auxin) and could enhance lateral root number, density and shoot biomass in Arabidopsis and rice. Exogenous auxin produced by ASBT1-KP1 could contribute to alteration of endogenous auxin accumulation, transport and pathway components in plant root. We further showed that it could enhance plant growth and development by modulating the expression of auxin-pathway components and key regulators of lateral root development. Thus, our results indicate that sewage-derived lanthanide-tolerant methylotroph ASBT-KP1 can potentially be used as plant growth promoting bacteria for sustainable agriculture as well as bioremediation. In a separate screen, we identified rice rhizospheric bacterial isolates with variable ability to produce auxin. Interesting, we also found a non-auxin producing isolate which could promote plant growth. Therefore, our findings suggest that isolates from different ecological niches can alter physiology and growth of plant potentially exploiting partially different mechanisms.

Cold Chain-Free Specimen Transportation & Amp; Preservation: Transforming Diagnostics, Microbiome Research, and Global Health Equity Through Deep-Tech Innovation

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Abstract:

Specimen degradation during transportation remains a critical bottleneck in diagnostic accuracy, microbiome research, and pathogen identification worldwide. Reliance on cold chains limits access in resource-limited settings, escalates carbon emissions, and undermines sustainability and health equity objectives. Innovation: Ruhvenile Biomedical pioneers cold chain-free preservation technologies deployed across five continents. Proprietary formulations BiomLife®, truGnom®, UroStabl™, and BloodGnom™ sustain specimen integrity at ambient temperatures without toxic additives, bypassing refrigeration needs for swift, dependable analysis. Key Applications: BiomLife®: Complete Sample Transport & Preservation. Collect & preserve ANY specimen. Revives all microbes. Ideal for Microbiome, Bio-Banking, and OMICS research (NGS, 16S, Metagenomics). truGnom®: Genetic Analysis Stabilization. Ensures long-term DNA/RNA stability from ANY sample type. Streamlined workflow and up to 3X more yield. Includes a color-shift integrity indicator. UroStabl™: Boric Acid-Free Urine Preservation. Risk-Free preservation for a broader range of sensitive pathogens. Enables Revival + PCR from one tube. Cold Chain-Free transport up to 120 hours. BloodGnom™ - cfDNA/cfRNA Liquid Biopsy Stabilization. Optimized for cell-free DNA/RNA integrity in plasma. Essential for cancer, prenatal, and rare variant detection in liquid biopsy and minimal residual disease assays. Impact & amp; Outcomes: Diagnostic accuracy: Prevents degradation-related errors, enhancing clinical decisions. Antimicrobial resistance identification: Improves pathogen profiling for targeted treatments and AMR control. Microbiome research: Advances personalized protocols and microbiota therapeutics. Environmental sustainability: Cuts cold-chain emissions; aids novel microbe identification for green applications. Health equity: Facilitates analysis in remote areas, equalizing advanced diagnostic access. This deep-tech breakthrough closes the diagnostic-transport-preservation divide, propelling personalized medicine, AMR strategies, and sustainability. Five-continent validation confirms scalability and impact.

Integrated Biomanufacturing Strategies for Sustainable Jackfruit Peel Valorization

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Abstract:

Jackfruit peel, a widely available lignocellulosic residue, offers an underexploited resource for advanced biomanufacturing. This work presents a systems-level biorefinery framework that fractionates the peel into its major biopolymeric components, pectin, lignin, cellulose, and hemicellulose, and channels each stream into targeted value-added products. Mild organic acid-assisted extraction enabled the production of high-purity pectin suitable for fabrication into PVA-blended electrospun nanofibers. These composite fibers demonstrated robust mechanical behavior, strong hydrophilicity, and intrinsic antibacterial performance, supporting their use as bioactive wound-healing materials. Lignin isolated through optimized alkaline processing exhibited structural features that facilitated its dual deployment. It functioned as a carbon source for polyhydroxybutyrate (PHB) biosynthesis by *Oceanimonas doudoroffii*, where metabolic response-surface optimization increased polymer yield by nearly an order of magnitude. The same lignin also acted as an efficient adsorbent for dye-laden effluents, achieving high uptake capacity governed by Langmuir and pseudo-second-order adsorption mechanisms. The remaining depectinated and delignified biomass was processed through acid-assisted steam pretreatment and enzymatic hydrolysis, generating a mixed-sugar stream amenable to co-fermentation. A dual-yeast system integrating *Saccharomyces cerevisiae* and *Kluyveromyces marxianus* enabled concurrent hexose–pentose conversion, producing ethanol titres of 17 g/L under ANN–GA optimization. Overall, this integrated biomanufacturing strategy transforms jackfruit peel from waste into a versatile feedstock for biomaterials, biopolymers, and biofuels, aligning with the SDGs on clean energy, responsible production, and climate action by lowering the carbon footprint and strengthening a resilient circular bioeconomy.

Integrated Computational Biology and Transcriptomic Profiling Reveal Potential Biomarkers and Therapeutic Targets in Sporadic Amyotrophic Lateral Sclerosis

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Abstract:

Amyotrophic lateral sclerosis (ALS) is a progressive neurodegenerative disorder characterized by the loss of both upper and lower motor neurons. Sporadic ALS (sALS), the most common form, is a multigenic condition, and its underlying molecular mechanisms remain only partially understood. Although recent advances have provided new insights, several pathogenic targets of ALS still require clarification. This study aims to identify potential protein biomarkers and therapeutic targets for sALS by analyzing gene expression profiles from motor neuron cells of sALS patients, available in the GSE68605 dataset. We applied computational systems and structural biology approaches, including differential expression analysis, protein interaction network, candidate protein biomarker (CPB) identification, functional module analysis, and molecular docking. The top ten up and downregulated genes were used to construct a protein protein interaction network (PPIN). Network analysis identified four CPBs (RIOK2, AKT1, CTNNB1, and TNF) that consistently overlapped across key topological network parameters (degree, bottleneck, and maximum neighbourhood component). Among these, RIOK2 emerged as a central mediator, associated with five major functional modules linked to RNA binding, lipoprotein particle receptor binding in pre-ribosomes, and interferon/cytokine-mediated signaling pathways. We found RIOK2 downregulated in expression datasets from sALS patients. It functions as a potential mediator of cross-talk among modules, which play an important role in signal propagation and network stability. Molecular docking further revealed that cyclosporine exhibited the strongest binding affinity with RIOK2 (-8.6 kJ/mol), outperforming FDA-approved ALS drugs such as riluzole and edaravone. This suggests cyclosporine may represent a promising candidate for counteracting the downregulation of RIOK2 in sALS. To substantiate these computational findings, future in vitro and in vivo studies are warranted to advance our understanding of ALS diagnosis, prognosis, and therapeutic intervention.

Magnetic Nanoworm-Based Screening for PEG-Binding Nanobodies

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Abstract:

PEGylation is commonly utilized to modify nanoparticles, vaccines, therapeutic proteins, and biomaterials. The increased use of PEG-containing cosmetics and medicines results in anti-PEG immunoglobulins in humans, including IgG, IgM, and IgE types. Recent studies have shown that high-affinity antibodies against PEG can be isolated through immunization. These antibodies have been used as standards in anti-PEG antibody immunoassays and for decorating PEGylated nanoparticles with targeting ligands. However, the limitations of conventional antibodies, such as their large size and potential stability issues, prompt us to explore the isolation of anti-PEG nanobodies (Nbs), which offer a smaller, more robust alternative. Here, we developed a protocol to isolate anti-PEG Nbs using yeast display. We utilized a set of PEGylated and non-PEGylated (control) iron oxide nano worms for negative and positive magnetic selection, followed by multi parameter flow-cytometry sorting using differently labeled PEGylated and non- PEGylated nano-worms or DiD-labeled PEGylated liposomes. The isolated Nb exhibited highly specific binding to PEGylated liposomes and nanoparticles and was able to compete with commercial anti-backbone PEG IgG but not with anti-methoxy PEG IgG for PEG binding. Nb showed no aggregation, high thermal stability, and reversible structural stability. Stable Nbs that target PEGylated surfaces will have numerous applications in drug delivery and nanomedicine.

Novel Human Antimicrobial Peptides Targeting Multidrug-Resistant and Biofilm-Forming Group B *Streptococcus*

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Abstract:

Group B *Streptococcus* (GBS) remains a leading cause of neonatal sepsis, meningitis, and invasive adult infections, with clinical management increasingly compromised by multidrug resistance and robust biofilm formation. In our analysis of clinical GBS isolates from India, 27% exhibited penicillin non-susceptibility a strikingly high rate for a pathogen historically considered uniformly penicillin-sensitive. All isolates produced biofilms, with 70% classified as strong producers using crystal violet quantification. Notably, biofilm strength showed a significant inverse correlation with penicillin MIC, indicating that biofilm formation may directly contributes to therapeutic failure. While key virulence determinants (cylE, pavA, cfb, lmb) were near-universally present, their carriage did not predict biofilm-forming capacity, suggesting independent regulatory pathways. To address the urgent need for non-antibiotic alternatives, we explored the endogenous human antimicrobial peptidome as a source of novel anti-GBS agents. Over 1,000 peptide-containing fractions derived from human hemofiltrate, neonatal foreskin, and vaginal tissue were screened against a panel of multidrug-resistant GBS isolates from India, Europe, and the USA. Multiple fractions displayed potent bactericidal activity and eradicated pre-formed biofilms. Active fractions were iteratively purified using reverse-phase HPLC, and candidate peptides were identified by MALDI-TOF/TOF mass spectrometry. These findings highlight the escalating threat of biofilm-protected, multidrug-resistant GBS and demonstrate that the human peptidome represents an underexploited reservoir of potent, naturally occurring anti-GBS molecules. This work lays the foundation for developing peptide-based therapeutics capable of combating both planktonic and biofilm-associated GBS infections.

Oral Talks

Biochemical Analysis of Gamma Radiation Processed Flax Seed

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Abstract:

Flax seed (*Linum usitatissimum* L.) is a fibre containing oil seed, rich in omega-3 fatty acid and lignans. It helps digestion, weight management, reduce risk of cancer regulates blood sugar level and calcium in human body. Radiation processing of flax seed was carried out for purpose of hygienization shelf-life extension. Dry and fresh flax seeds were packed in HDPE bags and subjected to 60Co gamma irradiation at different doses 1 to 5 kGy and further stored at room temperature (~25°C) for six months. Biochemical analysis of those stored samples was carried out for sensory analysis, aw activity, estimation of protein, phytic acid, totals phenolics and anti-oxidant capacity. Anti-nutritional (phytic acid) content found to be decreased with increasing gamma radiation doses (1, 2, 3 and 5 kGy). There was no significant change found in the content of protein, total phenolic and antioxidant capacity in radiation processed samples over the control. However, 2 kGy were found optimal dose for radiation processing of flax seed.

Regulation and odulation of Bacterial Biofilm by a Novel rspA Gene of *Salmonella Typhimurium*

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Abstract:

Salmonella enterica serovar Typhimurium (*S. Typhimurium*) is a major cause of foodborne illness worldwide. Despite progress in understanding its pathogenesis, many genes remain functionally uncharacterized. The rspA (STM14_1818) gene, predicted to encode a dehydratase, shows strong upregulation in intracellular environments and condition mimicking low Mg^{2+} and low pH. However, its role in Salmonella virulence remains unknown. This study aimed to characterize the function of rspA in intracellular survival, biofilm formation, and overall virulence. RspA deletion mutant (ΔrspA-STM) and a complemented (ΔrspAc- STM) were generated in *S. Typhimurium* 14028. Growth in intracellular-mimicking MGM-MES media, ROS sensitivity and antibiotic resistance were evaluated. Motility, flagella number, and biofilm formation at 20°C, 25°C, and 30°C were assessed. The qRT-PCR was used to measure virulence and biofilm associated genes expression. Adhesion, invasion, and intracellular proliferation were tested in various cells. Virulence and persistence were evaluated using *C. elegans*. ΔrspA-STM showed enhanced growth in MGM-MES, suggesting a regulatory role in intracellular proliferation. The mutant was more sensitive to ROS but resistant to antibiotics and complement-mediated killing. The rspA deletion had no effect on motility or flagella number. Biofilm formation was temperature-dependent and mutant formed less biofilm at 20°C and more at 25°C and 30°C. Genes for cellulose (bcsA, bcsB, bcsZ) and curli (csgA, csgB) were downregulated at 20°C but upregulated at 25°C, except for bcsC. SPI-1, SPI-2, biofilm, and stress-related genes were downregulated in the mutant under LB conditions. The ΔrspA-STM was less adhesive and invasive but showed hyperproliferation inside macrophages due to reduced ROS/RNS production. In *C. elegans*, the mutant showed increased bacterial burden, higher virulence, and modulation of host immunity.

Assessment of Pathogenic Microbial Contamination in Indian Smokeless Tobacco Products Using an RFLP-Based Approach

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Abstract:

India is the second-largest producer of tobacco and a major consumer of diverse smokeless tobacco (SLT) products such as dohra, zarda, khaini, pan masala, and others. Despite existing regulatory policies, inadequate implementation and unhygienic production conditions increase the likelihood of microbial contamination. These contaminants may include opportunistic pathogens posing serious health risks to users. This study aimed to detect and identify potential pathogenic bacteria present in commercially available Indian SLT products using a simple, cost-effective Restriction Fragment Length Polymorphism (RFLP)-based molecular approach. Twenty-three heterogeneous SLT samples representing multiple product categories were collected from Indian markets. Initial bacterial isolation was performed using conventional culture methods, followed by DNA extraction, amplification, and restriction digestion. Three restriction enzymes HaeIII, MnlI, and AluI were utilized to generate RFLP patterns for bacterial identification. RFLP analysis confirmed the presence of three opportunistic bacterial species *Pseudomonas aeruginosa*, *Enterococcus faecalis*, and *Staphylococcus aureus* in 16 of the 23 samples. *P. aeruginosa* was the most frequent isolate (52.9%), followed by *E. faecalis* (35.3%), while *S. aureus* was detected for the first time in SLT samples (11.8%). Distinct restriction profiles validated the accuracy of the method in differentiating bacterial species. The study demonstrates substantial microbial contamination in SLT products, underlining potential health hazards for consumers. Enhanced surveillance and enforcement of hygiene standards are necessary to minimize such risks. This is the first report of *Staphylococcus aureus* contamination in Indian SLT products. The study also establishes a single-primer, multi-enzyme RFLP assay as a rapid, economical, and reliable tool for pathogen detection in tobacco-based samples.

Conundrum in Bio Vanillin Production from *Pseudomonas*: Conventional Strategies vs Genetic Modification

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Abstract:

Vanillin is one of the natural flavoring compounds with high industrial demand in the world. The availability of this metabolite in nature is very scarce and majority is supplied as synthetic derivatives to fulfill need. This study aimed to compare three organisms with their bio vanillin production potential using different strategies Viz., Conventional (media optimization), Overexpressing feruloyl-CoA synthetase (FCS) and enoyl-CoA hydratase (ECH), and insertional inactivation of Vanillin dehydrogenase (VDH). for vanillin biosynthesis from ferulic acid by regulating. Medium formulation and optimization were carried out for the maximum production of vanillin using *Pseudomonas taiwanensis* strain NAU6 (PX376096.1). A sequential approach was used, where Placket Burman Design (PBD) was applied for the screening and identification of significant chemical and physical parameters affecting vanillin production. Among selected ten factors, Ferulic acid, FeCl3, MgSO4 and Ammonium Nitrate were found to be significantly affecting vanillin production using PBD by *Pseudomonas taiwanensis* strain NAU6 (PX376096.1). These factors were further optimized using Central Composite Design (CCD) of Response Surface Methodology (RSM). Quadratic model was suggested with optimized solution of 0.095 g% of FeCl3, 1.075 g% of Ferulic acid, 0.133 g% of MgSO4 and 0.755 g% of Ammonium nitrate by Design Expert Software. Sequential statistical exploration of PBD and CCD increased vanillin production 2.4 times as compared to the basal medium. Furthermore, the genes responsible for the bioconversion of ferulic acid into vanillin was cloned and expressed in *Bacillus subtills* to obtained cell free extract. Simultaneously the host was modified by mutating Vanillin dehydrogenase gene in order to obtained higher yield of vanillin during bioconversion process. It was observed that recombinant organism was able to produces higher vanillin compare to conventional strain due to lack of impurities in the final product and restriction of being used as substrate further metabolisms.

Developing Chikungunya and Dengue Subunit Vaccines

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Abstract:

Chikungunya is a febrile infectious disease caused by chikungunya virus (CHIKV) that leads to long term sequelae of arthritis. Dengue caused by the dengue virus (DENV) is also a febrile infectious disease that is endemic in many regions of the world. Severe dengue results in complications that may lead to death. Current vaccines to prevent CHIKV and DENV infection have limitations and restricted efficacy. The structural envelope protein spike of CHIKV and DENV are the target of broadly neutralizing antibodies and therefore suitable as subunit vaccine immunogens. The CHIKV envelope spike is a trimer of a heterodimer of the subunits E1 and E2 whereas the DENV envelope spike is a dimer of E. These subunits when expressed do not by themselves form CHIKV envelope trimer or DENV envelope dimer. We have developed a method to develop stable CHIKV and DENV oligomeric envelope spikes comprising the ectodomains of E1 and E2 for CHIKV and E for DENV using structure-guided, disulphide bond clipping strategy. We have biochemically, antigenically and structurally characterized the oligomeric form of CHIKV and DENV envelope. In mice immunization studies the CHIKV immunogen elicits robust neutralizing and cell-mediated immune response and is able to clear virus and reverse arthritic symptoms. Our initial immunization studies with the DENV4 E dimer shows that it is able to elicit robust neutralizing and cell mediated immune responses. This is the first report of a subunit vaccine strategy against CHIKV and DENV targeting the viral envelope spike.

Multidrug-Resistant Non-Tuberculous Mycobacteria in Sundarban Wetlands: An Emerging Threat to Public Health and Sustainable Development

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Abstract:

Non-tuberculous mycobacteria (NTM) are opportunistic pathogens with increasing clinical significance worldwide. Unlike *Mycobacterium tuberculosis*, NTMs are free-living organisms widely distributed in aquatic environments. Wetlands, particularly in ecologically sensitive regions such as the Indian Sundarbans, can serve as reservoirs of these pathogens, thereby posing significant risks to both environmental and public health. The emergence of multidrug-resistant NTMs has become a major concern, especially in ecosystems sustaining dense human populations and fragile biodiversity. This study investigated the occurrence of pathogenic NTMs in Sundarban wetlands and assessed their antibiotic susceptibility patterns. Samples were collected from selected wetland sites within the Sundarbans and processed using standard microbiological and molecular protocols. A total of 55 isolates were identified, representing five pathogenic species: *Mycobacterium fortuitum, M. chelonae, M. abscessus, M. avium*, and *M. kansasii*. Antibiotic susceptibility testing, performed by the broth microdilution method according to CLSI guidelines, revealed alarming resistance patterns. Approximately 89% of isolates were resistant to first-line anti-TB drugs (isoniazid, rifampicin, and ethambutol). Resistance was also observed against streptomycin and doxycycline, while partial susceptibility was retained for amikacin (78%), moxifloxacin (70%), ciprofloxacin (64%), and clarithromycin (55%). These results highlight the multidrug-resistant character of NTMs persisting in Sundarban wetlands. Given the high tuberculosis burden in adjacent human populations, the presence of resistant NTMs increases the risk of co-infections, misdiagnosis, and treatment failures. Moreover, the persistence of such pathogens in a UNESCO World Heritage ecosystem has broader implications, threatening progress toward United Nations Sustainable Development Goals (SDGs), particularly SDG 3 (Good Health and Well-being), SDG 6 (Clean Water and Sanitation), and SDG 14 (Life Below Water).The study underscores the urgent need for wetland health monitoring, prudent antibiotic stewardship, and integrated public awareness strategies to mitigate the growing threat of resistant NTMs in the Sundarbans.

Understanding Immunological Interactions: Antibody Cross-Reactivity Among Viruses in Endemic Regions

Kamini Jakhar[1], Sudipta Sonar[1], Gagandeep Singh[2], Tejeswara Rao Asuru[3], Garima Joshi[3], Sushma Mithina[1], Nisha Beniwal[1], Tania Sarkar[1], Mahima Tiwari[1], Jaskaran Kaur[1], Deepak Kumar Rathore[4], Banwari Lal[1], Sandeep Kumar[1], Puneet Srivastav[1], Satendra Kumar[1], Vikas Phagna[1], Sushma[1], Lokesh Kumar[1], Vishal Gupta[1,5], Pallavi Kshetrapal[6], Savita Singh[6], Nitya Wadhwa[6], Ramachandran Thiruvengadam[6], Sreevatsan Raghavan[6], Mudita Gosain[6], Tripti Shrivastava[1], Sankar Bhattacharyya[1], Shailendra Asthana[2], Prasenjit Guchhait[3] and Shailendra Mani[1]✉

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Abstract:

In the context of the SARS-CoV-2 pandemic, India witnessed a notable surge in symptomatic dengue cases. Our study investigates the role of antibody cross-reactivity, revealing that antibodies from SARS-CoV-2 spike protein enhance DENV2 infection in vitro. In silico analysis of protein-protein interactions between the SARS-CoV-2 spike protein and DENV2 envelope (E) protein demonstrated significant binding, suggesting potential cross-reactivity. Furthermore, monoclonal and polyclonal antibodies against SARS-CoV-2 were found to elevate DENV2 infection. In vivo, AG129 mice infected with SARS-CoV-2 prior to DENV2 infection showed increased dengue pathogenesis. These findings highlight the potential for aggravated dengue infection and severe disease in COVID-19 survivors, underscoring the importance of understanding antibody cross-reactivity in endemic regions.

Inhibiting *Plasmodium falciparum* Apicoplast DNA Gyrase B: An Integrative Computational and Experimental Approach to Next-Generation Antimalarials

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Abstract:

The escalating global crisis of drug-resistant *Plasmodium falciparum*, exemplified by the spread of artemisinin-resistant strains, necessitates the discovery of antimalarial agents with novel targets and distinct mechanisms of action. Here, we present the identification and characterization of potent inhibitors of the *P. falciparum* Gyrase B (PfGyrB), a validated, essential antimalarial drug target. Utilizing high-throughput virtual screening (HTVS), we prioritized compounds demonstrating stable, favorable binding within the PfGyrB active site. The most promising hits were validated biochemically for PfGyrB inhibition. In *P. falciparum* growth inhibition assays, UNC8153 and fexofenadine hydrochloride exhibited a time dependent delayed-death phenotype, evidenced by significantly reduced IC50 values after 96 hours of exposure, a finding corroborated by morphological analysis. Crucially, UNC8153 demonstrated 25-fold greater inhibition during the second intraerythrocytic cycle compared to the reference PfGyrB inhibitor, novobiocin. Furthermore, UNC8153 was found to be effective against the artemisinin-resistant C580Y mutant strain, exhibiting a high resistance index, and also showed a high selectivity index in the toxicity test. This compound is structurally distinct from current antimalarials, suggesting a low potential for cross-resistance. Collectively, these data establish UNC8153 as a structurally novel and highly potent lead compound for development as a next-generation antimalarial.

Microbial Production of Plant Product Degrading Enzymes: Isolation, Characterization, and Application as Eco-Friendly Biofertilizer

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Abstract:

Complex plant products like cellulose, lignin, and pectin are organic compounds that require simplification/degradation into usable biological forms that help improve soil structure, water retention, and aeration, all of which are necessary for healthy root development; enhance soil fertility by releasing trapped nutrients from plant debris on one hand while stimulating microbial activity that leads to a more robust and self-sustaining soil ecosystem. Microbes from various origins have proved to be useful enzyme sources to facilitate this degradation process. In our search for potential enzyme-producing microbes from natural soil and organic debris, we successfully isolated and characterized bacteria and fungi capable of degrading cellulose, pectin, amylase, and lipase. However, in this context, cellulase- and lipase-producing strains were particularly emphasized due to their synergistic effect in accelerating nutrient release, minimizing the use of chemical fertilizers while enhancing soil fertility, stimulating microbial activity, and demonstrating potent bioremediation. The Gram nature of the isolates was determined; they were physiologically and biochemically characterized for tentative identification. Growth curve patterns and antibiotic sensitivity profiles were also assessed. An attempt was made to formulate a practical model for utilizing native, enzyme-producing soil microbes as natural fertilizers, with promising implications for organic farming, waste recycling, and sustainable agriculture. The study thus focuses on sustainability, affordability, and environmental safety.

Simultaneous Environmental Surveillance of Viral Pathogens and Antibiotic Resistance Genes in a Wastewater Treatment Plant in Suwon City, South Korea

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Abstract:

Wastewater-based environmental surveillance has emerged as a vital tool for tracking infectious diseases and assessing community health. This study reports an integrated surveillance of viral pathogens, SARS-CoV-2, norovirus, and hepatitis A virus, and antibiotic resistance genes (ARGs) in the municipal wastewater of Suwon city, South Korea. Quantitative analyses using real-time digital PCR (RT-dPCR) revealed the consistent detection of all target viruses and ARGs, except for hepatitis A virus and the carbapenemase gene blaNDM, in influent samples. A strong positive correlation (r = 0.796) was observed between SARS-CoV-2 RNA levels and the number of reported COVID-19 cases in the catchment area. Norovirus exhibited distinct seasonal trends, with high concentrations (up to 6.73 log10 gene copies/L) and presence in effluent samples during the colder months. Among the monitored ARGs, blaTEM was observed at the highest abundance (8.67 log10 gene copies/L), followed by blaFOX (8.13) and blaKPC (8.02). The positive association between SARS-CoV-2 RNA and the prevalence of COVID-19 cases reveals the promising role of community-scale monitoring of pathogens in providing early signals of infection dynamics. Additionally, the strong positive associations between extended-spectrum β-lactamases (ESBL), extremely extended beta-lactamases, and plasmid-mediated AmpC β-lactamases (PABL) genes suggest their co-selection and possible horizontal gene transfer within microbial communities in wastewater. These findings collectively indicate the indispensable role of an integrated biological surveillance framework. Moreover, the detection of viral pathogens and antimicrobial resistance markers in wastewater can provide key insights into evaluating public health risks and formulating effective wastewater treatment methods to reduce infectious disease transmission and antibiotic resistance dissemination.

From Microbes to Nanoparticles: Nature-Based Innovations for River Ecosystem Restoration

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Abstract:

Rivers are essential lifelines for biodiversity, agriculture, and human settlements, yet they are increasingly threatened by pollution. The Shivnath River in Durg, Chhattisgarh, is subjected to domestic sewage, industrial effluents, and agricultural runoff, resulting in deterioration of water quality. Traditional treatment methods are costly and insufficient, making biological approaches involving microbes and aquatic plants highly relevant for sustainable river restoration. Systematic studies have been carried out on the Shivnath River to understand its pollution load and microbial potential for bioremediation. Physico-chemical analyses revealed marked variation between upstream and downstream sites. Downstream samples consistently showed higher biochemical oxygen demand (BOD), chemical oxygen demand (COD), turbidity, hardness, and suspended solids, with significantly lower dissolved oxygen (DO). Microbial investigations demonstrated heavy faecal contamination. Most probable number (MPN) counts for coliforms ranged between ~900 MPN/100 mL upstream to ~1600 MPN/100 mL downstream. Thermotolerant *E. coli* and *Salmonella species* were isolated, indicating potential health risks. Fungal diversity in riverbank soils at Mehmara, Chhatagarh, and Kotani sites, 24–49 species belonging to 16–21 genera were recovered. Many of these fungi are known decomposers of organic material, with potential to break down complex pollutants. Recent advances in green nanotechnology further extend these biological strategies. Nanoparticles synthesized from medicinal and aquatic plants exhibit remarkable catalytic, antimicrobial, and adsorptive properties. Silver, zinc oxide, and iron oxide nanoparticles derived from plant extracts have shown promise in degrading dyes, neutralizing pathogens, and immobilizing heavy metals. When integrated with microbial and phytoremediation processes, plant-based nanoparticles accelerate pollutant breakdown and enhance detoxification efficiency. This integrative approach uniting microbes, aquatic plants, and phyto-nanoparticles offers a low-cost, scalable, and environmentally benign strategy for restoring river ecosystems. By leveraging natural processes and green nanotechnology, it is possible to achieve significant reductions in organic load, pathogens, and toxic metals, while simultaneously strengthening ecosystem resilience. Such innovations align with national missions on river rejuvenation and global sustainable development goals, providing a blueprint for ecological restoration in Chhattisgarh and beyond.

Green Gold: Unlocking The Potentialities of Algal Pigments for Clean Energy Generation, Carbon Mitigation and Sustainable Bio-Based Circular Economy

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Abstract:

Bio photovoltaics (BPVs, also known as biological solar cells) have emerged as an environment friendly and low-cost approach for harvesting solar energy and directly converting solar energy into electrical power. The annual solar radiation incident on India's land area is massive, estimated about 5000 trillion kWh per year. States like Rajasthan, Gujarat, Tamil Nadu have large swathes of land combining high solar insolation and availability of wasteland or semi-arid areas. According to IEA, India's electricity demand is projected to rise by 4 % in 2025, underscoring the urgent need to diversify power generation through sustainable alternatives. Algae is explored to act as a green powerhouse for solar energy by providing not just natural, low cost pigments but also reduces carbon foot print capture during its growth supporting clean energy and carbon mitigation simultaneously. In the current study, *Scendesmus* sp. optimized for its growth with the highest count of 30.02 x 106 cells/mL. The pigment was extracted and characterized using infrared spectroscopy, figure represents the FTIR spectrums of chlorophyll with a CO stretch of 1092.79/ cm-1, C=C (1709.08/cm-1), CN (1422.16/cm-1) and Mg (530.88/cm-1). The photovoltaic performance of nanoparticle-sensitized solar cell with TiO2 was observed between the period of 10:00 h to 4:00 h to estimate the max power point (VMP-0.90), current at the max power point (IMP-0.04) and efficiency (η % 5.76). The NDSSC with TiO2 showed the efficiency of 5.76. The major focus is to enhance the performance by algal strains for higher electron yield and integration of nanomaterials to pilot scale operation of Bio-photovoltaic (BPV) cell technology.

Novel Antiviral Agent Against Hepatitis C Virus from Endophytic Fungi of *Penicillium citrinum* R2 Source in Medicinal Plant *Phyllanthus niruri*

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Abstract:

A novel source for discovering antiviral agents by examining endophytic fungi from *Phyllanthus niruri,* known for its medicinal uses in liver disease and viral infection treatment. The research underscores the critical demand for cost-effective therapies for Hepatitis C Virus (HCV), which was represents a major global health challenge with severe consequences like cirrhosis and hepatocellular carcinoma. The approach entailed isolating endophytic fungi from diverse parts of the *P. niruri* plant, among the 3 isolates from root *Penicillium citrinum* R2 and performing solvent extraction on these isolates, underwent screening for the production of secondary metabolites. Comprehensive phytochemical analysis was carried out to detect antiviral compounds such as lignans, flavonoids, alkaloids, tannins, coumarins, and saponins and the antioxidant property was evaluated by DPPH and ABTS assays, further demonstrating the 97% highest inhibitory concentration. The cytotoxicity assessment of the most promising fungal extract on HepG2 liver cell lines exhibited moderate effects at elevated concentrations, indicating a potential safety margin at lower doses for therapeutic applications. This investigation emphasizes the promise of endophytic fungi of *P. citrinum* R2 from *P. niruri* as a significant source of natural antiviral agents, facilitating the pursuit of alternative treatments for HCV.

Production of Cost-Effective, Pre- and Probiotic Novel Combinations Utilizing Fruit Wastes for Health Benefits, Sustainable Economy and Environmental Cleanup

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Abstract:

To produce a cost-effective formulation of novel pre-and probiotic combinations utilizing fruit wastes. Various kinds of waste generated from fruits are a global concern as it causes pollution of air, water and soil which damages human health and the environment. As per food waste index report 2021 (UNEP), on an average 121kg of food per capita is wasted globally with India ranked 50th. Fruit wastage comprises 4.58% to 15.88% of this huge loss with a financial loss of about Rs.40811 Crore. Different fruit wastes contain various untapped bioactive compounds including flavonoids, phenolics, triterpenes, alkaloids etc. along with several oligo- and polysaccharides and essential dietary fibres, which as prebiotics, may enhance the growth of probiotic consortia of yeasts molds or lactic acid bacteria. Such novel combinations of pre- and probiotics may improve digestive health, boost immunity, manage antibiotic associated issues and inhibit pathogenic bacteria. It is also promising to boost circular economy through promoting the waste-to-wealth concept as envisioned in the sustainable development goals. In the present study, fruit wastes from *Musa paradisiaca* (banana), *Citrus limetta* (mosambi), *Citrus sinensis* (orange), *Ananas comosus* (pineapple), and *Punica granatum* (pomegranate) showed the presence of important bio actives, with orange, pomegranate, and pineapple showing the richest prebiotic profiles. Aqueous extracts of these fruit wastes enhanced the growth of *Lactobacillus* from dahi and probiotic supplementary capsule blends. The strongest probiotic growth promoting results came from mixing all five fruit extracts, suggesting a synergistic effect.

Biological Studies of Silver Nanoparticles

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Abstract:

Synthesis of nanomaterials having bio-compatibility with definite surface functionality, precise shape and particular size is a promising area of research in the field of bio-nanotechnology. Hybrid nanomaterials combine multiple functionalities on a nanoscopic length scale. Chemical based synthesis of silver nanoparticles has been extensively studied due to huge application of such nano-systems in a wide range of areas. A major disadvantage of chemical reduction is its high toxicity which has led to the development of green synthesis protocols using biomolecules, phyto extracts and others. Single step rapid synthetic route where the molecule can act both as a stabilizer and a reducing agent has been the flavour of present synthesis techniques. These silver nanoparticles have been characterized by TEM, XRD, AFM, UV-Vis spectroscopy and other different tools. These synthesized nanoparticles also bind with calf thymus DNA and forms a ground state complex which is established by both UV-Vis spectrophotometrically as well as fluorimetrically having potential bio related applications. The antimicrobial activities of these nanoparticles on various microorganisms have also been studied. The antimicrobial tests against bacteria and the antitoxicity studies reveal that the stabilized NPs are safe and non-toxic having the potential for clinical applications in the medical field. These noble metal nanoparticles also exhibit specific selectivity to different cancer cell lines having potential anti-cancer properties.

Nanofertilizer-Based Agrotechnological Approaches for Enhancing Nutrition and Secondary Metabolite Production in Cannabis Species

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Abstract:

Excessive use of nitrogen-based fertilizers results in unnecessary costs and contributes to environmental degradation due to overabundance of urea. We synthesized a urea–hydroxyapatite nanofertilizer (UHAPF) for addressing this issue. Characterization studies showed that the reduced dissolution of hydroxyapatite enables controlled nitrogen release. When UHAPF was applied in combination with *Bacillus megaterium* and *Pseudomonas aeruginosa,* plant growth significantly improved in pot experiments compared to control and individual groups, indicating lower nitrogen loss under field-like conditions. In a vertical-column experiment, UHAPF exhibited gradual nitrogen release over approximately 30 days. We also examined variations in secondary metabolite production in industrial cannabis and found that nanofertilizers enhanced nutrient uptake, biofertilizers improved soil health, and both synergistically influenced cannabinoid accumulation. Additionally, the detection of 2,4-DTBP during GC–MS analysis prompted further environmental and health assessments. Overall, our findings highlight sustainable strategies for nutrient management and crop yield enhancement, emphasizing the potential of innovative nanofertilizer formulations to reduce excessive nitrogen losses.

A Perspective of Soil Microbial Dynamics and Azotobacter Species in Plant Health Modulation

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Abstract:

The growing concerns linked with the long-term use of chemical fertilizers, particularly their harmful influence on soil fertility, have accelerated the quest for sustainable alternatives. Several biological based approaches exist to improve soil health, among which plant growth promoting rhizobacteria (PGPR) represent a particularly promising group. Within this microbial community, Azotobacter species are generally recognized for their capacity to boost plant vitality by producing important phytohormones including auxins, cytokinins and gibberellic acid. These free-living nitrogen fixers aid in the growth of plants. Its application has demonstrated promise in restoring degraded soils, thus showing their value in transforming marginal or uncultivated land into productive agricultural systems. In addition to fixing nitrogen, Azotobacter species promote positive and healthy rhizospheric interactions by boosting microbial activity, increasing nutrient availability, inhibiting phytopathogens and enhancing plant resilience in general. A wide spectrum of soil microorganisms are now understood to exert similar favourable affects on crop performance. Rhizosphere-associated bacteria can either directly support plant growth by providing vital nutrients and growth-promoting substances, or indirectly by producing antimicrobial metabolites that fight soil-borne diseases. The contributions of Azotobacter species and other soil microbes to biological nitrogen fixation are highlighted in this review, along with their wider functions in fostering soil fertility and plant health.

Prevalence of Antibiotic Resistance in Drinking Water of Cyclone-Affected Sundarbans of West Bengal

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Abstract:

The Sundarbans biosphere reserve, the largest Gangetic delta and mangrove forest in West Bengal, is highly vulnerable to natural disasters, particularly cyclones, which may compromise the potable water distribution system and sanitation, potentially exacerbating the spread of antibiotic-resistant bacteria (ARB). The primary objective of this study was to assess the current landscape of antibiotic resistance in various drinking water sources, including tube-wells, ponds, and municipal tap water, across 21 distinct cyclone-affected locations of the Sundarbans. A total of 478 water samples, collected from designated locations, were analysed for total coliforms, Escherichia coli, and other indicator bacteria such as *Klebsiella* spp., *Enterobacteria* spp., *Citrobacter* spp., and *Enterococci* spp., using standard microbiological techniques. Additionally, specific pathogens such as *Salmonella* spp. and *Vibrio cholerae* were screened to detect high-risk environments. Bacterial isolates were subjected to antibiotic susceptibility testing (AST) against a panel of commonly used antibiotics. Environmental parameters, including pH, salinity, and turbidity, were also recorded to assess any correlation with bacterial resistance. Preliminary findings indicate a significant presence of antibiotic-resistant bacteria in drinking water sources, 71% of the samples tested positive for coliforms, with 32% showing *E. coli* contamination exceeding permissible limits. A high proportion of isolated bacteria exhibited multidrug resistance (MDR), with resistance rates to ampicillin and tetracycline exceeding 74% in some isolates. Ciprofloxacin resistance was also notably high, particularly in isolates from pond water sources. Statistical analysis demonstrated a positive correlation between higher salinity levels and increased prevalence of certain ARBs, potentially due to the impact of saline intrusion on microbial communities and horizontal gene transfer. These findings suggest enhanced water quality monitoring and robust public health interventions in the cyclone-affected Sundarbans.

Characterization of the Oral Bacteriome of Smokeless Tobacco Users with Oral Squamous Cell Carcinoma (OSCC) and Their Comparative Analysis with Healthy Individuals

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Abstract:

Consumption of smokeless tobacco in South Asian countries is widespread and a major cause of oral diseases, including oral cancer. The microbial diversity of smokeless tobacco has been less studied to understand its impact on oral cancer. Several nitrate-reducing bacteria participate in nitrite formation, which further reacts with certain tobacco metabolites to form tobacco-specific nitrosamines (TSNAs), a group I carcinogen. Additionally, acetaldehyde- producing bacteria provide a microenvironment to stimulate oncogenesis. Chewing smokeless tobacco for a longer period introduces several tobacco bacteria into the oral cavity. Therefore, a comprehensive analysis is required to understand the microbial dynamics of the oral cavity among OSCC patients. In this study, a culture-independent approach was used to compare the bacterial diversity of the oral cavities of smokeless tobacco chewers with Oral Squamous Cell Carcinoma (OSCC). The 16S rRNA-based amplicon (V3-V4 hypervariable) sequencing showed that the bacterial diversity of OSCC patients significantly differs among patients and healthy groups. Additionally, fourteen bacterial genera were significantly different (p-value < 0.05) in the oral cavities of OSCC patients. Dominance of tobacco-specific nitrosamine-forming bacteria, viz., Staphylococcus, Fusobacterium, and Campylobacter, was observed in the oral cavity of OSCC patients. These findings open pathways to further explore bacterial diversity among oral cancer patients and develop early diagnostic tools. Shotgun-based analysis of the smokeless tobacco microbiome can provide significant functional attributes.

Antibacterial Herbal Soap Preparation and Evaluation

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Abstract:

Herbal soaps are generally made from ingredients that are skin friendly. The ingredients present in herbal soap are generally kinder to the skin than some of the chemicals that are present in industrially made soaps. Commercial soaps contain many harmful ingredients may not be suitable for your skin. Herbal have become an item of global importance both medicinally and economically. Many skin infections are caused by bacteria and require proper care and treatment. Antibacterial soaps (sometimes called antimicrobial or antiseptic soaps) contain certain active ingredients not found in plain soaps. Some herbal plant extracts and their oils were found to have antibacterial activity. The present study aim is to prepare anti-bacterial herbal soap using *Azadirachta indica, Ocimum tenuiflorum* oils. The finding demonstrates that prepared herbal soap exhibit significant antibacterial activity when tested against most common skin infections causing bacteria such as *Pseudomonas aeruginosa*, *Staphylococcus aureus* and *Escherichia coli* by using the agar well diffusion method. Therefore, the use of herbal soap formulation may aid in progressing towards the world of green synthesis to save our environment. Furthermore, advanced standardization as well as assessment of the effectiveness of prepared herbal soap would assist in the commercialization of this product.

Role of Calcium Signaling in Ribosome Biogenesis via Interaction with an Eukaryotic Translation Initiation Factor a Possible Pathway for Cancer Drug Development

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Abstract:

The highly conserved eukaryotic translation initiation factor 6 (eIF6), is essential for 60S ribosome biogenesis, which is a nucleolar function. eIF6 also has to escort nascent pre-60S ribosomal particles from the nucleus to the cytoplasm for its final maturation and then again recycle back to the nucleolus. Well-regulated nucleo-cytoplasmic shuttling of eIF6 is controlled by phosphorylation-dephosphorylation events at positions Ser-174 and Ser-175. Phosphorylation of eIF6 by nuclear Casein Kinase 1 (CK1) promotes its cytoplasmic localization. On the other hand, nuclear import is mediated by eukaryotic Ca2+ - and calmodulin-dependent Calcineurin phosphatase, thus linking calcium signaling with ribosome biogenesis. A highly conserved putative calcineurin binding motif is present in eIF6 of only nucleated species, at amino acid positions 177-180, which are immediately adjacent to the CK1 phosphorylation sites. Site directed mutagenesis studies in this motif proves the importance of these conserved residues of eIF6 in calcineurin binding and nuclear import. Immunoprecipitation studies show that calcium signalling (via Ca+2/ionomycin) induces association between eIF6 and Calcineurin phosphatase and promotes their subsequent transport to the nucleus as a complex. Inhibition of the process can eventually lead to defects in ribosome synthesis and maturation. This eIF6 pathway can be explored for drug designing in cancer. Cancer cells need to produce more and more ribosomes to rapidly synthesize more and more proteins in order to sustain continuous and uncontrolled proliferation and unrestrained growth. This ribosome dependency is a potential vulnerability that can be exploited in designing effective, targeted cancer therapies.

Computational Stability Analysis of Keratinases in Ionic Liquids for Sustainable and Efficient Keratin Recovery

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Abstract:

Keratin from human hair represents a high-value biomaterial with broad biomedical potential. Although ionic liquids (ILs) and keratinases have individually been utilized to enhance keratin hydrolysis, their synergistic application for sustainable extraction is still largely unexplored. In this work, the structural stability of two keratinases one from *Stenotrophomonas maltophilia* and the other from Bacillus subtilis was examined using molecular models generated by AlphaFold2. All-atom molecular dynamics simulations of 200 ns duration were conducted in aqueous medium and in six selected ILs known for effective keratin dissolution. Keratinases stability was assessed through root mean square deviation (RMSD) and root mean square fluctuation (RMSF) analyses. The *S. maltophilia* keratinase maintained stability in water as well as in two ILs, namely 1-allyl-3-methylimidazolium chloride ([AMIM]Cl) and 1-butyl-3-methylimidazolium bromide ([BMIM]Br), whereas the B. subtilis keratinase remained stable only in [AMIM]Cl. These computational insights highlight the potential of integrating ILs with keratinases for environmentally responsible and efficient recovery of keratin from human hair waste, thereby contributing to sustainable biomaterial valorization strategies.

Effect of Pollutants on the Gut Microbiota Leading to Behavioural and Physiological Abnormalities Associated with Autism

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Abstract:

Neurodevelopmental disorders, including Autism Spectrum Disorder (ASD), are defined by core behavioural impairments; however, subsets of individuals display a spectrum of gastrointestinal (GI) abnormalities. Although autism spectrum disorder (ASD) is defined by core behavioural impairments, gastrointestinal (GI) symptoms are commonly reported. Subsets of ASD individuals display dysbiosis of the gut microbiota, and some exhibit increased intestinal permeability. Recent systematic reviews have reported that exposure to air pollution is associated with an increased risk for ASD. In particular, studies from the United States, Israel, and Taiwan have reported positive associations between particulate matter (PM), nitric oxide (NO), and nitrogen dioxide (NO2) exposures and increased risk for ASD. As per the epidemiological and clinical evidences co-morbid gut dysfunction exists in many individuals with neurodevelopmental disorders. Air pollutants can cause gut dysbiosis by altering the composition of gut microbiota. This can include a decrease in beneficial microbes and an increase in pro-inflammatory species. Recent case studies suggest that gut microbiota shapes cognitive networks encompassing emotional and social domains in neurodevelopmental disorders. This is attributed to the changed ratio of the bacteria of Gut microbiome. In children with ASD, there is a tendency of the Bacteroidetes to Firmicutes ratio to be lower than individuals with no ASD, which corresponds to gastrointestinal and behavioural abnormalities.

Mucuna pruriens: Leaves Extraction, Antifungal Activity, Minimum Inhibitory Concentration (MIC) and Minimum Fungicidal Concentration (MFC)

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Abstract:

Mucuna pruriens (L.) DC., commonly known as Velvet Bean, is a medicinally important legume widely used in traditional systems of medicine for its therapeutic and antimicrobial potential. The present study was conducted to evaluate the antifungal activity of M. pruriens leaf extracts along with the determination of Minimum Inhibitory Concentration (MIC) and Minimum Fungicidal Concentration (MFC) values. Leaf samples were collected, shade-dried, powdered, and extracted using the Soxhlet extraction method with solvents of increasing polarity petroleum ether, chloroform, acetone, ethanol, and methanol. The methanolic extract, found to be the most potent, was tested for antifungal activity against *Aspergillus niger* (MTCC-282) and *Trichoderma reesei* (MTCC-164) using the agar well diffusion method. The extract exhibited significant antifungal activity, with inhibition zones increasing proportionally to concentration (25, 50, and 100 mg/ml) compared to the standard antifungal drug Itraconazole. MIC and MFC were determined using broth dilution and sub-culturing techniques respectively, revealing the minimum concentrations required for growth inhibition and fungicidal action. The results indicated that *M. pruriens* possesses strong antifungal potential, suggesting that its bioactive phytochemicals could serve as promising natural alternatives to synthetic antifungal agents. This study provides a scientific basis for the traditional use of *M. pruriens* and supports its further exploration in pharmaceutical and agricultural applications.

Biochemical and Antibiotic Profiling of Stress-Tolerant Microorganisms from Fresh and Aged Landfill Environment

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Abstract:

Antimicrobial resistance (AMR) has become a pressing global health challenge, with increasing evidence of its emergence in environmental reservoirs such as landfills. Landfills receive a heterogeneous mixture of municipal, biomedical, and industrial wastes enriched with antibiotic residues, heavy metals, and organic pollutants, creating a multifactorial stressful environment that fosters microbial adaptation. Among these stressors, desiccation and low water activity represent critical selective pressures that favor the survival of stress-tolerant microorganisms. To assess such desiccation-tolerant and halotolerant populations, Mannitol Salt Agar was used to isolate stress-tolerant, potentially human-associated commensals and opportunistic microorganisms and assess their antimicrobial resistance profiles. In this study, aeromicroflora samples were collected from fresh and aged landfill sites at the Bhalswa dumpsite, New Delhi. Profiling is done for the isolates by characterization through biochemical and sugar fermentation tests. Antibiotic susceptibility profiling using the Kirby-Bauer disc diffusion method was performed to assess resistance patterns and compare isolates across landfill age and stress gradients. The study aims to elucidate the landfill environment's role as a reservoir for potential human associated antibiotic-resistant microbes and their potential risk to human health. Expected outcomes will contribute to environmental AMR surveillance within the One Health framework.

Gold-Doped Lignin Nanoparticles from *Azadirachta indica*: A Novel Sustainable Drug Delivery Platform for Breast Cancer Therapeutics

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Abstract:

The creation of biocompatible nano carriers that offer improved therapeutic effectiveness continues to be a significant hurdle in the field of oncology, especially in the case of breast cancer, where traditional treatments show restricted success and considerable systemic toxicity. This study presents the innovative synthesis and thorough characterization of gold- functionalized lignin nanoparticles (LNP-Au) derived from *Azadirachta indica*, responding to the critical demand for eco-friendly drug delivery systems with enhanced anticancer efficacy. Lignin was effectively extracted from *A. indica* wood using an alkaline extraction method, and then functionalized with gold nanoparticles through a novel combination of self-assembly and acid precipitation methods, resulting in a reproducible yield of 52.56±0.97%. Through systematic physicochemical characterization, we observed monodisperse nanoparticles exhibiting a mean hydrodynamic diameter of 142.20 nm, a D90 of 169.9 nm, a polydispersity index of 0.6526, and a surface charge of -38.92 mV, which suggests excellent colloidal stability. Morphological analysis through FESEM revealed a quasi-spherical structure, while elemental composition investigations using EDAX and XPS confirmed the successful incorporation of gold. The spectroscopic analysis (FTIR) showed that the functional groups of lignin were preserved, along with specific signatures related to gold. Meanwhile, XRD indicated beneficial amorphous characteristics for drug encapsulation. Thorough assessments of biocompatibility via erythrocyte hemolysis assays and HEK-293 cytotoxicity studies demonstrated outstanding safety profiles. LNP-Au showed remarkable antioxidant properties and displayed selective cytotoxic effects on MDA-MB-231 breast cancer cells, which serve as a key model in cancer research and represent important therapeutic targets in the field of oncology. The innovative blend of lignin's bioactive characteristics with the proven anticancer properties of gold nanoparticles presents a groundbreaking approach to therapy. These findings position LNP-Au as promising theranostic agents that can tackle the bioavailability and toxicity challenges present in existing cancer treatments, especially in the context of breast cancer therapy.

Antimicrobial Susceptibility of Multidrug-Resistant Bacterial Pathogens from Freshwater Ornamental Fish: Efficacy of Conventional Antibiotics and Antimicrobial Extracts from *Azadirachta indica* Leaves and *Trigonella foenum-graecum L.* seeds

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Abstract:

The ornamental fish industry is a multi-billion dollars global enterprise. It is grappling with escalating threats from multidrug-resistant (MDR) bacterial pathogens such as *Pseudomonas* species, *Aeromonas* species and *Edwardsiella* species exacerbated by antibiotic overuse in fish farming. The study was conducted using a comprehensive Kirby-Bauer disk diffusion susceptibility profiling assay using HiMedia kits (Hexa G-plus 9, Dodeca Enterobacteriaceae-2, Dodeca Pseudomonas, Hexa Pseudomonas, Icosa UTI-1), ethanolic extracts of neem (*Azadirachta indica*) leaves and fenugreek (Trigonella foenum-graecum L.) seeds (100 mg/ml) were also evaluated as natural antimicrobials. Bacterial isolates from infected freshwater ornamental fishes (*Poecilia reticulata* and *Carassius auratus*) were studied. The results revealed a high MDR profile (approximately 65% in 31 antibiotics). Fluoroquinolones (ciprofloxacin 100% sensitivity) and carbapenems (meropenem 100% sensitivity) showing superior efficacy. Cephalosporins and tetracyclines exhibited >60% resistance. Significant inter-species differences in resistance ($\chi^2 = 25.37$, $p < 0.0001$) was confirmed statistically, with *Pseudomonas* species showing the highest rate (60%). Neem (*Azadirachta indica*) leaves extract showed intermediate inhibition against *Aeromonas* species (15 mm zone of inhibition), while fenugreek (*Trigonella foenum-graecum* L.) seeds extracts displayed marginal activity against *Edwardsiella* species (14 mm zone of inhibition). These results are helpful in minimizing the use of antibiotics and encourages the exploration of integrated plant-based therapies and region-specific surveillance to sustain ornamental aquaculture amid rising antibiotic resistance.

Deploying Virus-Like Particles Platform by One Health Approach to address Public Health Challenges

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Abstract:

Global Public Health has been continuously threatened by several epidemics of infectious diseases which at times assume a pandemic proportion. Virus-like particles (VLPs) are ideal tools which can be easily efficiently and economically deployed for the One Health Approach in addressing this challenge. They are transforming the field of diagnostics, biotherapeutics and vaccine development. VLPs, which share structural similarities with native viruses but lack genetic material, present a non-infectious and highly immunogenic platform. This makes it a highly valuable platform technology in addressing many challenges in global health like emerging & re- emerging infectious diseases, zoonotic spillovers, pandemic preparedness, etc. VLPs fundamentally consist of nanoscale assemblies made up of one or more viral proteins. The intrinsic immunogenicity enables VLPs to function as both carriers of antigens and stimulators of robust immune response. VLPs can also be tweaked by genetic engineering or chemical modification which greatly enhances their adaptability and applications. Several VLP based vaccines such as Gardasil and Cervarix for HPV associated cancers have already been commercialized. The *Medicago* VLP COVID-19 vaccine, developed using plant-based technology, has demonstrated significant immunogenicity and safety in clinical trials, highlighting the adaptability of VLP platforms. The production of VLPs involves the selection of an appropriate scaffold protein and the incorporation of relevant antigens or therapeutic payload. In addition to preventive vaccines, the potential of VLPs is being investigated as carriers for antimicrobial peptides, bacteriophage lysins, or CRISPR-Cas constructs. VLP-based vaccines and therapy present a sustainable, cost- effective and easily scalable platform technology for Low-Middle Income Countries.

Microbial Degradation of Hydrocarbons from Petroleum Assisted by Biosurfactants

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Abstract:

Microbial degradation of hydrocarbons is a crucial process for the natural removal of these pollutants from the environment, with significant implications for bioremediation strategies. The successful removal of these pollutants depends on the native hydrocarbon-degrading bacteria producing a large amount of biosurfactants. Biosurfactants are amphiphilic molecules composed of hydrophobic and hydrophilic moieties. They interact with surfaces of diverse polarities and reduce the surface and interfacial tension of solutions. Given the potential of these biomolecules, the aim of this work was to develop a biosurfactants, characterize its chemical and surfactant properties, and investigate its potential for removing hydrocarbon pollutants from the environment. Many researchers reported that the bacteria which produce biosurfactants can react with hydrocarbon contaminants to raise the emulsification and facilitate other non biosurfactants producing microorganisms to access these contaminants uptake and use them as a source of carbon for their growth. In present study isolates from sewage, sludge, oil swab of ground nut extraction machine, and marine water showed positive results. Screening tests for biosurfactant producer viz., hemolysis on blood agar, drop collapse, oil displacement, emulsification activity, and surface tension (ST) reduction were done. Highest emulsification index (68 ± 0.1), the maximum yields (2.2 g/L) under optimized conditions and reduced surface tension (SFT) at 32.75 ± 1.50 mN/m was measured using surface tensiometer. The biosurfactants were further characterized by FTIR and NMR. Biosurfactants were found highly stable in terms of surface activity and EI indices at different environmental factors i.e. temperature, pH and various NaCl concentrations. By using stalagmometer drastic change in surface tension of engine oil was measured after mixing it with biosurfactant. The Gas Chromatography-Mass Spectrometry (GC-MS) profile revealed that most of the hydrocarbon peak intensities had been totally broken down by the biosurfactants produced by all these isolates.

Unearthing Hidden Microbial Potential through Metagenomics for Novel Antimicrobials

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Abstract:

The growing prevalence of antimicrobial resistance has intensified the global demand for new and effective therapeutic agents with low toxicity. Traditional culture-based screening methods have reached a plateau, capturing only a small fraction of microbial diversity. Metagenomics has revolutionized natural product drug discovery by enabling direct access to the vast genetic potential of uncultivable microbes, often termed as "microbial dark matter," inhabiting diverse and extreme ecosystems. This paradigm shift allows the identification of previously inaccessible novel biosynthetic gene clusters (BGCs) encoding antimicrobial metabolites possessing unique scaffolds. Recent advancements in high-throughput sequencing, heterologous expression systems, and bioinformatics pipelines have further enhanced the capacity to predict, clone, and characterize genes responsible for secondary metabolite biosynthesis. Studies from diverse ecosystems such as soil, marine sediments, and extreme environments like polar regions and thermal springs have revealed unprecedented structural and functional novelty among metagenomic-derived molecules. Harnessing these untapped genetic reservoirs offers immense potential to reinvigorate antimicrobial discovery pipelines. Integrating metagenomic data with cheminformatics, metabolomics, and synthetic biology approaches can pave the way for the rational design and scalable production of next-generation antimicrobials, offering a promising and innovative route to counteract the global AMR crisis and sustain global health security.

Mgat4b-Mediated Selective N-Glycosylation Regulates Melanocyte Development and Melanoma Progression

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Abstract:

Melanocyte development involves key pathways that are often recapitulated during melanoma initiation, underscoring the importance of understanding these regulatory processes. We identify mgat4b, a glycosyl transferase involved in selective N-glycan branching enriched in pigment progenitors, as a regulator of directional cell migration and establishment of the melanocyte stem cell (McSC) pool during early development. Targeted disruption of mgat4b in zebrafish followed by single-cell RNA sequencing revealed that migratory melanocyte progenitors marked by galectin expression fail to persist. Lectin affinity proteomics demonstrated that glycosylation of key melanocyte proteins, including GPNMB, KIT, and TYRP1, is under MGAT4B regulation. Furthermore, mislocalization of junctional plakoglobin (JUP) explained the observed defects in cell adhesion and migration, implicating MGAT4B but not its isozyme MGAT4A in these processes. Meta-analysis of melanoma datasets revealed that patients harboring both the BRAFV600E mutation and elevated MGAT4B levels exhibit significantly worse survival outcomes compared to those with BRAFV600E mutation alone. Using the zebrafish MAZERATI platform to model BRAFV600E-driven melanoma, we observed that mgat4b-deficient cells fail to aggregate and initiate tumors. Transcriptomic profiling of transformed melanocytes further highlighted cell-cell junction, adhesion, and extracellular matrix interactions as critical factors underlying tumor initiation failure. Importantly, pharmacological inhibition of complex N- glycosylation attenuated early-stage melanoma progression. Collectively, our findings underscore the role of selective N-glycan branching in melanocyte development and melanoma initiation, establishing MGAT4B as a promising therapeutic target for melanoma treatment.

Experimental Demonstration of Dissemination of Specific ESBL Genes from *Klebsiella pneumoniae* to *Pseudomonas aeruginosa* Under Simulated Environmental Conditions

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Abstract:

Extended-spectrum β-lactamases are enzymes produced by Drug Resistant Bacteria belonging to the family Enterobacteriaceae like *Escherichia coli* and *Klebsiella pneumoniae*. These enzymes are plasmid-coded enzymes that provide resistance to antibiotics belonging to Penicillins and Cephalosporins, also to sulbactam and clavulanic acid combinations and monobactams such as aztreonam. WHO has categorised ESBL producing *Klebsiella pneumoniae* as a serious threat. In this study we demonstrate the experimental evidence of transfer of selected Specific ESBL Genes (blaTEM and blaSHV) from *Klebsiella pneumoniae* to *Pseudomonas aeruginosa* under simulated environmental conditions. Phenotypic and genotypic studies were conducted on selected clinical isolates of drug resistant *Klebsiella pneumoniae*. Similar studies were also conducted on strains of *Pseudomonas aeruginosa* which were not showing ESBL antibiogram. Co-Cultivation of the strains of the test organisms under experimental setup was done. Sub-cultures were evaluated for their phenotypic and genotypic characterisation. Eventual transfer of resistance was noted in antibiogram supported by transfer of genes in PCR studies.

Traditional Knowledge and Biological Activities of Ethnomedicinal Plants in the Darjeeling Hills, West Bengal

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Abstract:

Ethnomedicinal plants represent an invaluable source of therapeutic agents and play a vital role in bridging traditional knowledge with modern medicine. This study explores the ethnomedicinal plant diversity of the Darjeeling Hills in West Bengal, India, emphasizing their therapeutic applications and potential for drug discovery. A quantitative ethnobotanical survey was conducted using semi-structured, face-to-face interviews with 104 respondents, including seven traditional healers, selected through purposive, snowball, and random sampling methods across nine villages. The investigation identified 148 medicinal plant species belonging to 132 genera and 68 families, with Zingiberaceae, Asteraceae, Lamiaceae, Rubiaceae, and Poaceae as predominant families. These plants were widely used for gastrointestinal disorders (44 taxa), respiratory problems (43 taxa), general ailments (42 taxa), and dermatological conditions (32 taxa). Key species with significant traditional relevance included *Ageratina adenophora, Artemisia indica, Aloe vera, Centella asiatica, Bergenia ciliata,* and *Drymaria cordata*. Notably, preliminary findings revealed quorum-sensing inhibitory activity in three plant species, suggesting promising anti-virulence properties with applications against microbial pathogens. The study underscores the rich ethnomedicinal heritage of the Darjeeling Hills and the urgent need to preserve indigenous knowledge systems. By integrating ethnobotanical documentation with biological activity assessment, this research highlights the dual importance of safeguarding cultural traditions and unlocking novel therapeutic agents for future drug development. The findings not only provide a scientific basis for traditional practices but also encourage cross-community knowledge exchange, biodiversity conservation, and the promotion of sustainable healthcare solutions.

Antimicrobial Peptides and Biotechnological Potentials of a Thermophilic, Antibiotic-Resistant *Stenotrophomonas maltophilia* from Bakreshwar Hot Spring

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Abstract:

The present study describes the isolation and characterisation of a consortium of antimicrobial peptides (AMPs) from an antibiotic-resistant, thermophilic, and biofilm-forming bacterial isolate, *Stenotrophomonas maltophilia* (MBST-100), obtained from the Bakreshwar hot spring in West Bengal. The investigation focuses on the antimicrobial potential of these AMPs against diverse Gram-positive and Gram-negative bacteria exhibiting resistance to contemporary antibiotics. The peptide consortium was analysed using LC–MS to elucidate its composition and putative mechanism of action. The study also reports a partial antibiogram of heat-resistant bacteria from the hot spring, revealing inhibition by naturally derived antimicrobial agents. The observed antibiotic resistance in MBST-100 is likely attributed to plasmid-mediated mechanisms, biofilm formation, and motility. Enzymatic assays demonstrated that streptomycin exposure enhanced gelatinase expression, whereas amylase activity remained comparatively low. Additionally, MBST-100 exhibited notable dye-degrading capabilities, effectively breaking down crystal violet and malachite green, indicating its potential role in bioremediation. Collectively, these findings identify *S. maltophilia* MBST-100 as a thermophilic, antibiotic- resistant strain capable of producing potent AMPs and extracellular enzymes. Its unique combination of antimicrobial, enzymatic, and degradative properties suggests promising prospects for industrial utilisation and the development of alternative strategies to mitigate antibiotic-resistant bacterial infections.

Zinc Oxide (ZnO) Nano-Bioformulation as Bio-Emergent strategy for Sustainable Agriculture

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Abstract:

Zinc oxide (ZnO) nano-bioformulation is synthesized or modified form of traditional fertilizers, nanotechnology tool is used to improve, soil fertility, quality and productivity of agricultural products. Total 29 bacterial trains were isolated from the agricultural field of sugarcane, chickpea and rice. During screening of microbial isolates for heavy metal zinc sulfate tolerance, as compared to other bacterial strains, Z-1, Z-19 and Z-23 showed maximum tolerance of zinc sulfate (600 to 800 mg/ml). Out of These three isolates, Z-19 showed significant ability for ZnO (colorless to milky white) nanoparticle synthesis. Size of ZnO nanoparticles synthesized by Z-19 was checked by particle size (40 nm) distribution and zeta potential (-37.0) was also checked. FTIR analysis of ZnO was also studied to observed the arrangements of functional groups. GC-MS analysis and SDS-PAGE electrophoresis were carried out for metabolite study and enzyme study which involved in ZnO nanoparticles synthesis by *Bacillus pumilus*. Optimization of media components for maximum ZnO and selenium nanoparticle synthesis was carried out by OFAT along with statistical analysis like PBD. Z-19 isolate showed maximum plant growth promotion as compare to Z-1 and Z-23 during seed germination (100%), pot and field assay. In field assay, as compared to isolates Z-1 and Z-23, ZnO nanoparticles synthesized by Z-19 isolate enhances major soil nutrients like nitrogen (from 125 to 138), phosphorus (22.54 to 25.62) and potassium (822 to 900 kg/h) and also enhanced growth of maize plant and watermelon in a rapid manner, salinity of the soil get decreased. Rhizosphere soil isolate Z-19 showed noteworthy ability to enhance soil fertility and plant growth promotion. Based on the result of 16s rRNA sequencing, this Z-19 bacterial strain showed maximum sequence similarity with *Bacillus pumilus*. Zinc oxide nano-bioformulation is economical, ecofriendly and versatile.

Resilient Agriculture: Harnessing Alkaliphilic *Actinomycetes* for Sustainable Phosphorus Management and Enhanced Crop Yields

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Abstract:

Phosphorus (P) is a critical nutrient necessary for the growth of plants; however, its availability in soil is frequently restricted due to its fixation in insoluble compounds. *Actinomycetes*, a group of Gram-positive, filamentous bacteria, have demonstrated significant potential in solubilizing these insoluble phosphates, thereby enhancing plant growth through various mechanisms, including phosphate solubilization, phytohormone production, and the suppression of phytopathogens. This research aims to isolate and characterize alkaliphilic *actinomycetes* from extreme environments to assess their capacity to improve phosphorus bioavailability and promote sustainable agricultural practices. Utilizing molecular and biochemical techniques, the study seeks to explore their functional diversity and optimize their application as bioinoculants. By harnessing their metabolic adaptability and resilience, this project aspires to create an environmentally friendly alternative to chemical fertilizers, reduce soil degradation, and enhance crop yields. This research highlights the importance of *actinomycetes* in advancing sustainable agricultural methods while tackling the pressing issues of food security and environmental sustainability.

Bridging Antigen Engineering and Protection: His-Tag and Signal-Peptide- Free SPy_2191-Alum Formulation for GAS Immunity

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Abstract:

Group A *Streptococcus* (*S. pyogenes*) continues to cause substantial global morbidity, emphasizing the need for a safe and effective vaccine. In this study, we assessed a refined, bioengineered SPy_2191 antigen, lacking both the his-tag and signal peptide, adjuvanted with Alum for its safety, immunogenicity, and protective potential in mice. The formulation was well tolerated, with no clinical or histological signs of toxicity. Vaccination elicited strong humoral immunity, characterized by high SPy_2191-specific IgG levels with balanced IgG1 and IgG2b responses, indicative of coordinated Th1/Th2 activation. Cellular responses were robust, as evidenced by increased antigen-specific $CD4^+$ and $CD8^+$ T cell activity accompanied by elevated IFN-γ, IL-4, and IL-17 production, demonstrating engagement of Th1, Th2, and Th17 pathways. Enhanced chemokine expression (MCP-1/CCL2, MIP-1α/CCL3, MIP-1β/CCL4, and RANTES/CCL5) further reflected a coordinated and controlled immune environment. Upon lethal challenge, vaccinated mice demonstrated 88% survival and significantly reduced bacterial burden across major organs. Complementary in vitro and in vivo toxicology analysis confirmed the non-toxic nature of the cleaved SPy_2191 protein. Collectively, these findings demonstrate that the his-tag and signal peptide-free SPy_2191 antigen, formulated with alum, is safe, highly immunogenic, and capable of eliciting integrated humoral and cellular responses that translate into meaningful protection. This work highlights cleaved SPy_2191 as a strong candidate for continued preclinical advancement and underscores its promise as a broadly protective vaccine approach against Group A Streptococcal disease.

Unveiling the Phytocytotoxic Effects of Dual Antibiotic Stress in Spinach

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Abstract:

In this growing era, there has been a distinguishable increase in the emerging contaminants, particularly antibiotics, in agricultural lands and water bodies, raising concerns about both health and environmental consequences. These antibiotics end up being released into sewers and wastewater treatment plants, contaminating the soil and water systems. In light of this, the current study examines the effects of two antibiotics, viz., azithromycin (AZI) and ciprofloxacin (CIP), as well as their combined effect on *Spinacia oleracea* (spinach). At varying concentrations (10, 25, 50, and 100ppm), germination rates displayed a clear inverse correlation, with the control group achieving a germination rate of 85.56%, while the 100ppm AZI, CIP, and combined treatment resulted in a decline to 34.4, 47.8 and 28.9% respectively. Statistical analysis ($p \leq 0.05$) upholds a marked reduction in seedling growth indices, including radicle and plumule lengths, which measured 3.63 and 4.03 cm, respectively, in the control, but diminished to 0.53cm and 1.30cm at 100ppm in AZI. A similar trend was observed in CIP as well as combined treatment. An increase in electrical conductivity was measured, from 7.15 µS cm^{-1} in the control to 16.92 µS cm^{-1} at the highest dose in the mixture. A concurrent cytological evaluation revealed a significant decrease in the Active Mitotic Index (AMI), from 10.8 in the control to 6.3% at the highest concentration, accompanied by various chromosomal abnormalities, such as stickiness, scattering, unorientation, and loop formation. The total abnormality percentage in the highest dose of the combined treatment was 5.49%. These results suggested that both AZI and CIP serve as potential toxins to plant cells, and continuous exposure can pose a genotoxic risk to living organisms, and antibiotic resistance may potentially develop in the near future.

Evaluating the Properties of a Novel Membrane Active Peptide with Potent Activity Against Carbapenem Resistant *Acinetobacter Baumannii*

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Abstract:

In India, *Acinetobacter baumannii* accounts for approximately 22.3% of hospital-acquired pneumonia cases, with more than 70% of isolates showing resistance to carbapenems. In addition to effective antibiotic stewardship practices, there is an urgent need to develop novel antimicrobial agents to address the escalating threat of antimicrobial resistance. Antimicrobial peptides (AMPs) possess broad-spectrum activity, high safety, and minimal drug resistance, acting through multiple mechanisms. CDAP-2 (patent filing under process) is a novel membrane-active peptide showing broad-spectrum antibacterial activity. This study investigates the antibacterial properties and mechanism of action of CDAP-2 against carbapenem-resistant *Acinetobacter baumannii* (CRAB) in vitro. It has shown a minimum inhibitory concentration of 5 μM against CRAB. Time kill kinetics studies show that it starts to exert its effect within 15 minutes of treatment. Microscopic studies reveal that it primarily works by damaging the cell membrane, leading to the release of extracellular contents. Moreover, CDAP-2 has been shown to induce membrane depolarization and the production of reactive oxygen species (ROS), demonstrating its multi-mode of action. Further studies are underway to understand its mechanism and assess its therapeutic potential.

Synergistic, Anti-Microbial and Probiotic Potential of Bacteriocins Identified from Rhizospheric Soil-Derived *Enterococcus Mundtii*

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Abstract:

Due to the ever-increasing global threat of antibiotic resistance, bacteriocins have gained attention among researchers due to their potential clinical applications. Bacteriocins, as antimicrobial peptides, represent one of the most important natural defense mechanisms among bacterial species, particularly lactic acid bacteria (LAB), that can fight against infection-causing pathogens. To tackle this menace, novel and alternative approaches are being explored. Bacteriocins from probiotic lactic acid bacteria (LABs) appear to be a promising, futuristic alternative in preventing the dissemination of MDR pathogens. Isolation of novel probiotic lactic acid bacteria from an economical source is becoming a prime importance, having lesser damaging effects on health and the environment. Hence, soil as a bioresource has become our source of interest in isolating potential LABs. Soil harbors a diversity of microbes, among which lactic acid bacteria (LABs) are of prime clinical importance. In this study, we isolated and functionally characterized Enterococcus mundtii from the rhizospheric soil of the grape fruit tree as probiotics. Enterococcus mundtii exhibited significant antimicrobial activity against several multidrug-resistant (MDR) and food-borne pathogens. The *Enterococcus mundtii* (OQ991274) showed the highest and remarkable survival against varying acid and bile salt tolerance, aggregation, and coaggregation, along with cell surface hydrophobicity and exopolysaccharide (EPS) production, with the potential to enhance the gut survivability and colonization. Safety assessments confirmed their safety with no hemolytic activity. Antibiotic susceptibility testing (AST) showed that Enterococcus mundtii was susceptible to all the tested conventional antibiotics. Moreover, growth curve kinetics displayed a strong bactericidal effect up to 48 h. The synergistic interaction of *Enterococcus mundtii* with traditional antibiotics revealed that combinatorial treatments can be a better alternative in controlling resistant pathogenic microbes.

Exploring the Bio-Efficacy of Streptomyces 130 Crude Extract and Its Biogenic Silver Nanoparticles: A Comparative Approach

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Abstract:

Multidrug-resistant fungi have become a major threat to both human health and agriculture. Their toxic metabolites not only lead to severe and often fatal infections but also damage crops, reducing yield and impacting food security. Although chemical fungicides provide temporary control, they frequently leave harmful residues and may induce toxicity, underscoring the urgent need for safer, natural, and sustainable antifungal alternatives. Natural microbial metabolites are a rich source of bioactive compounds effective against a wide range of pathogenic fungi. In our study, Streptomyces strain 130 exhibited noticeable antifungal potential against the pathogenic fungus *Aspergillus fumigatus*. However, the crude extract showed only moderate efficacy, with growth inhibition achieved at concentrations between 0.5 and 0.25 mg/mL in the MIC assay. To enhance its antifungal performance, biogenic silver nanoparticles (Ag-NPs) were synthesized using the bioactive metabolites of Streptomyces strain 130. Nanoparticle formation was confirmed by a UV–Vis absorption peak at 410 nm. DLS analysis indicated a hydrodynamic diameter of 101.3 nm with a PDI of 0.207, reflecting a uniformly dispersed nanoparticle population, while TEM revealed spherical particles with an average size of 25.07 ± 2.95 nm. FTIR spectra further confirmed the role of hydroxyl, amine, alkyne, and amide groups in nanoparticle stabilization. The synthesized Ag-NPs exhibited significantly enhanced antifungal efficacy against *A. fumigatus*, as demonstrated by MIC, disc diffusion, and spot assays. This improvement suggests increased bioavailability and more efficient, targeted action compared to the crude extract.

Probiotics as a Solution to Antibiotic Resistance: Mechanistic Insights into Gram-Positive and Gram-Negative Bacteria

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Abstract:

The development of various resistance mechanisms by bacteria such as *Staphylococcus aureus* (gram-positive) and *Escherichia coli* (gram-negative), including enzymatic degradation, target alteration, competition for nutrition and efflux pump overexpression, makes antimicrobial resistance a serious worldwide health burden. Especially in areas where antibiotic overuse and misuse is highly common, these processes raise morbidity and mortality rate and reduce the effectiveness of therapy. A possible alternative approach to lower antimicrobial resistance is provided by probiotics, which are live good bacteria such as *Lactobacillus, Bifidobacterium*, and *Bacillus subtilis*. Their mechanism includes reducing horizontal gene transfer, improving gut barrier integrity, modifying immunological responses, and suppressing harmful bacteria through the formation of mucins and bacteriocin. Its ability to reduce side-effects associated to antibiotic and inhibit colonisation by resistant microorganisms is supported by multiple evidences. Limitations in regulations, inadequate clinical trials, and strain-specific studies continue to be a major gap. Probiotics may play a more significant role in preventing antimicrobial resistance if their usage is optimized through multi-strain combinations, standardized clinical studies, and integration with global One Health initiatives.

Metagenomic Approach for Unveil Resistant Genes for Last-Resort Antibiotics in The Wastewaters of Delhi

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Abstract:

Antimicrobial resistance (AMR) is a global health concern contributing to 9% of global deaths. Existing drugs have become ineffective, making it crucial to track both existing and evolving AMR genes. One of the causes of AMR is gene mutations, leading to SNPs or indels, affecting the bacteria's resistance capabilities. The study employs two main NGS approaches: shotgun sequencing to unveil the bacterial and AMR profiles, and Nanopore sequencing to determine SNPs in the ORFs of the resistant genes. Wastewater samples were collected from six STPs in the Delhi region. 49 bacterial phyla were identified, with Bacteroides (41%) being the most dominant, followed by Pseudomonadota, Campylobacterota, and Bacillota. At the bacterial genus level, *Segatella, Aliarcobacter, Bacteroides*, and *Thauera* were abundant. The ESKAPE pathogens were present in the samples but at lower abundance (< 1%), except Pseudomonas, which occupied 3% of the community. Most of the genes in the samples conferred resistance to β-lactams, tetracycline, MLS, aminoglycosides, multidrug and sulfonamides. Nanopore amplicon sequences from metagenomic DNA of oxa-48, ges, kpc, mcr, and tet(X) were analysed for variant calling using Medaka, Clair3, and VarScan, and the effect was studied by using the SnpEff tool. In total, 35 SNPs were found to be common in three pipelines, with more than 30X depth. The ges gene showed the highest genetic diversity with missense mutations in the omega-loop region. tet(X) exhibited two missense mutations in the ORF region with the highest coverage and quality. The in-silico analysis was done to characterise the structural and functional changes due to SNPs. Our work highlights the presence of ARGs of last resort antibiotics in the environment, raising concerns. The SNPs present in the ORF region of the resistant genes indicate that novel resistant genes are arising and might be of a greater risk.

Bioprospecting and Characterization of Pigmented Halophiles for the Extraction and Analysis of Carotenoids

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Abstract:

Halophilic microorganisms are special types of microbes that can live and grow in salty environments. Many of these halophiles produce colorful pigments, mainly carotenoids, which have great importance in health, cosmetics, and food industries because of their antioxidant properties. In this study, samples were collected from saline habitats to find and study pigmented halophiles. The isolates showing bright colors such as yellow, red, orange, or pink are selected for further analysis. They are identified and characterized based on their physical and biochemical properties. Carotenoids are then extracted using solvents and analyzed to estimate their quantity and quality. The study shows that some of the isolated halophiles produced a high amount of carotenoids. These findings suggest that pigmented halophiles can be an excellent natural source of carotenoids and could be used for various industrial applications in the future.

Green Process for ε-polylysine and γ-linolenic Acid Production Using Ionic Liquid

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Abstract:

A process for extraction and purification of ε-polylysine and γ-linolenic acid from generated microalgal biomass of *Coelastrella thermophila* was developed through biorefinery model. A green extraction and purification protocol was developed using ethylammonium nitrate (EAN), synthesized via acid-base neutralization in methanol and characterized through CHNS analysis, DSC, moisture content, and NMR spectroscopy. Simultaneously, a green extraction and purification strategy was developed using trihexyltetradecylphosphonium bis(2,4,4- trimethylpentyl) phosphinate for selective recovery of γ-linolenic acid from the total crude oil obtained. Monoalgal cultures of *Collestralla thermophila* from CSIR-CSMCRI were cultivated in CSMCRI-P2 medium under autotrophic conditions (12:12 h light-dark cycle, 25°C, 100 μmol m^{-2} s^{-1}) with regular manual agitation. Fresh inoculum added to P2 medium at a concentration of 30% w/w and kept at incubator shaker for 96h at 80 rpm. After 96h, the culture was centrifuged and the obtained biomass was dried at 60 °C. The biomass is subjected to then soxhlet extraction for recovery of total lipids containing γ-linolenic acid which was purified using phosphonium based ionic liquid in a single step through selective recovery. Further, the residual biomass was subjected to detergent based hydrolysis and hydrolysate was further processed for microbial fermentation using *Bacillus licheniformis* for production of ε- polylysine. ε-polylysine was recovered from fermentation broth in a single step through selective recovery using ethylammonium nitrate (EAN), synthesized via acid-base neutralization in methanol and characterized through CHNS analysis, DSC, moisture content, and NMR spectroscopy.

Genomic Clues to Resistance Evolution in *Staphylococcus aureus*

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Abstract:

Staphylococcus aureus, recognized worldwide as a major "superbug", a leading cause of bloodstream infections, sepsis, and hospital-acquired infections, contributing to over 1.1 million deaths globally in 2019. Its multidrug resistance, including methicillin and vancomycin resistance, high prevalence affecting billions as carriers with methicillin-resistance *S. aureus* (MRSA) present in up to 2.7% of the population pose a critical public health challenge. In this in silico study, we investigated the genetic adaptability, evolutionary dynamics, antimicrobial resistance (AMR) determinants, virulence factors, and selective pressure on the mecA gene, which mediates methicillin resistance. We also identified mutations associated with vancomycin-intermediate *S. aureus* (VISA) and predicted therapeutic targets in *S. aureus* strains associated with bacteremia. Analysis revealed an open pangenome, reflecting extensive genetic diversity and the bacterium's remarkable ability to acquire new genes for survival in diverse environments. Multiple AMR and virulence factors including mecA, pvl, spa, hla, clfA/B, and icaA/D were identified, highlighting their roles in immune evasion, adhesion, toxin production, and biofilm formation. Selection pressure analysis of the mecA gene indicated strong purifying selection with a few positively selected codons (1M**, 4S**, 15S**, 22T**, 279I**, 303K**, 443S**) suggestive of adaptive evolution. For vancomycin resistance, mutations such as T24K in vraR and D147Q in graR were consistently detected, indicating molecular adaptation toward the VISA phenotype. Additionally, functional classification of core proteins revealed enrichment in categories related to translation, transcription, and defense mechanisms, emphasizing their essential role in pathogenicity. Subtractive proteomics further identified 272 stable, essential, and non-homologous cytoplasmic proteins, among which 20 displayed strong druggability potential. Overall, this study provides genomic evidence.

Biodegradation of H-Acid from Industrial Wastewater by *Pseudomonas aeruginosa*: Microbial Pathway and Environmental Implications

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Abstract:

The biodegradation of 1-amino-8-naphthol-3,6-disulfonic acid (H-acid), a persistent sulfonated naphthalene dye intermediate, was investigated using Pseudomonas aeruginosa under controlled laboratory conditions. Batch degradation experiments were conducted with varying H-acid concentrations (50, 100, and 200 ppm) to determine the degradation efficiency and transformation pathways. The optimized degradation occurred at 100 ppm after 24 h of incubation, as confirmed by UV–Visible spectrophotometry. Fourier-transform infrared (FTIR) analysis of the degraded samples revealed significant structural modifications, including the disappearance of sulfonic (–SO3H) stretching bands (1040–1180 cm−1) and the appearance of new peaks at 3289 cm−1 and 1638 cm−1 corresponding to hydroxyl (O–H) and carbonyl (C=O/C=C) groups, respectively, indicating desulfonation, aromatic ring cleavage, and oxidation of intermediates. A minor shoulder near 2350 cm−1 suggested CO_2 evolution, confirming partial mineralization. The proposed degradation pathway, supported by FTIR evidence, involves sequential desulfonation, deamination, and ring-cleavage reactions, ultimately forming low-molecular-weight carboxylic acids and aldehydes. These findings establish *Pseudomonas aeruginosa* as an efficient microbial system for the bioremediation of sulfonated aromatic pollutants and demonstrate its potential for treating industrial effluents containing H-acid residues.

Role of Transmembrane Protein RSN-1 in Cellulose Sensing, Stress Tolerance, and Cellulase Production in *Talaromyces pinophilus*

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Abstract:

This study investigates the functional role of the transmembrane protein RSN-1 in the filamentous fungus *Talaromyces pinophilus*, with a focus on its involvement in cellulose sensing, stress tolerance, and cellulase secretion. Transmembrane proteins are critical mediators of external signal perception, particularly in complex environmental conditions such as cellulose rich, stress inducing environments. Bioinformatic analyses identified RSN-1 as a CSC1/OSCA1-like 7-transmembrane domain protein, suggesting its potential role as a mechanosensitive calcium-permeable ion channel. Differential gene expression studies under various carbon sources revealed that RSN-1, along with other transmembrane proteins like MFS1 and MFS6, are significantly upregulated during growth on polysaccharides, indicating their potential involvement in cellulose sensing and transport. Functional characterization through knockout and rescue strains demonstrated that RSN-1 is crucial for optimal growth, stress tolerance (ionic, chemical, and osmotic) and cellulase secretion. The RSN-1 knockout strains exhibited reduced biomass and cellulase production under stress conditions, whereas wild-type and rescue strains maintained higher growth and enzyme activity, as measured by CMC assays. The study further elucidates that RSN-1 operates via a calcium-mediated signalling pathway, contributing to the cellular stress response and enzyme secretion mechanisms. These findings support the hypothesis that RSN-1 functions as a primary sensor for cellulose presence, activating downstream pathways to enhance cellulase production, vital for industrial applications. The research provides valuable insights into fungal perception of cellulose as a stress signal and presents RSN-1 as a potential target for genetic engineering aimed at improving cellulolytic enzyme yields. Future directions include examining Golgi apparatus dynamics and secretory vesicle trafficking upon RSN-1 modulation. Overall, this work advances our understanding of membrane-based sensing mechanisms in filamentous fungi and offers prospects for optimizing biotechnological processes for biomass degradation and biofuel production.

SPy_2191, A Novel Protein Subunit Vaccine Candidate Against Group A *Streptococcus* Infection

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Abstract:

Group A *Streptococcus* (*Streptococcus pyogenes*, GAS) is a flesh-eating pathogen causes widespread infections ranging from mild pharyngitis and skin disease to life-threatening invasive illness, yet no vaccine licensed so far. To address this gap, we formulated a vaccine using cleaved GAS surface protein SPy_2191. In this formulation His tag and signal peptide free (cleaved SPy_2191) used in order to avoid unwanted immune responses. The purified protein was formulated with alum, a human compatible adjuvant. Vaccine was further tested for its in vivo toxicity and protective efficacy in mice. We investigated the immunological mechanisms by which cleaved, His tag-free SPy_2191 induces protective immunity in C57BL/6 mice. We found immunization with cleaved SPy_2191 significantly expanded antibody-producing B-cell subsets ($CD19^+$, $CD27^+$ memory B cells, and plasma memory B cells), indicating robust humoral activation. Also, vaccinated mice showed enhanced recruitment and activation of splenic innate immune cells, including macrophages and dendritic cells accompanied by elevated cytokine levels of IFN-γ, IL-4, and IL-17, indicating activation of Th1, Th2, and Th17 pathways. Overall, cleaved SPy_2191 formulated with alum is safe, highly immunogenic, and imparts protection, indicating it is a promising preclinical vaccine candidate against GAS infections.

Ethylphenyl Sulfate: A Gut Microbiota-Derived Metabolite with Anticancer Potential Against Colon Cancer Cell

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Abstract:

Metabolites originating from the gut microbiota have recently received attention as potential anticancer agents. Among these, 4-ethylphenyl sulfate (4-EPS), a gut microbial metabolite, has not been investigated for its anticancer activity. This study deals with evaluation of anticancer activity of 4-EPS using HCT-116 human colorectal adenocarcinoma cells and CCD841 normal colon epithelial cells. For evaluating the anticancer activity, cell viability, proliferation, ATP levels, colony formation, and apoptosis were measured after 4-EPS treatment to HCT-116 and CCD841 colon cell lines. The changes in morphology were seen under a microscope. Cell cycle distribution was also investigated, together with the expression of apoptotic and cell cycle regulating proteins (Bax, Bcl-2, and cyclins). Histone deacetylase (HDAC) isoform interactions with 4-EPS were investigated using in silico molecular docking. 4-EPS treatment greatly increased apoptosis while considerably decreasing HCT-116 cell viability, proliferation, ATP generation, and colony-forming potential. Cell shrinkage, vesicle formation, and loss of membrane integrity were among the morphological changes. Mechanistic investigation showed G2/M phase arrest, downregulation of Bcl-2, and overexpression of Bax. Strong binding affinity of 4-EPS to HDAC isoforms was seen in silico investigations, indicating epigenetic modification. Notably, 4-EPS demonstrated its selective action on cancer cells by not causing any cytotoxic effects on CCD841 normal colon epithelial cells. For the first time, these results demonstrated therapeutic potential of 4-EPS which can specifically target colorectal cancer (CRC) by inducing apoptosis, cell cycle arrest, and epigenetic modification. The novelty of this work lies in repositioning a metabolite previously considered uremic toxin into a promising anticancer candidate, thereby offering new avenues for microbiota-based interventions in colorectal cancer therapy.

Production of Cost-Effective, Pre- and Probiotic Novel Combinations Utilizing Fruit Wastes for Health Benefits, Sustainable Economy and Environmental Cleanup

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Abstract:

To produce a cost-effective formulation of novel pre-and probiotic combinations utilizing fruit wastes. Various kinds of waste generated from fruits are a global concern as it causes pollution of air, water and soil which damages human health and the environment. As per food waste index report 2021 (UNEP), on an average 121kg of food per capita is wasted globally with India ranked 50th. Fruit wastage comprises 4.58% to 15.88% of this huge loss with a financial loss of about Rs.40811 Crore. Different fruit wastes contain various untapped bioactive compounds including flavonoids, phenolics, triterpenes, alkaloids etc. along with several oligo- and polysaccharides and essential dietary fibres, which as prebiotics, may enhance the growth of probiotic consortia of yeasts molds or lactic acid bacteria. Such novel combinations of pre- and probiotics may improve digestive health, boost immunity, manage antibiotic associated issues and inhibit pathogenic bacteria. It is also promising to boost circular economy through promoting the waste-to-wealth concept as envisioned in the sustainable development goals. In the present study, fruit wastes from *Musa paradisiaca* (banana), *Citrus limetta* (mosambi), *Citrus sinensis* (orange), *Ananas comosus* (pineapple), and *Punica granatum* (pomegranate) showed the presence of important bio actives, with orange, pomegranate, and pineapple showing the richest prebiotic profiles. Aqueous extracts of these fruit wastes enhanced the growth of *Lactobacillus* from dahi and probiotic supplementary capsule blends. The strongest probiotic growth promoting results came from mixing all five fruit extracts, suggesting a synergistic effect.

Unveiling the Immunomodulatory Effects of Sacha inchi (*Plukenetia volubilis* L.) derived Omega Fatty Acids: A Network Pharmacological Perspectives

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Abstract:

Human body is incapable of synthesizing ω-3 PUFA due to limitation in bioconversion of ALA to EPA subsequently to DHA. The natural sources of PUFA are animals, plants, microalgae including fungi and single cell and are limited especially the proportion that essential to cater appropriate physiological functions. Plukenetia volubilis L. (Euphorbiaceae), is also known as “sacha inchi”, “mani del monte” and grown in Mizoram, India are considered as super-food due to its immunomodulatory potential and seed oil of sacha inchi contains omega 3, omega 6 polyunsaturated fatty acids and omega 9 monounsaturated fatty acid and is a good source of ‘healthy fats’. Traditionally roasted seeds are used for neurodegenerative disorders, anti-inflammatory and digestives. Fresh leaves used as laxative and in treatment of burns. This study aims to understand the network pharmacological annotations of immunomodulatory potential of essential and non-essential fatty acids found in sacha inchi. The major precursor in biosynthetic pathway of omega-3, 6 and 9 fatty acids (viz. palmitic, oleic, linoleic and stearic) obtained from published literature. The systems level network pharmacology of biomolecules was further subjected to predict the toxicity, target identification, disease genes, pathway enrichment analysis and associated (protein-protein) interactions using SWISS ADME, ToxPred, gprofiler, Swiss target prediction, STITCH, STRING and Cytoscape (cytohubba) respectively. In-vitro anti-inflammatory efficacy was investigated by using Heat-Induced Haemolysis and Heat-induced Albumin Denaturation Inhibition Assay. In this study, total 1768 disease genes were obtained from the Genecards and 802 target related genes. Gene enrichment analysis using Enrichr tool generated significant functional enrichment analysis results for signalling by interleukin, immune system, cytokine signaling, and interleukin-4 and 13 pathways. This natural source of omega fatty acids with appropriate proportions essential for physiological functions will be open a new avenue to consider sacha inchi as important natural source of omega-3,6 and 9 fatty acids.

Revealing MDR *Aerococcus viridans* in Diabetic Wounds and the Healing Potential of *Syzygium cumini* Seed Extracts

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Abstract:

Aerococcus viridans is an understudied, often misidentified, catalase-negative, Gram-positive organism increasingly associated with endocarditis, urinary tract infections, bacteremias, and (Diabetic) wound infection in immunocompromised individuals or those on immunosuppressants. It is frequently misidentified as *Staphylococcus*. This study focuses on identifying and isolating an MDR strain of *Aerococcus viridans* from a diabetic foot wound and on assessing an alternative treatment strategy for MDR infections. Using a full-thickness excision wound model, phytochemicals from *Syzygium cumini* seeds were converted into topical ointments and tested in streptozotocin-induced diabetic Wistar rats. The formulation's capacity to heal wounds was assessed against control groups and a traditional commercial ointment (Mega Heal). By the 21st day, animals treated with the ointment showed full epithelial closure and much faster wound contraction. The identification of MDR *A. viridans* and the observed therapeutic efficacy of *S. cumini* seed phytochemicals highlight the dual importance of precise microbiological diagnosis and plant- based interventions. This approach offers a promising path to managing chronic diabetic wounds caused by resistant bacterial strains.

A Hybrid Ensemble Framework for Robust Classification of Breast Cancer in Histopathology Slides

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Abstract:

Breast cancer (BC) is one of the most prevalent forms of cancer and second highest cause of mortality among women worldwide. In 2022, BC were detected in 2.3 million women, of which 0.67 million fatalities occurred globally. Early identification and accurate diagnosis of BC are decisive for boosting patient survival rates from 30% to 50%. Histopathological diagnosis is fundamental to contemporary preventative medical care, directing the therapy and treatment of early-stage breast cancer. The manual analysis of histologic data, reliant on the clinician's subjective expertise, is also a labour-intensive, time-taking, and costly procedure that requires clinical intervention and proficiency for an equitable assessment. With the advancement of techniques in healthcare, deep learning (DL) plays a crucial role in processing and analysing a vast array of X-ray, CT, MRI, and histopathology images. This study utilizes a dataset from the public repository Kaggle, comprising a total of 277,524 breast cancer histopathology images, of which 198,738 depict benign tumors and 78,786 represent malignant tumors. In image classification difficulties, convolutional neural networks (CNNs) exceeded alternative DL architectures. CNNs automatically learn hierarchically feature representations from unprocessed picture data, therefore removing the requirement for human feature engineering. The data was imbalanced, so to balance the data, we have used under-sampling. After balancing the data. We first used three pre-trained models, Xception, MobileNet, and VGG19. After getting the result from all three pre-trained models, we created an ensemble model of these three models, achieving 93% precision, recall, F1- score, and accuracy comparable to other state-of-the-art outcomes. This research will enable researchers and medical professionals to select an appropriate approach for tumor classification. It will assist medical practitioners in accurately and effectively classifying the sickness. The proposed ensemble architecture, combining VGG19, MobileNet, and Xception, is showcasing the superior performance in classifying BC histopathology images into benign and malignant classes. The evaluation metrics and comparison analysis show that the balanced dataset which obtained by under sampling and optimized training process allowed robust generalization.

Plasmodium falciparum Molecular Mechanism of Heme Binding and Sensitivity to Artemisinins

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Abstract:

Heme is critical to activating artemisinins (ARTs), drugs essential for malaria control. *Plasmodium falciparum* Kelch13 (K13) protein binds heme in vitro, but its in vivo functions remain unknown. As precise regulation of free-heme levels is not feasible in infected erythrocytes, we developed mammalian cell model to study molecular properties of K13 at biological heme concentrations. We show that K13 levels are exquisitely responsive to nanomolar and micromolar amounts of heme. Heme stabilizes K13 with chemical and molecular specificity, raises its oxidative-stress responses and association with autophagic-endosomes. Targeted disruption of lysosomal autophagy further increases K13 levels to fuel ART-induced redox-cell death that is proportional to K13 intensities at physiological heme levels. K13's kelch-domain confers both heme and ART responsiveness to its mammalian orthologue KEAP1. These data suggest a novel molecular mechanism for K13 heme-binding in regulating ART- sensitization and the power of models to study frontiers of pro-oxidant stress.

Investigation of Novel Drug Targets; Advances in Anti- Tubercular Drug Development Through Structure Guided Approach

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Abstract:

Tuberculosis remains a formidable global health challenge, with *Mycobacterium tuberculosis* demonstrating sophisticated survival strategies that render conventional antibiotics increasingly ineffective. The emergence of multidrug-resistant and extensively drug-resistant strains, coupled with treatment-associated toxicity and prolonged therapy duration, necessitates urgent identification of novel therapeutic targets. Our research focuses on discovering and characterizing previously unexplored mycobacterial proteins that orchestrate multiple virulence mechanisms simultaneously. Through comprehensive genomic analysis and functional characterization, we have identified key enzyme families including peptidyl-prolyl isomerases and protein tyrosine phosphatases as promising therapeutic targets. These enzymes exhibit dual functionality coordinating immune evasion strategies while establishing drug-tolerant biofilm architectures that protects the pathogen from antibiotic action. Our investigations revealed that Mtb PpiB (peptidyl-prolyl isomerase B), plays a critical role in biofilm formation and tolerance to anti-mycobacterial drugs. Surface plasmon resonance spectroscopy confirmed predicted interactions between PpiB and FDA-approved drugs including cyclosporine-A and acarbose. While acarbose and cyclosporine-A demonstrated bacteriostatic effects against Mycobacterium smegmatis, gallium nanoparticles (GaNP) exhibited bactericidal activity. Analysis of binding sites across PpiB homologs revealed conservation across biofilm- forming pathogens, suggesting broad therapeutic applicability. Parallel investigations of inhibitors for Mtb PtpB (protein tyrosine phosphatase B), a recognized virulence factor with unique structural properties, employed molecular docking of ChemBridge compound libraries followed by quantum mechanical calculations. Two novel derivatives bearing pyrazolo[4,3-c]pyridine and 1,4-diazepane nuclei demonstrated significant PtpB inhibition with favorable molecular descriptors and binding free energies. In vitro enzymatic assays using recombinant PtpB confirmed inhibitory potency and selectivity of these compounds. This approach addresses critical gaps in tuberculosis therapy by targeting distinct but complementary pathogenic mechanisms. The identification of biofilm-disrupting agents and novel phosphatase inhibitors provides promising scaffolds for next-generation anti-tubercular drug development, offering potential for shorter treatment regimens and enhanced efficacy against drug- resistant strains.

Development and Evaluation of Serological Assays and Pseudovirus Platforms for Rabies and Nipah Viruses: Advancing Safe and Scalable Vaccine Strategies

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Abstract:

Rabies and Nipah viruses are highly pathogenic zoonotic viruses that impose severe yet distinct public health challenges. Rabies, a neglected tropical disease, causes nearly 60,000 deaths each year worldwide, with the greatest burden in Asia and Africa. Human infection usually results from bites or scratches inflicted by infected animals, or from contact with their saliva. Although rare, human-to-human transmission has also been reported. Once clinical symptoms appear, rabies is universally fatal. Nipah virus (NiV), designated as a BSL-4 pathogen, is less common but far more lethal, with recurrent outbreaks reported in South and Southeast Asia. Globally, from 1998 to 2024, Nipah has been linked to 754 confirmed cases and 435 deaths, corresponding to a case fatality rate of approximately 58%. Both viruses are neurotropic, capable of invading the central nervous system, leading to severe neurological disease and, ultimately, death. Research on these viruses is constrained by stringent biosafety requirements, creating a pressing need for surrogate systems that can accelerate vaccine and therapeutic development under safer laboratory conditions. To address this, we established pseudovirus-based platforms for both Rabies and Nipah, engineered using VSV-ΔG backbones expressing respective viral glycoproteins along with a reporter gene (luciferase). These pseudo-viruses are non-replicative, enabling safe handling under lower biosafety conditions. The rabies pseudovirus was validated using anti-rabies equine serum, demonstrating specific neutralization profiles and assay robustness. For Nipah, the pseudovirus was successfully generated and optimized, with neutralization assays performed using sera from immunized animal models to evaluate vaccine-induced and cross-neutralizing antibody responses. Multiplexed antibody assays were further integrated to allow simultaneous detection of antigen-specific responses. By integrating multiplexed antibody detection with pseudovirus neutralization assays, this dual-platform strategy offers a powerful tool for preclinical vaccine evaluation, antiviral screening, and immunological studies. Importantly, it provides a scalable, safe, and cost-effective alternative to live virus experimentation, expanding the scope of research beyond high-containment laboratories. This work establishes a next-generation serological platform for Rabies and Nipah, with direct implications for advancing vaccine candidate development against these high-priority viral threats.

Probiotic Fermented Milk Beverage Using Kokum: A Novel Approach for Microbial Therapeutics

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Abstract:

Probiotic fermented milk beverages have gained significant attention as functional foods due to their ability to support gut health, immunity, and overall well-being. Integrating kokum (*Garcinia indica*), an underutilized fruit rich in anthocyanins, hydroxycitric acid, and natural antioxidants, offers a promising approach to enhancing both the nutritional and therapeutic potential of such beverages. This study explores the formulation and functional evaluation of kokum-based probiotic fermented milk beverages. Kokum extract was incorporated into milk, followed by fermentation using selected probiotic strains such as *Lactobacillus rhamnosus* and *Lactobacillus plantarum*. The addition of kokum not only improved the sensory attributes—including color, flavor, and acidity balance—but also provided an excellent substrate for probiotic growth due to its bioactive compounds. The developed beverages demonstrated high viable cell counts (>10^7 CFU/mL), strong antioxidant activity, and enhanced stability during refrigerated storage. Overall, kokum-fortified probiotic fermented milk beverages represent a novel, natural, and consumer- friendly therapeutic option. Their combined probiotic and phytochemical benefits position them as valuable candidates for future health-promoting foods, especially in addressing oxidative stress, gut dysbiosis, and lifestyle-related disorders.

Plantaricin VN-25 from Probiotic Neera Isolate *Lactiplantibacillus plantarum* 1625: A Multifunctional Bacteriocin with Antimicrobial, Wound-Healing, and Anticancer Potential

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Abstract:

The emergence of multidrug-resistant (MDR) pathogens and drug-resistant cancers has intensified the search for safe, naturally derived bioactive molecules with broad therapeutic applications. This study reports the isolation, purification, and multifunctional evaluation of Plantaricin VN-25, a potent bacteriocin produced by lactic acid bacteria isolated from the traditional probiotic drink Neera. Plantaricin VN-25 a novel bacteriocin was produced by *Lactiplantibacillus plantarum* strain 1625 were purified and characterized. Multi-stage purification method was used, salt precipitation, organic solvent precipitation and purity was checked by Reversed Phase High Performance Liquid Chromatography (RP-HPLC) with retention time of 3min indicating the homogeneity of bacteriocin and was characterized by Liquid Chromatography-Tandem Mass Spectrometry (LC-MS/MS) with a molecular mass of 663 Da belongs to class II bacteriocins and amino acid sequence was determined by LC-MS and analyzed using ProtParam, yielding a composition of C-86, H-147, N-23, O-22, and S-2. Peptide's nominal mass and isoelectric point confirmed its cationic nature. Leucine was the most abundant residue, followed by Glycine, Alanine, and Methionine. Primary structure analysis using Pep Draw revealed hydrophobicity contributing +9.13 kcal/mol. Secondary structure prediction using I- TASSER and Alpha Fold v2 indicated alpha-helical content with high confidence. Tertiary structure modeling via TrRosetta revealed triple-stranded beta-sheets and a disulfide bridge, with a TM-score of 0. 412. Parallel screening of fish and waste samples from retail markets in Navi Mumbai revealed the prevalence of ESBL-producing E. coli harboring blaTEM, blaSHV, and blaCTX- M genes, displaying extensive resistance to β-lactams and other antibiotic classes. Plantaricin VN- 25 demonstrated remarkable pH and thermal stability, potent activity against ESBL *E. coli*, and enhanced fibroblast cell migration in vitro, comparable to ascorbic acid. These findings establish Plantaricin VN-25 as a promising biocontrol and wound-healing agent for combating antimicrobial resistance and promoting tissue regeneration PlantaricinVN-25 displayed dose-dependent cytotoxicity against HCT116 cancer cells, HCT116 cell lines, with an IC50 = 65.10 µg/ml approaching the effectiveness of standard chemotherapeutics. These results demonstrate that Plantaricin VN-25 are a promising dual-function therapeutic platform with antibacterial and anticancer potential.

Re-Evaluating Shankhpushpi's Anti-Aging Mechanism: A Study in *Paramecium* Suggests Non-Oxidative Pathways

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Abstract:

This study investigates the geroprotective potential of the traditional Ayurvedic herb Shankhpushpi (Convolvulus pluricaulis) using the ciliate-Paramecium as a model organism. Initially, a database was manually curated compiling plants, herbs, and phytochemicals known for longevity-enhancing or anti-aging properties. From this database, Shankhpushpi extract was selected for detailed study on cellular longevity. Our findings revealed that high doses of Shankhpushpi exerted toxic effects on Paramecium, while low doses significantly decreased generation time, indicating enhanced longevity. We also established that hydrogen peroxide is potently cytotoxic to Paramecium, causing complete cell death at concentrations as low as 0.05%. Importantly, co-treatment with Shankhpushpi did not confer protection against hydrogen peroxide-induced oxidative stress at any tested concentration. These results suggest that the anti-aging benefits of Shankhpushpi may not involve antioxidant mechanisms but are likely mediated through other, yet-to-be-elucidated pathways affecting cellular survival and replication. Future work will focus on uncovering these non-antioxidant mechanisms to better understand the therapeutic potential of Shankhpushpi in healthy aging

Evaluating the Efficacy of Alternative Medicine in the Evidence-Based Treatment of Uterine Fibroids: A Case Study

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Abstract:

Hysterectomy, the surgical removal of the uterus, is often performed due to conditions like uterine fibroids or cancer. Uterine fibroids are common benign tumors in women of reproductive age. While conventional treatments are effective, they can be costly and have side effects. This has led to growing interest in alternative approaches such as botanical medicines, dietary changes, and yoga. This study highlights individual and synergic botanical agents (*Bauhinia variegata* (Kanchnaar) *Boerhavia diffusa*, (Punarnava) *Emblica officinalis* (Amla), etc.) and polyherbal formulations (Kanchnaar Guggulu, Punarnava, Triphala, etc.) that have demonstrated anti-fibroid activity, based on evidence drawn from Ayurvedic text. Herein, a case of a 40-year-old woman with multiple uterine fibroid and ovarian polyp are presented. She undergone specific yoga, ayurvedic medicines, naturopathic therapy on a regular basis for three months. This resulted in highly significant reductions in the size of the fibroid and associated polyps. When first identified, uterus showed bulky in size, measured multiple intramural and subserosal fibroids within the uterine wall, primarily in the upper body, and also reported endometrial polyp, confirmed on the basis of ultrasonography images. Follow-up ultrasonography conducted 50 days after initiating treatment showed complete regression of all uterine fibroids and the endometrial polyp, indicating significant clinical improvement along with reduction of symptoms. The positive response highlights the potential effectiveness of natural, herbal, Ayurvedic, and naturopathic therapies as non-invasive approaches for managing uterine fibroids.

Omics Insights into Symbiotic Intelligence of *Serendipita Indica*, A Model Endophyte for Engineering Climate-Smart Agriculture

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Abstract:

Serendipita (*Piriformospora indica)*, a root-colonising endophytic fungus discovered in the Indian Thar Desert in 1998, has rapidly emerged as a key model for studying plant-host interactions. Exceptionally broad spectrum of hosts ranging from cereals, legumes, vegetables, fruits, medicinal herbs, forest trees, and even aquatic plants-sets it apart from most fungi with limited host preference. Colonisation by *S. indica* promotes plant growth, yield, nutrient acquisition, while fortifying immunity against diverse pests and pathogens. Additionally, it improves plant tolerance to extreme temperatures, drought, salinity, and heavy metal toxicity, thus finds utility in phytoremediation and soil health restoration. These multifunctional ecological and agricultural roles position *S. indica* as a key bioinoculant for climate-resilient sustainable agriculture. Advances in multi-omics technologies - genomics, transcriptomics, proteomics, and metabolomics - have decoded the symbiotic plasticity underlying its broad functionality. The compact ~24 Mb genome encodes a rich repertoire of secreted proteins, symbiotic effectors, carbohydrate-active enzymes (CAZymes), and transporters central to nutrient exchange and stress response. Integrated omics analyses reveal strategic programming of host signaling through transcriptional rewiring, hormonal crosstalk, metabolic modulation, transcription factor and small RNA mediated regulation, thereby enhancing plant-resilience and crop productivity. *S. indica's* ability to grow axenically, further enables precise molecular and functional characterization, while CRISPR/Cas-based genome editing and genome-wide association studies (GWAS) accelerate trait dissection and comparative evolutionary analyses. The convergence of omics, systems biology, and AI/ML-driven network modeling now strengthens effector prediction, interaction mapping, and predictive frameworks for microbiome engineering for precision agriculture. Collectively, these molecular, ecological, and computational insights underscore *S. indica's* transformative potential as a catalyst for omics-led "Evergreen Revolution" advancing the goals of climate-resilient, sustainable agriculture in "Viksit Bharat".

Green Synthesized Nanoparticles from Moringa, Neem, and Tulsi: A Sustainable Approach to Biocontrol and Plant Growth Promotion

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Abstract:

The green synthesis of metallic nanoparticles using plant extracts offers a sustainable, eco-friendly, and cost-effective alternative to conventional chemical and physical synthesis methods. This study focuses on three potent medicinal plants Moringa oleifera, *Azadirachta indica* (Neem), and *Ocimum sanctum* (Tulsi) as bio-reducing agents for the synthesis of silver (Ag), copper (Cu), and gold (Au) nanoparticles. These phyto-mediated nanoparticles exhibit potent antimicrobial properties and have demonstrated significant potential as biocontrol agents against various phytopathogens. Furthermore, their emerging roles in enhancing plant growth, akin to the functions of plant growth-promoting rhizobacteria (PGPR), are explored. The study also outlines recent advancements, challenges, and prospects for integrating these green nanoparticles into mainstream agricultural practices.

Study of Microbiota from Sweet Spices for Gluten Degradation and Probiotic Potential

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Abstract:

Gluten, a ubiquitous protein found in wheat and other cereals, is known to trigger celiac disease, wheat allergy, and type 1 diabetes in genetically predisposed individuals. The incomplete degradation of gluten by human digestive enzymes results in the accumulation of toxic peptides that elicit inflammatory and immune responses in the intestine. Therefore, microbial enzymes capable of degrading gluten are of great therapeutic importance for gluten-sensitive individuals. In this study, bacterial isolates were obtained from sweet spices and evaluated for their gluten-degrading potential. A total of sixteen bacterial isolates were screened, among which three promising strains—identified as *Bacillus cereus*, *Bacillus subtilis*, and *Pantoea cypripedii* demonstrated significant gluten hydrolyzing ability. The purified enzyme, referred to as glutinase, efficiently degraded gluten into smaller, non-toxic peptides. Enzymatic assays confirmed the catalytic efficiency and stability of glutinase under simulated gastrointestinal conditions. Moreover, the selected bacterial isolates exhibited notable probiotic attributes, including tolerance to bile salts and low pH, as well as antioxidant activity, suggesting additional health benefits beyond gluten degradation. These findings highlight the potential of spice-derived microbiota as a source of novel gluten-degrading enzymes and probiotic candidates. The study opens new avenues for the development of safe and effective therapeutic supplements for individuals suffering from celiac disease and other gluten-related disorders.

Development of Cost-Effective and Ecofriendly Microbial Growth Media Using Fruit and Vegetable Waste

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Abstract:

The high cost of conventional microbial culture media has led to growing interest in developing affordable and sustainable alternatives. Fruit and vegetable wastes, which are commonly discarded as household or market refuse, contain valuable nutrients such as carbohydrates and proteins that can support microbial growth. In this study, locally available waste materials including spinach leaves, cabbage residues, pomegranate peels, banana peels, and spoiled gooseberry were utilized to formulate alternative growth media. The media were tested for their ability to support the growth of bacterial isolates (*Escherichia coli, Pseudomonas spp., Bacillus spp., and Staphylococcus spp.)* and fungal species (*Aspergillus spp., Candida spp.)* under both agar and broth conditions. All tested microorganisms exhibited satisfactory growth, confirming the nutritional adequacy of the prepared media. Comparative analysis with standard selective media such as MacConkey agar, Dettol agar, and Czapek-Dox agar revealed similar morphological characteristics and growth patterns. These findings suggest that fruit and vegetable waste-based media can effectively replace conventional culture media for bacterial and fungal cultivation. This approach provides a sustainable, low-cost, and environmentally responsible solution for microbial research and routine laboratory applications.

Sustainable Production and Functional Health Properties of Herbal Fruit Wines

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Abstract:

Medicinal wine possesses therapeutic properties and is typically prepared by incorporating herbs and medicinal plants, hence referred to as herbal wine. Such formulations offer consumers numerous health advantages and can serve as functional foods. *Ficus carica* is rich in bioactive secondary metabolites such as flavonoids, furanocoumarins, anthocyanins, pectin, and phytosterols, which contribute to various health benefits. The "drumstick tree" (*Moringa oleifera*) is recognized for its exceptional nutritional value, containing phytosterols like stigmasterol, sitosterol, and kampesterol that act as hormone precursors. *Bryophyllum pinnatum*, also known as the air plant or miracle leaf, is renowned for its wound-healing and haemostatic properties. In this study, *Saccharomyces cerevisiae* isolated from fig fruit was used as the fermenting organism. The combination of *Moringa oleifera* and *Bryophyllum pinnatum* with *Ficus carica* fruit wine resulted in functional beverages with potential antioxidant, antidiabetic, and prebiotic properties. Herbal wines were produced in varying ratios based on herb and fruit concentrations and subjected to physicochemical, qualitative, and quantitative analyses. The alcohol yield was found to be 7.89%–8% across the formulations. Additionally, the herbal wines exhibited bactericidal activity against common foodborne pathogens (*Staphylococcus aureus, Pseudomonas aeruginosa*, and *Escherichia coli*) and showed prebiotic potential when tested with *Lactobacillus sporogenes*. The resulting formulations demonstrated a novel and functional product with enhanced sensory and health-promoting qualities.

Zn Resistance is Modulated by Five Homologous Ciar-Controlled Ccn sRNAs in *Streptococcus pneumonia*

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Abstract:

Zinc is a vital transition metal for *Streptococcus pneumoniae*, but is deadly at high concentrations. In *S. pneumoniae*, elevated intracellular free Zn levels result in mis- metallation of key Mn-dependent metabolic and superoxide detoxifying enzymes resulting in Zn intoxication. Here, we report our identification and characterization of the function of the five homologous, CiaRH-regulated Ccn sRNAs in controlling *S.pneumoniae* virulence and metal homeostasis. We show that deletion of all five ccn genes (ccnA, ccnB, ccnC, ccnD, and ccnE) from *S. pneumoniae* strains D39 (serotype 2) and TIGR4 (serotype 4) causes Zn hypersensitivity and an attenuation of virulence in a murine invasive pneumonia model. We provide evidence that bioavailable Zn disproportionately increases in *S. pneumoniae* strains lacking the five ccn genes. Consistent with a response to Zn intoxication or relatively high intracellular free Zn levels, expression of genes encoding the CzcD Zn exporter and the Mn-independent ribonucleotide reductase, NrdD-NrdG, were increased in the ΔccnABCDE mutant relative to its isogenic ccn $^{+}$ parent strain. The growth inhibition by Zn that occurs as the result of loss of the ccn genes is rescued by supplementation with Mn or Oxyrase TM, a reagent that removes dissolved oxygen. Lastly, we found that the Zn-dependent growth inhibition of the ΔccnABCDE strain was not altered by deletion of sodA, whereas the ccn + ΔsodA strain phenocopied the ΔccnABCDE strain. Overall, our results indicate that the Ccn sRNAs have a crucial role in preventing Zn intoxication in *S. pneumoniae.*

Phytochemical Profiling and Multifunctional Biological Activities of *Tridax procumbens* Extracts: A Comprehensive Evaluation

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Abstract:

The present study explores the potential medicinal and biological applications of *Tridax procumbens*, a traditionally used herb with well-known therapeutic properties. Plant samples were collected from the Dharmabad region of Maharashtra. The dried and powdered plant material underwent successive solvent extraction using a Soxhlet apparatus. Solvents such as water, ethanol, methanol, ethyl acetate, and hexane were selected based on a polarity gradient to ensure a broad spectrum of phytochemicals. The crude extracts were subjected to preliminary phytochemical screening to identify the presence of bioactive compounds, including alkaloids, flavonoids, saponins, tannins, and terpenoids. Further analyses were carried out to evaluate the biological activities of *T. procumbens* extracts. Antimicrobial activity was assessed using the disc diffusion method against selected bacterial strains to determine inhibitory potential. Anticancer activity was analyzed using the MTT assay on human cancer cell lines to evaluate cytotoxicity and cell viability. The antioxidant capacity was determined through the DPPH (2,2-diphenyl-1-picrylhydrazyl) radical scavenging assay, indicating strong free radical neutralizing potential. Additionally, the insecticidal and larvicidal efficacy of the extracts was tested against mosquito larvae to assess mortality rates at varying concentrations. Fourier-transform infrared spectroscopy (FTIR) was employed to characterize the functional groups and chemical constituents present in the extracts. The findings suggest that *Tridax procumbens* is a rich source of bioactive compounds with promising antimicrobial, anticancer, antioxidant, and insecticidal properties. This comprehensive study supports the pharmacological and therapeutic potential of *T. procumbens* and lays a foundation for future drug development and pest control applications.

Survival-Primed Evolution of p53–MDM2 Interaction in Hypoxia- Adaptive Rodents

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Abstract:

Our study investigates how the blind mole rat (Spalax), a hypoxia-adapted and cancer-resistant rodent, has evolved unique amino acid substitutions in its p53 transactivation domain (TAD1) and its regulator MDM2. Using phylogenetic and sequence analyses, these substitutions were found to be under positive selection and present in other hypoxia-adapted rodents, suggesting convergent evolution. Molecular dynamics and flexible docking demonstrated that the Spalax variants increase conformational rigidity in p53 and MDM2, restricting induced-fit motions and reducing their binding affinity, as confirmed by MM-GBSA calculations. This weakened interaction is predicted to expand the pool of transcriptionally active p53. Transcriptomic analysis of brain RNA sequencing data under hypoxia revealed upregulation of cell cycle arrest and survival genes (e.g., CDKN1A/p21, BCL-xL) and downregulation of few important hub genes of apoptotic activation pathway (eg. APAF-1). The findings suggest that these coevolved p53-MDM2 substitutions attenuate their interaction, fostering a survival-primed upregulation of active p53- a key adaptation enabling Spalax to thrive in chronic low-oxygen environments, with broader implications for understanding tumor suppression and hypoxia tolerance in mammals.

Novel Molecular Complex for Photoantimicrobial Therapy

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Abstract:

Antimicrobial Resistance (AMR) has become a critical global health threat, driving the need for alternative infection control strategies beyond conventional antibiotics. In this study, we investigated the efficacy of SHURAZ complex as novel photoantimicrobial agents, comparing their performance with free SHURAZ under various laser irradiation conditions (808nm, 915nm, Dual Laser). SHURAZ complex were prepared via thermal induction and characterized for their spectral properties, stability, and photostability. Their photoantimicrobial activity was evaluated against Escherichia coli, with bacterial viability assessed by spot plate and Alamar Blue assays, and mechanistic insights obtained through Reactive Oxygen Species (ROS) quantification, temperature measurements, and scanning electron microscopy (SEM). The results demonstrate that SHURAZ complex exhibit a pronounced red-shift in absorption (896 nm) and superior photostability compared to free SHURAZ. In antimicrobial assays, SHURAZ complex achieved complete bacterial eradication at lower concentrations (20 μM) and with less energy input than free SHURAZ, which required higher doses (30 μM) for similar effects. Dual wavelength irradiation further enhanced the bactericidal effect, with SHURAZ complex displaying synergistic photodynamic and photothermal action. ROS assays and thermal measurements confirmed that both oxidative and hyperthermic mechanisms contributed to bacterial killing. SEM analysis revealed severe membrane disruption in bacteria treated with complex and laser, supporting the combined mode of action. This work establishes SHURAZ complex as highly effective photoantimicrobial agents with distinct advantages over conventional SHURAZ, including improved stability, deeper tissue penetration, and dual-mode bactericidal activity. Their ability to achieve efficient bacterial killing at lower concentrations and energy doses positions them as promising candidates for clinical photoantimicrobial therapy, particularly in the context of rising AMR.

The Future of Bio-Signaling Molecules: Lipo-chitooligosaccharides

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Abstract:

Lipo-chitooligosaccharides (LCOs) are a unique class of bio-signaling molecules central to plant–microbe communication. These compounds, first discovered as Nod and Myc factors, are naturally produced by rhizobia and mycorrhizal fungi to establish symbiotic associations with plants. Structurally, LCOs consist of a chitin-derived oligosaccharide backbone linked to a fatty acyl chain, allowing them to specifically bind plant receptor kinases. Upon recognition, they activate intracellular signaling cascades that promote root hair deformation, nodule initiation, mycorrhizal colonization, and improved nutrient acquisition. Beyond symbiosis, LCOs play a crucial role in modulating plant immune responses, enhancing tolerance to abiotic stresses, and stimulating overall plant growth, making them promising molecules for sustainable agriculture. Advances in synthetic biology have revolutionized the study and production of LCOs. Through heterologous expression systems, This allows precision-controlled biosynthesis of LCO variants with defined structural and functional properties. Metabolic pathway engineering, promoter optimization, and CRISPR-based gene editing further enable increased yields and structural diversification of LCOs. Such synthetic biology approaches not only facilitate detailed functional studies but also support scalable biomanufacturing processes for commercial deployment. Bioreactor-based fermentation and downstream purification strategies are now being developed to enable cost-effective production of LCOs at industrial scales. These bio-signaling molecules hold significant potential as biofertilizer additives, biostimulants, and eco-friendly plant growth regulators. Harnessing LCOs through advanced biotechnology can redefine future agricultural practices by merging molecular precision with environmental sustainability.

Unveiling the Nexus Between Emerging Contaminants and Antimicrobial Resistance in Urban Wastewater

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Abstract:

Wastewater treatment plants (WWTPs) play a crucial role as both potential reservoirs and conduits of emerging contaminants (ECs). ECs such as pharmaceuticals (PHs) and microplastics (MPs) often persist through conventional treatment processes, fostering the development and dissemination of AMR. WWTPs serve as hotspots where bacteria are exposed to sub-lethal levels of antibiotics and chemical stressors, promoting horizontal gene transfer and the spread of antibiotic resistance genes (ARGs). This study aims to understand the correlation between MPs and AMR, which in turn can be used to improve wastewater treatment strategies. Influent and effluent samples from five WWTPs in the Pune region were analysed to study the correlation between MPs and antimicrobial resistance (AMR). MPs were extracted by the wet oxidation process and visualised under an optical microscope. PHs in the water samples were ascertained via LC-MS. Antibiotic-resistant bacteria (ARB) were isolated using a clinical concentration of seven antibiotics, including Tetracycline, Cefixime, Erythromycin, Imipenem, Kanamycin, Clindamycin and Ciprofloxacin. Of 78 resistant bacterial isolates obtained, 38 were isolated from WWTP inlet water samples and 40 were from effluent water, indicating poor ARB removal. Further, 18% of the total isolates exhibited resistance to both Cefixime, a third-generation cephalosporin, and Clindamycin, a lincosamide antibiotic. While there was no significant difference in the MP count, effluents had more particles of size <100 µm, suggesting fragmentation during treatment. Beyond size, the colour and size of MPs. These results highlight WWTPs as hotspots for EC transformation and AMR propagation, underscoring the need for improved treatment strategies. The persistence of emerging contaminants and antibiotic-resistant bacteria in WWTP effluents reveals the limitations of conventional treatment. The link between smaller MPs, residual antibiotics, and resistant isolates highlights the need for integrated monitoring and advanced treatment. A holistic approach is vital for effective wastewater management and public health protection.

Designing a Rapid PCR-Based Test Kit at Point-of-Care Detection of Antimicrobial Resistance

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Abstract:

Antimicrobial resistance (AMR) has emerged as one of the most pressing global health challenges, threatening the effectiveness of existing antibiotics and complicating the management of infectious diseases. Conventional antimicrobial susceptibility testing (AST) requires 24–72 hours to deliver results, forcing clinicians to rely on empirical use of broad-spectrum antibiotics often accelerating the spread of resistance. Rapid, accurate, and portable diagnostic tools are urgently needed to guide targeted therapy, particularly in low-resource healthcare settings. This project focuses on the development of a rapid, PCR-based molecular diagnostic kit designed for point-of-care detection of antimicrobial resistance genes directly from clinical specimens. The system employs multiplex real-time PCR with customized primers and TaqMan probes targeting blaCTX-M-15 and aac(6')-Ib-cr genes, which mediate resistance to β-lactams and fluoroquinolones/aminoglycosides, respectively. DNA was extracted using the HiGeno MB rapid extraction kit, allowing high-quality DNA recovery within 45 minutes. The optimized workflow enables simultaneous amplification and detection on portable qPCR platforms, producing interpretable results in under 60 minutes. Performance evaluation against conventional AST methods demonstrated 100% sensitivity and 87.5% specificity, validating the accuracy and reliability of the assay. The prototype integrates simplified DNA extraction, closed-cartridge amplification, and fluorescence-based detection within a compact, field-deployable unit. Identified challenges such as reagent stability, power limitations, and cost constraints are being addressed through the use of lyophilized reagents, solar-powered thermocyclers, and cost-effective modular designs. This study underscores the potential of rapid molecular diagnostics to transform AMR surveillance and clinical decision-making. By enabling precise detection at the point of care, this innovation could reduce unnecessary antibiotic use, improve patient outcomes, and strengthen antimicrobial stewardship initiatives in both urban and remote healthcare environments.

Phenotypic and Genotypic Analysis of the Blakpc-2-Producing *Pseudomona Aeruginosa* Isolates Collected from Tertiary-Care Hospitals in India

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Abstract:

Carbapenem-resistant *Pseudomonas aeruginosa* (CRPA) is a major cause of healthcare-associated infections, especially in intensive care units, where treatment options are increasingly limited. In India, resistance has been dominated by metallo-β-lactamases (MBLs), while, KPC-type carbapenemases have rarely been documented. Here, we provide the first nationwide report with phenotypic and genotypic characterization of blaKPC-2 positive CRPA collected from 16 tertiary-care hospitals across Pan-India between 2016 and 2019. Of 419 clinical isolates, indicated majority of carbapenem resistance isolates belonged to metallo- beta -lactamse producer class while ten (2.4%) harbored the blaKPC-2 gene. Isolates producing blaKPC-2 belonged to the globally disseminated, high-risk clone ST235. These isolates exhibited multidrug resistance with significant higher MIC for carbapenem and other beta-lactam antibiotics, and showed limited restoration of susceptibility to novel BL-BLI combinations, namely; ceftazidime/avibactam, imipenem/relebactam, and cefepime/taniborbactam. None of these combinations were prescribed during isolation period. Notably, only cefepime/zidebactam (combination that is undergoing USFDA Clinical Phase III) emerged as the sole agent to achieve complete activity across all isolates. Whole-genome sequencing revealed conserved mutations in regulatory genes; ampR, ampD, mexR, nalC, mexZ and truncation of OprD, implicating non-enzymatic resistance mechanisms in these KPC producing CRPA isolates. Time-kill assays demonstrated initial bactericidal activity of β-lactam/β-lactamase inhibitor combinations, but regrowth occurred within 24 hours, suggesting tolerance rather than resistance selection. The emergence of blaKPC-2 in ST235 P. aeruginosa in India signals a paradigm shift in the resistance epidemiology beyond MBL dominance, demanding a close monitor. These findings carry major implications for antimicrobial stewardship, surveillance strategies, and the urgent need for next-generation therapies to counter this evolving threat.

Surgical Site Bacterial Infection and Related Antimicrobial Resistance Pattern in Aurangabad City

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Abstract:

Surgical Site Infections (SSIs) are among the most common postoperative complications, significantly contributing to patient morbidity, prolonged hospital stay, and increased healthcare costs. The emergence of antibiotic-resistant bacteria has further complicated the management of these infections. A total no. of 150 clinical samples were collected from patients with suspected SSIs admitted to various surgical wards of Hospital, Aurangabad City. Samples were processed using standard microbiological techniques. Bacterial isolates were identified based on cultural, morphological, and biochemical characteristics. Antimicrobial susceptibility testing was performed using the Kirby-Bauer disk diffusion method as per CLSI guidelines. Among the isolates, *Staphylococcus aureus* was the predominant organism, followed by *Escherichia coli*, *Pseudomonas aeruginosa*, and *Klebsiella pneumoniae*. A significant proportion of S. aureus isolates were Methicillin-resistant (MRSA). Gram-negative isolates showed high resistance to β-lactam antibiotics but were more sensitive to carbapenems and aminoglycosides. The study highlights the predominance of multidrug-resistant bacteria in surgical site infections. Regular surveillance of antimicrobial resistance patterns and strict infection control measures are essential to reduce the incidence of SSIs and improve patient outcomes.

Material-Specific Bio interface Behavior of Two-Dimensional Nanomaterials in Cancer Models: In-Vitro and In-Silico Insights

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Abstract:

Two-dimensional nanomaterials are widely explored for application in targeted drug delivery, photodynamic therapy, bio sensing, and imaging. With their expanding therapeutic potential, it is critical to elucidate their interactions at biological interfaces to ensure both safety and clinical applicability. This study presents a comparative evaluation of Molybdenum Disulfide (MoS_2) nanosheets and Mg-Al Layered Double Hydroxides (LDHs), emphasizing biological stability, cytotoxicity, and cellular uptake in cancer models. Defect-rich MoS2 Nano sheets were synthesized hydrothermally, whereas Mg-Al LDHs were prepared by co-precipitation. Crystalline structure and phase purity were confirmed via HR-TEM, XRD, and XPS. Dispersion stability was systematically assessed across diverse biological and environmental media (BSA, natural organic matter, DMSO, RPMI, RPMI + FBS, and Type I water), following NaNoReg and NanoEcotox guidelines. Both nanomaterials demonstrated stable suspension in Type I water for up to 72 hours, as validated by DLS parameters (effective diameter, polydispersity, span, D10, and D90 values). ICP-MS analysis revealed a significant cellular uptake of Mo in HepG2 cells exposed to MoS2 nanosheets for 48 hours, compared to 1 hour. Significant cytotoxicity was observed at 500 mg/L ($p \leq 0.05$) in HepG2 and at 500–1000 mg/L ($p \leq 0.01$) in HL-60 cells. Flow cytometric apoptosis and mitochondrial permeability assays revealed no alteration of cellular morphology and no loss of mitochondrial permeability at clinically relevant concentrations. However, no substantial toxicity was detected at clinically relevant concentrations, indicating concentration-dependent biosafety. Computational docking revealed weak binding affinities to apoptotic proteins, implying dominance of non-apoptotic pathways in MoS2-induced toxicity at higher doses. In contrast, Mg- Al LDHs showed distinct internalization kinetics and induced alternative cytotoxic patterns, including subcellular perturbations indicative of organelle-specific stress responses. This study underscores the strong correlation between nanomaterial physicochemical properties, bioavailability, and biosafety. The findings highlight the necessity for material-specific assessments to advance the safe integration of 2D nanomaterials into cancer drug delivery and therapeutic strategies.

Extraction and Characterization of Microbial Laccases from Agrowastes and their Applications in Bioremediation

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Abstract:

In recent years, enzymes have gained great importance in Industries; laccases are one among them which are widely present in nature. Laccases are enzymes belonging to the group of oxidases. Oxidation of a variety of phenolic compounds, diamines and aromatic amines. Laccases catalyze the Laccases are the oldest and most studied enzymatic systems. These enzymes contain 15–30% carbohydrate and have a molecule mass of 60–90 kDa. These are copper containing 1,4-benzenediol: oxygen oxidoreductases (EC 1.10.3.2) found in higher plants and microorganisms. These are glycosylated polyphenol oxidases that contain 4 copper ions per molecule that carry out 1 electron oxidation of phenolic and its related compound and reduce oxygen to water. When a substrate is oxidized by a laccase, it loses a single electron and usually forms a free radical which may undergo further oxidation or non-enzymatic reactions including hydration, disproportionation, and polymerization. These enzymes are polymeric and generally contain 1 each of type 1, type 2, and type 3 copper centre/subunit where the type 2 and type 3 are close together forming a trinuclear copper cluster. Laccases are widely distributed in higher plants, bacteria, fungi, and insects. In plants, laccases are found in cabbages, turnips, potatoes, pears, apples, and other vegetables. They have been isolated from Ascomycetous, Deuteromycetes and Basidiomycetous fungi to which more than 60 fungal strains belong. The white-rot Basidiomycetes fungi efficiently degrade the lignin in comparison to Ascomycetes and Deuteromycetes which oxidize phenolic compounds to give phenoxy radicals and quinones. Laccases play an important role in the food industry, paper and pulp industry, textile industry, synthetic chemistry, cosmetics, soil bioremediation and biodegradation of environmental phenolic pollutants and removal of endocrine disruptors. These enzymes are used for pulp delignification, pesticide or insecticide degradation, organic synthesis, waste detoxification, textile dye transformation, food technological uses, and biosensor and analytical applications.

Compartment-Specific ROS Responses in Chloroplast and Mitochondrial Activity upon Targeted Perturbation of Either Organelle in *Chlamydomonas reinhardtii*

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Abstract:

Reactive oxygen species (ROS) act as a key signaling intermediate in plant metabolism, defense and stress adaptation. In the photosynthetic organisms, both chloroplast and mitochondria serve as a major hub of ROS production, thereby coordinating stress responses across cellular compartments. However, the extent of cross-organellar communication following the compartmentalized oxidative stress remains poorly understood. In the present study, we investigated whether the ROS generation in one organelle triggers any functional responses in the other organelle by externally inducing compartmentalized oxidative stress in chloroplast using Methyl viologen (MV) and in mitochondria using menadione (MD) in *Chlamydomonas reinhardtii*. Using compartment-specific roGFP imaging, we demonstrated that at sublethal drug concentration both MV and MD induce transient ROS production in the specific compartment without interfering with the other compartment. Comprehensive functional analyses using organelle morphology imaging, chloroplast photosynthetic performance (using Handy-PEA and 77K Spectroscopy) and mitochondrial respiratory rate (using Sea Horse analyzer assay) was performed to reveal the impact of ROS perturbation in one organelle on the activity of the other. We observed compartment-specific ROS production by MV and MD and the absence of cross-compartmental activity changes at sublethal drug concentrations. The absence of cross-compartmental functional interference highlights the organelle-specific redox homeostasis. This compartmentalized response may be attributed to the effective antioxidant buffering within each organelle, and it suggests that cross-organellar ROS signaling may require threshold levels of oxidative stress that exceed local antioxidant capacity or involve specific signaling mechanisms beyond localized ROS accumulation.

Isolation of Organophosphate Degrading Bacteria from Agricultural Soil and In-Vivo Analysis of Monocrotophos Degradation

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Abstract:

The extensive application of organophosphate pesticides (OPs) like monocrotophos (MCP), chlorpyrifos, and malathion in agriculture has led to their pervasive accumulation in the environment. Chronic human exposure to contaminated produce and water can cause severe health issues, including endocrine dysfunction, birth defects, and nervous disorders. This study aimed to isolate and characterize bacteria capable of degrading these OPs from a local cotton cultivation field. We isolated a bacterial consortium tolerant to MCP up to 2000 ppm. The consortia on 16S rRNA sequencing were identified as *Micrococcus luteus* SBR2, *Rhodococcus* SBR5, *Bacillus aryabhattai* SBR8, *Ochrobactrum intermedium* SBK2. In vitro assays demonstrated significant individual strain tolerance to MCP, chlorpyrifos, and malathion in the range of 500-5000 ppm. Gene screening revealed the presence of plasmid-borne opdA and mpd genes in *O. intermedium* and *B. aryabhattai*, while all strains harbored genomic opdA and mpd; the opd gene was not detected. In vitro HPLC analysis of individual strains incubated with each pesticide (MCP, chlorpyrifos, and malathion) showed complete degradation, indicated by the disappearance of the respective pesticide peaks. For in vivo validation with MCP, soil samples amended with the consortium showed complete MCP degradation within four weeks, as confirmed by HPLC. Subsequent GC-MS analysis identified non-toxic degradation products, including cyclotrisiloxane compounds and acetic acid. In summary, this consortium efficiently degrades multiple OPs in vitro, and its application successfully remediates MCP-contaminated soil in vivo, presenting a potent bioremediation strategy for pesticide-polluted agricultural soils.

Hispolon: A Green Bioactive Weapon Against *Candida* Biofilms

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Abstract:

Candida albicans develops intricate and robust biofilms that greatly increase its resistance to antifungal agents and lead to long-lasting infections. Conventional antifungals mainly synthetic or semi-synthetic often fail to deliver effective outcomes because of rising drug resistance, unintended interactions, and toxicity to the host. This makes the exploration of natural compounds an attractive, safer, and more sustainable strategy for addressing fungal diseases. Consequently, the search for environmentally friendly bioactive molecules with strong antifungal and anti-biofilm potential has become increasingly important. In this study, we investigated Hispolon, a naturally derived flavonoid, for its ability to inhibit *C. albicans* biofilm formation and virulence. Through in silico molecular docking, Hispolon was tested against two major virulence-related proteins HSP70 (PDB ID: 6CJJ) and SAP5 (PDB ID: 2QZX) both essential for adhesion and biofilm development. Hispolon showed notable binding affinities of 6.6 kcal/mol with HSP70 and 5.4 kcal/mol with SAP5, indicating its capability to disrupt adhesion processes and enzymatic pathways involved in biofilm formation. Overall, these results suggest that Hispolon is a promising, eco-friendly biofilm inhibitor and may offer a natural, sustainable approach for antifungal treatment. Further experimental and clinical research is needed to validate Hispolon as a potential next-generation therapeutic candidate for managing biofilm-associated Candida infections.

Isolation of Bacteriophages for Controlling Bacterial Phytopathogens from the Agricultural Fields of South Gujarat

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Abstract:

Crop productivity is facing the threat of bacterial diseases, whereas overuse of copper and antibiotics has led to resistance and environmental degradation. There is an urgent need to explore alternative and ecofriendly biocontrol agents. Bacteriophage, the bacteria eating virus, is an effective controller of bacterial population. This work was undertaken to isolate the bacteriophages against plant pathogenic bacteria. Phages act specifically against bacterial species, self- replicate at the site of infection, and are harmless to plants, animals, and humans. The studies entail isolating natural phages from agricultural fields and evaluating their lytic ability in-vivo for its future application as biocontrol agent. This work helps in reducing resistance and decreasing chemical dependency through providing a sustainable alternative to chemical treatments hence improving disease management techniques of resilient and sustainable crop production.

Development of Monobodies as Antibody Mimetic that Target DENV

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Abstract:

Monobody is a synthetic non-immunoglobulin customizable protein built using the fibronectin protein domain III (FN3) as a molecular scaffold. The advantages of monobody are their small size, low molecular weight, and lack of a disulfide bond, and hence, they are potential antibody mimetics. Among pathogenic diseases, Dengue is one of the most common. Dengue virus is a +ssRNA virus and has 4 serotypes. Dengue virus encodes a single polyprotein, which upon cleavage produces structural (Capsid protein(C), precursor membrane protein(prM), envelope protein(E)) and non-structural (NS1-NS5) proteins. The DIII domain of E-protein is the prime target of neutralizing antibodies. Therefore, we are trying to develop a monobody that targets specifically the DIII domain of the E protein of DENV. Here, we present the development and validation of a monobody that specifically targets the DENV serotype 2 using a combination of computational, structural, protein biochemistry, and molecular/cell biology approaches. My work is focused on the designing, expression, and functional evaluation of monobodies, a class of synthetic antibody mimetics. DENV remains a persistent global health challenge therefore we have specifically engineered monobodies to target the domain III (EDIII) region of the envelope glycoprotein E in all four serotypes of Dengue virus (DENV). Traditional antibodies have limitations such as high production cost, and batch to batch variability, this leads us to explore the alternative scaffolds. The fibronectin type III (FN3) domain acts as an ideal scaffold due to its structural similarity to antibody CDRs, robust bacterial expression, and flexibility to targeted mutational engineering. Monobody constructs library were designed by incorporating mutations within the BC, DE, and FG loops of the FN3 domain, aiming to study the contributions of individual loop in antigen recognition and binding. Constructs were cloned and expressed, using bacterial expression systems, and purified by affinity chromatography and size-exclusion chromatography. To study the antigen-binding properties we used western blotting, biolayer interferometry (BLI), and solution-phase nuclear magnetic resonance (NMR) spectroscopy, which enabled high-resolution mapping of the interaction surface and kinetic parameters of binding. Antigen binding data analysis of Biolayer Interferometry and NMR chemical shift revealed that incorporating all three BC, DE and FG engineered segments, consistently exhibited markedly superior affinities for DENV EDIII, pointing out the crucial residues involved in enhanced specificity. Site-directed mutagenesis further refined the monobody repertoire, and interactions were evaluated across all dengue serotypes. In conclusion, the present study not only establishes a robust platform for dengue-neutralizing monobodies but also laid the groundwork for a new generation of engineered therapeutic molecules applicable to other viral pathogens. The translational significance lies in the ability of these synthetic mimetics to combine high-affinity, and ease of production, thus offering an adaptable solution for rapid-response antiviral therapies in regions with endemic dengue and similar emerging diseases.

Reprogramming the Host T Cell Metabolism to Mitigate Tuberculosis Recurrence

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Abstract:

Tuberculosis (TB) is the most contagious infectious disease globally with a very high burden in low-income regions. The availability of modern synthetic therapeutic agents left behind ethnomedical therapy. However, these synthetic agents possess serious side effects and toxicity including the dampening of immune responses, thus making the host vulnerable to TB recurrence. Injudicious use of available antibiotics and treatment non-compliance may further worsen global TB statistics, leading to the emergence of Drug-resistant TB. Considering the rapid emergence of drug-resistant TB, it is highly imperative to develop a new method of therapy that minimizes these obstacles, which is needed to combat this deadly disease and prevent a possible future epidemic. Recently, we have demonstrated that a combination of antibiotics and an immunotherapeutic agent significantly enhances therapeutic efficacy, reduces the risk of generating drug-resistant variants, and mitigates hepatotoxicity. In this study, we demonstrate that the tetraterpenoid compound, Astaxanthin (ASX) exerts substantial modulatory effects on both the innate and adaptive branches of the host immune system. ASX polarises macrophages towards the M1 phenotype through the ERK/NF-kB signalling pathway, thereby enhancing M.tb phagocytosis and the secretion of pro-inflammatory cytokines. This activation subsequently elicits robust Th1 and Th17 responses, leading to effective bacterial clearance. Furthermore, ASX fortifies the Th1 central memory reservoir in the lungs, significantly diminishing TB reactivation and reinfection rates. Interestingly, LC-MS-based proteomics analysis of ASX-treated M.tb-specific CD4+ T cells deciphered that ASX upregulates glutaminase activity in CD4+ T cells, promoting glutamine catabolism, also evidenced by metabolomics. This metabolic reprogramming results in enhanced Th1 and Th17 responses, conferring long-term protection against TB recurrence. Furthermore, Astaxanthin (ASX) alone has shown substantial efficacy against MDR and XDR TB in murine models. Altogether, this study substantiates that ASX acts as a potent immunomodulator and, when administered alongside ATT, ASX can serve as an effective adjunctive treatment for both drug- susceptible and drug-resistant TB.

Occurrence of Drug-Resistant Microbes and Associated Resistance Genes in Potable Water Supplies of Solan City, Himachal Pradesh

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Abstract:

Water is life for every living organism on earth and everyone have right to get safe drinking water. But overcrowded population, industrialization, use of pesticides, insecticides and poor sewage disposing planning are responsible for water contamination and water pollution. In the present study we have analyzed the water quality of Solan city of Himachal Pradesh. From the 150 water samples collected, total 239 bacterial isolates were isolated and identified as *E.coli*, *Klebsiella* spp., *Salmonella enterica subsp enterica, Pseudomonas* spp., *Staphylococcus aureus*. All the isolates were screened for drug susceptibility using the Kirby-Bauer disc diffusion method. Out of 239 total bacterial isolates, 95 were found to be drug-resistant to at least one, two, or more antibiotics. High resistance pattern was noticed for *E. coli* followed by *Staphylococcus aureus, Klebsiella* spp., *Salmonella enterica,* whereas *Pseudomonas* spp. were sensitive for most of the antibiotics tested. Among all, 18 isolates of *E. coli* and 15 isolates of *Klebsiella* spp. were found multi-drug resistant while all other isolates of three genera were resistant either to one or two antibiotics. Proportion of drug resistance was found more threatening for water samples collected from MWDS followed by baories. E10 isolate of *E. coli* and K5 isolate of *Klebsiella* spp. were selected for MDR gene identification. *Klebsiella* spp. was found positive for the presence of blaSHV, bla KPC, tet32, and erm genes, while E. coli except for blaKPC was found positive for rest of the genes like *Klebsiella* spp.

From Lab to Field: Seed Nano-priming as a Novel Strategy for Enhanced Agricultural Productivity

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Abstract:

Global climate change, as well as other biotic and abiotic factors, severely impacts agriculture. Contemporary agriculture faces mounting pressures from environmental stressors and the rising food demand of a growing population. Nanotechnology offers a transformative solution to this universal challenge. Seed nano-priming involves treating seeds with nanoparticles before planting to enhance crop performance. This technique offers advantages over conventional seed treatments by utilizing the distinctive characteristics of nanomaterials, including increased surface reactivity and enhanced cellular penetration. The process stimulates specific biochemical pathways, promotes enzyme activation, and optimizes plant hormone regulation, resulting in improved germination rates and seedling establishment. Traditional seed enhancement methods provide a limited duration of benefit and insufficient protection against multiple stress factors. In contrast, nano-priming treatments can establish adaptive responses in plants, potentially improving their capacity to cope with drought conditions, soil salinity, temperature fluctuations, and contaminated environments. Despite its promises, current limitations include concerns regarding nanoparticle safety, the absence of standardized treatment procedures, insufficient field-scale testing, and unclear regulatory guidelines. Future research should emphasize the development of environmentally safe nanomaterials and the establishment of international regulatory standards. Nano-priming technology offers significant potential for improving crop performance while supporting the transition toward climate-resilient and resource-efficient agricultural practices. This study presents a comprehensive overview of the applications of nanoparticles in sustainable agriculture, providing valuable insights into their potential uses.

Nature's Pharmacy: Aloe Vera for the Fight Against Tuberculosis

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Abstract:

A long way we have already come, but a long way is still to be covered. The world has come forward in all terms, but diseases like Tuberculosis still hold the potential to take us back, especially when it comes to middle and low-income countries. TB's contribution to the world's mortality rate remains significantly high, compounded by the rise of multidrug-resistant (MDR) TB and the adverse side effects of commonly administered first-line drugs for the disease. Medicinal plants have been a cure for most diseases since time immemorial, and half of our population still relies on them. Regarded as the backbone of traditional medicine, they are now central to efforts to combat diseases. According to WHO estimates, about 80% of the population in developing and underdeveloped countries depend on traditional herbal or botanical medicines for their primary health care needs. India has a rich diversity of medicinal plants with over 3,500 discovered species. There has been an accelerating interest in phytotherapy, integrating natural products as complements to boost the treatment efficacy and to scale down the side effects. This review explores the possibility of Aloe vera as an adjunct in the TB treatment. It also assesses its potential synergy with first and second-line anti-TB drugs, examines its activity against multidrug-resistant TB, and evaluates its safety and pharmacokinetics. The aim is to critically study Aloe vera's contribution to anti-TB drug discovery and propose a roadmap for its integration into global TB control programs.

Antibiotic Resistance Profiling and Molecular Characterization of Multidrug – Resistant Enterobacteriaceae Isolates from Humans

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Abstract:

In this study, the emergence and rapid dissemination of antibiotic-resistant bacteria which represent a serious global health challenge were evaluated, Enterobacteriaceae, a diverse family of Gram-negative bacteria, are among the most common causes of hospital- and community-acquired infections and have shown increasing resistance to multiple antibiotic classes. This study aims to evaluate the antibiotic resistance profiles of human Enterobacterial isolates and to characterize multi-drug resistant (MDR) strains at the phenotypic and molecular levels. Clinical samples has been collected and subjected to bacterial isolation, followed by antimicrobial susceptibility testing using standard disc diffusion and minimum inhibitory concentration (MIC) methods. Isolates demonstrating resistance to three or more antibiotic classes will be categorized as MDR and further analyzed for the presence of resistance determinants, efflux mechanisms, and plasmid-mediated resistance. The outcomes of this study will provide insights into the prevalence and resistance trends among Enterobacterial pathogens, contributing to better infection control strategies and guiding the rational use of antibiotics in clinical practice. Ultimately, this research will strengthen surveillance efforts and offer valuable data for the design of targeted therapeutic interventions to combat antibiotic resistance.
In this study, the emergence and rapid dissemination of antibiotic-resistant bacteria which represent a serious global health challenge were evaluated, Enterobacteriaceae, a diverse family of Gram-negative bacteria, are among the most common causes of hospital- and community-acquired infections and have shown increasing resistance to multiple antibiotic classes. This study aims to evaluate the antibiotic resistance profiles of human Enterobacterial isolates and to characterize multi-drug resistant (MDR) strains at the phenotypic and molecular levels. Clinical samples has been collected and subjected to bacterial isolation, followed by antimicrobial susceptibility testing using standard disc diffusion and minimum inhibitory concentration (MIC) methods. Isolates demonstrating resistance to three or more antibiotic classes will be categorized as MDR and further analyzed for the presence of resistance determinants, efflux mechanisms, and plasmid-mediated resistance. The outcomes of this study will provide insights into the prevalence and resistance trends among Enterobacterial pathogens, contributing to better infection control strategies and guiding the rational use of antibiotics in clinical practice. Ultimately, this research will strengthen surveillance efforts and offer valuable data for the design of targeted therapeutic interventions to combat antibiotic resistance.

Efficient Bioethanol Production from a Scenedesmus–cyanobacteria Co-culture via Wet-Biomass Enzymatic Hydrolysis

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Abstract:

Among the simplest photosynthetic forms, microalgae such as Scenedesmus and cyanobacteria hold immense promise for sustainable energy. Their rapid growth, minimal nutrient requirements, and biochemical versatility render them ideal candidates for third-generation bioethanol production via wet-biomass processing. This study explored a wet-biomass route for third-generation bioethanol production using a Scenedesmus- Cyanobacteria co-culture. Five comparative treatments, control, autoclaved, acid, acid + enzyme, and enzyme-only, were designed to evaluate hydrolytic efficiency. Fermentation was carried out using an indigenous Saccharomyces cerevisiae K3 strain, and ethanol yield was estimated via the potassium dichromate oxidation method. The enzyme-only treatment, utilizing *Aspergillus niger* cellulase, achieved the highest yield (100.87 mg ethanol per 10 mL broth), outperforming acid-based processes, demonstrating superior saccharification and fermentation efficiency while eliminating energy-intensive drying and harsh chemical pretreatments. Each milligram of ethanol represented a fragment of a larger vision, a way to convert sunlight and simplicity into motion and meaning. The findings validate the concept of a cleaner, low-cost, and eco-efficient process for microalgal bioethanol generation. Furthermore, the use of co-cultures enhanced biomass recovery and sugar availability, offering an integrated model for sustainable fuel production. Building upon this foundation, future work will explore algal phenolics and extracellular polysaccharides as potential antibiofilm and antivirulence agents against Staphylococcus aureus and MRSA. By extending the same microalgal platform from biofuels to microbial therapeutics, this research seeks to reveal new dimensions of algal potential. Together, these efforts affirm that innovation can align with empathy, showing that the future of biotechnology lies not in dominating nature but in collaborating with it.

Poster Presentation

Poster Presentation

Hospital Wastewater Inorganic and Organic Pollutants as Chemical Drivers of AMR. An In Vitro Toxicity Assessment and Modulatory Actions on Biofilm Development

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Abstract:

Hospital effluents are a complex source of contamination, containing organic compounds, heavy metals, and pathogenic microorganisms that pose risks to aquatic ecosystems and their vitality. In this study, the chemical composition and biological effects of hospital wastewater collected during 2022–2023 in Aligarh City, India, were evaluated, focusing on its toxicity and its impact on biofilm production in Gram-negative bacteria. Different site-specific variations were recorded in pH, ionic content, salinity, and microbial load. ICP-AES was used for heavy metal analysis, and GC-MS was used to analyse contaminants in wastewater. The ICPAES revealed metals such as copper, cobalt, chromium, nickel, zinc, and Cd were measured, with copper showing the highest level (0.079 mg/L) at Site 1. GC–MS analysis of dichloromethane (DCM) extracts revealed alkanes, fatty acids, esters, and phthalate derivatives. The phytotoxicity test on V. radiata seedlings showed up to 75% growth reduction and oxidative stress at a 25% effluent concentration, and was confirmed by CLSM stained with propidium iodide. Genotoxicity assessment via plasmid-nicking at Site 1 showed a high conversion of supercoiled DNA to open circular DNA. High DCM extract levels reduced bacterial survival rate (4.1–8.3 $\log_{10}$ CFU/mL). Heavy-metal tolerance ranged from 50 to 800 µg/mL, and sub-inhibitory concentrations (≤ MTC/8) notably promoted biofilm development, while higher doses reduced biomass. Microscopic evaluation using SEM and CLSM confirmed these biofilm trends. The findings indicate that even low levels of pollutants can trigger stress-induced biofilm formation and may help sustain resistant bacterial populations. The detected chemicals and some organic pollutants are known to exert selection pressure on resistant bacteria, and biofilm development can provide a mechanism for survival. Therefore, in addition to their ecotoxicological effects, these chemicals can also drive AMR. However, regular evaluation and treatment of hospital effluents are crucial to reduce ecological harm and protect public health.

Poster Presentation

Nanotechnology: A Novel Approach to Combat Antibiotic Resistance

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Abstract:

Global public health is seriously threatened by the upsurge of drug-resistant microorganisms, which significantly limits the therapeutic options in infectious diseases. The antibiotic resistance is primarily influenced due to lack of new and effective antimicrobial agents for harboured or inherited resistomes as well as overuse and misuse of existing ones, although other factors like environmental stress (such as the build-up of heavy metals), unsanitary surroundings, unawareness, and scarce financial resources also play major roles. The standard and conventional treatment options are lagged behind the rapid emergence of antibiotic- resistant bacteria, leading to infection persistence and spreading, novel strategies are fundamentally necessary in order to avoid critical health issues. There are several ongoing studies exploring the alternatives to combat AMR, such as bacteriophages, antimicrobial peptides, nanotechnology etc. The cutting-edge technology of utilising nanoparticles, focused on manipulating materials at the nanoscale, has emerged in the medical field by offering new approach to combating infectious diseases. Nanoparticles can be engineered to target specific biosynthetic and enzymatic pathways to penetrate bacterial membranes and function as antibiotic delivery systems (nanocarriers) or exhibit intrinsic antibacterial properties. Also, their encapsulation properties protect antimicrobial agents from degradation and allow for controlled drug release. The subcellular size of nanoparticles enables higher intracellular uptake of the drug which results in the reduction of the concentration of free drugs, reducing their toxic effect. Additionally, their small size and distinctive physical traits enable them to effectively target and dismantle biofilms, which are commonly associated to resistance development. Nanoparticles have demonstrated the ability to inhibit biofilm formation and disruption of established biofilms, which leads to membrane damage and reduced viability of the bacteria. Further understanding of this technology is vital for developing effective treatments and regulatory policies to mitigate critical health concerns due to antibiotic resistance.

The Synergistic Effect of Conventional Antibiotics and Antimicrobial Peptides (AMPs) in Ciprofloxacin Resistant *Escherichia coli* Strains

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Abstract:

Escherichia coli (*E. coli*) is the leading cause of urinary tract infections (UTIs) worldwide. Antimicrobial Resistance (AMR) associated with UTI poses serious public health concerns. The decline in the development of new antimicrobial drugs and misuse of last-resort antibiotics have worsened the AMR crisis in E. coli infections. The inappropriate clinical use of ciprofloxacin over the past three decades has further intensified this issue, emphasizing the urgent need for new antimicrobial therapies. Antimicrobial peptides (AMPs) are promising alternatives to traditional antibiotics because they offer broad-spectrum activity against various pathogens and are less likely to induce resistance. Previous laboratory adaptation experimental studies revealed that microbial strains evolved resistance to AMPs at a slower rate and required higher fitness costs. AMPs are characterized by net positive charge, high hydrophobicity, and amphiphilicity, contributing to their rapid killing at micromolar concentrations. This study aims to investigate the synergistic effect of conventional antibiotics and AMPs against clinical ciprofloxacin (Cip)-resistant *E. coli* strains. The antibacterial effects of AMPs, including Batroxicidin, Crotalicidin, and Latarcin-2a, were assessed against ciprofloxacin-resistant *E. coli* isolates. All AMPs demonstrated low minimum inhibitory concentration (MIC) of 8µg/mL, whereas ciprofloxacin exhibited MIC values from 16-128µg/mL. Furthermore, a checkerboard assay was conducted to assess the synergistic effect of ciprofloxacin with AMPs. The results showed that the MIC of ciprofloxacin decreased fourfold when compared to ciprofloxacin alone, indicating an additive effect with a fractional inhibitory concentration index (FICI) between 0.5-0.8. Finally, combination of ciprofloxacin, AMPs, and carbonyl cyanide 3-chlorophenylhydrazone (CCCP, efflux pump inhibitor) significantly reduced MIC of Cip to ≤ 0.001µg/mL. Our findings reveal that there is synergistic effect of Cip, AMPs, and CCCP. Thus, the observed resensitization of resistant E. coli strains to ciprofloxacin is mostly due to reduced efflux pump activity caused by CCCP that improves ciprofloxacin's intracellular retention.

Poster Presentation

Bacteriophages Targeting ESKAPE Pathogens: A Potential Strategy Against AMR

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Abstract:

The global rise of multidrug-resistant (MDR) pathogens poses a critical challenge to antimicrobial therapy. The presence of resistance determinants such as metallo-β-lactamases and carbapenem-hydrolyzing oxacillinases enables these pathogens to survive even in the presence of last-resort antibiotics. In this study, we screened multiple bacteriophages against *Acinetobacter baumannii*, *Escherichia coli*, and *Klebsiella pneumoniae* for the selective targeting of MDR pathogens. A diverse set of MDR isolates was used for bacteriophage screening, and the identified phages were subsequently purified and sequenced. We confirmed the strong lytic activity of these bacteriophages against MDR pathogens, along with their tolerance to a wide range of pH and temperature conditions. The ability of these phages to reduce bacterial growth and achieve targeted killing suggests their potential use in treating MDR infections where conventional antibiotics are ineffective. This work establishes a strong foundation for targeting these ESKAPE pathogens using bacteriophage-based approaches.

Poster Presentation

Genome-Resolved Metagenomics of House Floors with Phylogenomic Insights into the Origin, Resistome, and Virulence of *Escherichia coli* Strains

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Abstract:

Metagenome-assembled genomes (MAGs) deliver high-resolution insights into the diversity and metabolic capabilities of microbes inhabiting built environments. Through the analysis of 90 house floor metagenomes, 2304 dereplicated MAGs were reconstructed, including 662 genomes of high quality and 75 near-complete drafts possessing comprehensive rRNA and tRNA marker sets. Taxonomic classification using GTDB-Tk identified 300 unique species, while over half the MAGs remained unclassified at the species level, revealing substantial genomic novelty within indoor microbial communities. Notably, rare and phylogenetically distinct taxa such as Candidatus Kapabacteria, Sumerlaeota, and members of Abditibacteriaceae were observed, representing previously uncharacterized lineages from domestic environments. Functional annotation revealed an extensive repertoire of carbohydrate-active enzymes, with glycoside hydrolase (GH13, α-amylase family) and glycosyltransferase (GT2, family 2) modules being the most prevalent, suggesting widespread potential for starch degradation and polysaccharide biosynthesis among floor-associated microbes. Auxiliary Activity (AA) enzyme families were enriched in MAGs related to the Pseudomonadota phylum, indicating considerable redox capabilities and adaptation to detergent- and pollutant-exposed surfaces typical of house settings. Antimicrobial resistance gene (ARG) profiling detected 196 unique genes distributed across 440 MAGs. Among these, 49 clinically relevant ARGs—including resistance determinants to β-lactams, aminoglycosides, macrolides, tetracyclines, and chloramphenicol—were found in 130 genomes, highlighting a potential reservoir for the persistence and spread of clinically important resistance traits indoors. Pathogenic taxa were also present, including several Escherichia coli lineages related to both pathogenic and commensal groups, as confirmed by phylogenomic analysis and virulence trait profiling. Collectively, this genome-resolved study recasts the house floor microbiome as a dynamic reservoir housing novel environmental lineages and multiple clinically significant strains bearing virulence and resistance features.This work is funded by project “A Comprehensive Approach to Addressing Antimicrobial Resistance (AMR), Grant Id: MMP075202.”

Poster Presentation

Actinomycetes: An Emerging Tool for the Development of Antibiotics

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Abstract:

Antibiotic resistance is becoming a severe global problem. Therapeutics with novel chemical scaffolds and modes of action are urgently required to address infections caused by multidrug resistant pathogens such as bacteria, fungi, and viruses. The discovery of new natural compounds remains a critical step in the development of novel antibacterial drugs. The rapid growth of drug-resistant infections highlights the critical need for continued research into actinomycetes as a sustainable supply of next-generation antibiotics. Actinomycetes are among the most promising bacteria for producing antimicrobial chemicals; they are responsible for about two-thirds of all clinically used naturally derived antibiotics. These filamentous bacteria, which primarily belong to the genus Streptomyces, have a remarkable metabolic variety that allows them to produce a broad range of bioactive secondary metabolites with antiviral, antifungal, and antibacterial properties. Systematic isolation, morphological and molecular characterization, fermentation condition optimization, and activity screening against pathogenic strains are all part of the investigation of actinomycetes for the manufacture of antimicrobial compounds. Combining actinomycete-derived antimicrobials with existing antibiotic may prolong drug effectiveness and overcome resistance. The manufacturing of antibiotics stimulates innovation in the fields of microbiology, biotechnology, and pharmaceuticals. It's likely that genetically engineered bacteria will be used in the synthesis of antibiotics in the future to create new medications more quickly and sustainably. The world health gap can be closed and the death rate from treatable infections decreased by making investments in the development of antibiotics that is both affordable and scalable. This work summarizes antibiotic compounds isolation and analysis from microorganism. Strengthening collaborations between academia, industry, and healthcare systems is crucial to bring novel compounds from the lab to clinical use.

Poster Presentation

How Does *Toxoplasma gondii* Influence the Brain and Body? – A Systematic Review Using PRISMA Framework

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Abstract:

Toxoplasma gondii is an obligate intracellular, neurotropic protozoan parasite that can infect almost all warm-blooded animals, including humans. When infection becomes chronic, it leads to the formation of latent cysts mainly in neural and muscular tissues. Growing evidence shows that Toxoplasma gondii influences host neurochemistry, immune responses, and systemic physiology, which may cause changes in brain function and behaviour. This systematic review aimed to gather and synthesize evidence on how Toxoplasma gondii infection affects the host's brain and body, encompassing molecular, neurological, behavioural, and systemic effects. Following PRISMA 2020 guidelines, literature searches were performed in PubMed, Scopus, Web of Science, and Google Scholar (up to October 2025). Keywords used included "Toxoplasma gondii," with "neuroinflammation," "host behavior," "neurotransmitters," and "systemic effects." Inclusion criteria comprised experimental, clinical, and epidemiological studies on humans or animals connecting T. gondii infection to neural or systemic outcomes. Exclusion criteria involved case reports lacking mechanistic data or reviews without primary evidence. Screening process: 2,146 records identified → 164 records screened → 57 studies included Results. Evidence shows that T. gondii affects brain and body functions through several mechanisms: Vertical Transmission: Toxoplasmosis is a potential sexually transmissible infection (Tong HW et al., 2023). The infection influences dopamine and GABA pathways, which may affect behavior and risk-taking (Prandovszky et al., 2011). Neuroinflammation & Glial Activation: Ongoing microglial activation and cytokine release lead to subtle changes in cognition and emotion (McConkey et al., 2013). Behavioral Links: Epidemiological data associate Toxoplasma gondii seropositivity with altered reaction times, mood disorders, and sometimes schizophrenia-like conditions (Flegr et al., 2014). Systemic Impact: Outside the brain, T. gondii infection changes immune and endocrine responses, affecting inflammation, metabolism, and cardiovascular health during chronic stages (Kumar V et al, 2014) (Vasudevan A, Kumar V et al., 2015) Toxoplasma gondii affects the brain and body through various neurochemical, immune, and behavioral pathways. Understanding these interactions is essential for creating interventions for vulnerable groups, particularly those who are immunocompromised.

Production of Naringinase Enzyme by Bacterial Strain and Its Applicability for Debittering of Fruit Juice

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Abstract:

Naringinase (E.C.3.2.1.40) is a kind of glycosidase that catalyzes the biotransformation of naringin into naringenin. Total 52 bacterial isolates were isolated from citrus waste and rhizospheric soil of different plants. Out of these isolates, 14 isolates showed ability for break down of naringin and zone of hydrolysis was observed. Among these, isolate no. PS8 showed maximum zone of hydrolysis (25 mm). Total flavonoid and naringin content of different isolates. Maximum production of Naringinase enzyme (89.3 U/ml) was showed by PS8 isolate by solid state fermentation process using substrate sugar cane baggases as compared to other substrates like rice straw and orange peel etc. To increase production of Naringinase, optimization of culture conditions was carried out by OFAT and statistical analysis was carried out by Plackett-Burman Design (PBD) and Response surface methodology (RSM). The mature fruit juice was taken and naringin content before and after enzyme treatment was carried out by Davis method. The enzymatic debittering of sweet lime juice using Naringinase enzyme produced by bacterial isolates PS8 shows maximum decrease of naringin was obtained at Naringinase concentration of 1.0 µg/100ml with incubation time of 3 hrs at room temperature (30˚C).

Poster Presentation

Biochemical Profiling of Marine Cyanobacterial Strains

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Abstract:

Cyanobacteria, also formerly called “blue-green algae”, are photosynthetic prokaryotes with ~3500 million years of existence on the planet earth. In the last decade, Cyanobacteria have been in the center of interest as a rich and sustainable source of highly valuable natural products and bioactive compounds. In this present study, four marine water cyanobacterial strains, namely AP20 (GQ355490), AP25 (Leptoelongatus litoralis, EU908684), AP17 (Oxynema aestuarii, FJ847842) and AP 3b (Aerofilum fasciculatum, FJ847843) have been used for study. Different biochemical constituents of the strains were analyzed and comparative qualitative analyses of different enzyme activities were done in this study. The quantitative analyses of the cyanobacterial strains revealed the presence of catalase, urease and amylase enzymes, along with some bioactive compounds, such as phycobiliproteins, neutral carbohydrates, and chlorophylls, which were species-dependent and detected in variable amounts in the sample extracts. The analysis showed that AP20 contains maximum amount of total carbohydrate, total lipid and phycobiliprotein content but minimum amount of chlorophyll content. Maximum amount of total protein was observed in AP3b. AP25 showed higher amount of chlorophyll content than others. On performing the qualitative biochemical tests, all four marine cyanobacterial strains demonstrated comparable levels of distinctive catalase, amylase and urease activity. For Triple Sugar Iron(TSI) test, it was observed that only one sample (AP17) was able to ferment glucose and the other three samples generated negative result for sugar fermentation while all four samples were positive for H2S production. Only AP20 exhibited phosphate solubilization for pikovskaaya agar test. All four samples were observed to be negative for the oxidase and gelatin hydrolysis tests.

Poster Presentation

Metagenomic Insights into Urban and Rural Freshwater Microbiomes: Diversity, Pathogen Risks, and Antimicrobial Resistance

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Abstract:

Water is one of the crucial natural resources, to an extent that global concerns suggest future conflicts could arise over its scarcity. Water is a recyclable resource, but its availability is limited, leading to a widening gap over time between its supply and demand. Freshwater lake or pond ecosystems are among the most valuable and heavily utilized natural systems, providing resources to millions around the globe. Besides being vital for natural life forms, these water bodies are central to various ecological, economic and cultural human activities, and are undergoing rapid shifts due to multiple environmental and anthropogenic pressures. To investigate how anthropogenic activities shape microbial community composition and functional potential, we analyzed 61 lake and pond water samples collected from Urban and Rural regions. The study explored microbial diversity, potential pathogens, antibiotic resistance and virulence genes, and reconstructed metagenome-assembled genomes (MAGs) to assess the ecological and functional status of these freshwater bodies. Phylum-level analysis revealed a reciprocal abundance pattern between phylum Cyanobacteria and Proteobacteria, which were the most dominant phyla with 59.58% and 39.08% abundance respectively. Many members of Candidatus Radiata Phyla (CRP), the uncultured bacteria, were also reported. Species level diversity did not differ significantly between rural and urban settings; however, the presence of harmful algal blooms, primarily Microcystis aeruginosa, contributed to a reduced diversity across these waterbodies. Environmental factors such as pH, temperature, copper and phosphate significantly influenced diversity. Pathogens such as Vibrio cholerae (Rural), Aeromans veronii (both regions) were detected, with a higher prevalence of gut-associated bacteria in rural samples. ARGs diversity was closely linked to the presence of gut bacteria, with aminoglycoside, beta- lactam, macrolide, MDR drug classes being predominant. More than 3,000 high- and medium quality MAGs were reconstructed from the metagenomic data with more than 80% classified only up to the genus level. Overall, this study provides an integrative view on how environmental and human-driven factors alter the microbial ecology and functional landscape of urban and rural freshwater systems. Such knowledge is critical for susutainable water management approach and for preserving microbial functions crucial for ecosystem balance.

Poster Presentation

Functional Characterization of LPMO from Bacterial Endophytes of Medicinal and Aromatic Plants

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Abstract:

Endophytic and pathogenic microbes associated with medicinal and aromatic plants (MAPs) play crucial roles in influencing plant growth, defence, and overall health. These microorganisms produce lytic polysaccharide monooxygenases (LPMOs), a class of copper-dependent enzymes that oxidatively cleave polysaccharides such as cellulose/chitin. Endophytic LPMOs are proposed to facilitate mutualistic interactions by promoting nutrient exchange and enhancing plant defence mechanisms, whereas pathogenic LPMOs assist in host invasion and disease establishment. Understanding the structural and functional diversity of these enzymes is essential to elucidate their roles in maintaining the balance between plant protection and infection. In this study, a LPMO AA10 protein from Serratia marcescens (PDB ID: 2BEM) was used as a reference to identify and compare homologous enzymes from bacterial endophytes associated with MAPs. The LP1 protein, selected from Bacillus cereus, was analysed for its sequence, structure, and functional characteristics. Phylogenetic analysis indicated that LP1 closely relates to chitin-active LPMOs within the AA10 family. SignalP 6.0 predicted a Sec-type signal peptide of 23 amino acids, suggesting secretion via the classical pathway. InterPro analysis classified LP1 under the IPR004302 family (cellulose/chitin-binding, N-terminal domain). Protein–protein interaction analysis of LP1 in STRING showed it interacts strongly with endo- and exo-chitinases, supporting its role in extracellular chitin degradation. Structural modelling using AlphaFold 3 (ipTM/pTM = 0.96, pLDDT > 90) and alignment with 2BEM confirmed the conservation of copper-binding residues (His1, His85) in LP1 and chitin-recognition motifs (TAXH) in the L2 loop region. These findings strongly indicate that LP1 functions as a chitin-active LPMO AA10 enzyme. Cloning and expression studies of LP1 are ongoing for further biochemical validation.

Poster Presentation

Interactions Between Host Immune Modulation and Antibiotic Resistance in *Helicobacter pylori*

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Abstract:

Helicobacter pylori is a prevalent pathogen responsible for causing chronic gastritis, peptic ulcers, and gastric cancer. It is a Gram-negative, S-shaped, or helical microaerophilic bacterium belonging to the genus Helicobacteraceae. Its pathogenesis is driven by a multifaceted set of virulence factors, including CagA, VacA, and urease, which promote mucosal colonization, subvert host immune responses, and sustain chronic inflammation. Despite its global prevalence, the mechanisms by which *H. pylori* modulates host immune responses to persist and simultaneously develop antibiotic resistance remain incompletely understood. Chronic infections create a dynamic host-pathogen interface, where immune invasion strategies may contribute to bacterial survival and reduced susceptibility to standard eradication therapies. This study aims to elucidate the interactions between host immune modulation and the emergence of antibiotic resistance in *H. pylori*. By manipulating cytokine signalling, altering macrophage polarization, and inducing regulatory T-cell responses, H. pylori creates a tolerogenic microenvironment that enhances bacterial survival. These immune evasion strategies reduce bacterial clearance, prolong infection, and indirectly promote the emergence of antibiotic-resistant subpopulations. Persistent bacterial survival under immune pressure facilitates adaptive mechanisms such as efflux pump activation, biofilm formation, and stress-response gene expression, which contribute to decreased susceptibility to standard eradication therapies. This study elucidates the interplay between host immune modulation and the emergence of antibiotic resistance in *H. pylori*, providing critical insights into persistent infections and therapeutic failures. Targeting both bacterial virulence factors and the host immune pathways they manipulate may provide innovative strategies to enhance eradication efficacy and reduce the development of resistant strains. This integrative perspective underscores the importance of considering host–pathogen crosstalk in designing next-generation interventions for *H. pylori* infections.

Poster Presentation

Identification and Immunogenicity Assessment of Protective Epitopes in *Vibrio alginolyticus* ATCC 17749

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Abstract:

Vibrio alginolyticus is an opportunistic marine pathogen that causes severe vibriosis in aquatic species and occasional zoonotic infections in humans, leading to significant aquaculture losses and public health concerns. Despite advances in antimicrobial therapy, the rapid emergence of multidrug-resistant (MDR) strains and the limited availability of effective vaccines underscore the need for alternative control strategies. This study aimed to identify and evaluate potential vaccine candidate genes in V. alginolyticus using an integrative approach combining reverse vaccinology and immunoinformatics analyses. The complete proteome of V. alginolyticus ATCC17749 was retrieved from NCBI databases, and computational pipelines were implemented for subcellular localization, transmembrane topology, and antigenicity screening. Surface-exposed, non-toxic, and non-allergenic outer membrane and secretory proteins with high antigenicity scores were shortlisted for epitope prediction. Cytotoxic T lymphocyte (CTL), helper T lymphocyte (HTL), and B-cell epitopes were identified using NetMHCpan 4.1, IEDB, and ABCpred servers, respectively. Immune simulation predicted robust humoral and cellular immune responses. This study demonstrates that integrated computational vaccinology can efficiently reveal promising antigenic targets for V. alginolyticus, laying a foundation for the rational design of next-generation polyvalent vaccines against Vibrio infections in aquaculture and beyond.

Poster Presentation

Isolation and Screening of Potential PET Degrading Microorganisms from Bhalswa Landfill Soil Samples

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Abstract:

Plastic such as Polyethylene terephthalate (PET) is one of the most widely used plastics in bottles and packaging, which is non-biodegradable. Over 350 million tons of plastic waste are produced annually, with polyethylene terephthalate (PET) accounting for a significant portion, around 70 million tons each year. Accumulation of such plastic waste has become a major ecological concern that affects both terrestrial and aquatic ecosystems. Conventional disposal methods such as landfilling and incineration cause secondary pollution via emission of volatile organic compounds (VOCs), nitrogen oxides, and sulphur oxides. Our present study aims to isolate and identify potential PET-degrading microorganisms from soil samples collected from the Bhalswa landfill site, Delhi. A total of forty microbial isolates were obtained and screened using Mineral Salt Medium (MSM) supplemented with Polyethylene glycol (PEG) as the sole carbon source. Among these, ten isolates exhibited significant growth on PEG-containing media, indicating their potential for plastic degradation. PET degradation efficiency was assessed by incubating pre-weighed PET beads (1%) with individual isolates for 15 days, followed by determining residual PET weight to calculate biodegradation. Among the isolates tested, one isolate demonstrated the highest PET-degrading ability, recording 22.5% degradation, while another isolate showed 10.76% degradation. These isolates were further subjected to detailed morphological and biochemical characterization. The results highlight the biodegradation potential of naturally occurring landfill microbes and support their future application in sustainable bioplastic recycling and environmental bioremediation.

Poster Presentation

Unveiling Novel CRISPR-Cas Systems: Insights from Lake Reservoir Metagenomes

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Abstract:

CRISPR-Cas is an adaptive immune system found in bacterial and archaeal systems to prevent invasion from phages or other viral substances. With rising advancements in genome editing technologies, the requirement for new CRISPR-Cas systems has alarmingly increased. In search for such novel CRISPR-Cas systems, exploration of new sites is crucial. Therefore, in our research we have focussed upon lake microbiome to find new CRISPR-Cas systems through in-silico analysis. 3862 metagenomic assembled genomes (MAGs) from lake microbiome were selected for further studies. CRISPRCasTyper tool classified the MAGs data into the types and subtypes of CRISPR-Cas systems. Our research interest lied on Class II systems, specifically on Type II and Type V Cas proteins because of the requirement of single effector protein for interference. Therefore, for these Class II systems, locus architecture was analysed and complete systems were selected. Multiple sequence alignment and domain analysis gave further structural insights for our proteins. Along with this, RNAFold utilised the repeat sequence information and predicted the structures. At last, spacer analysis was done through CRISPRTarget which provided an insight on PAM sequences and also gave information regarding the types of phages/viruses affecting the microorganisms residing in lake. All this information led to identification of novel CRISPR-Cas systems with a possibility for genome editing applications in future. Therefore, with our research work, it expands the understanding of CRISPR diversity in aquatic microbial ecosystems and helps in discovering new CRISPR-Cas systems with unique structural and functional properties.

Poster Presentation

CRISPR Cas System Diversity in Indian House Microbiome

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Abstract:

CRISPR Cas systems are RNA guided endonucleases that have been repurposed for genome editing and can be used to target gene of interest. Among the diverse CRISPR Cas systems available, spCas9 form Streptococcus pyogenes is the most widely used system for this purpose but using spCas9 poses some limitations such as the large size of the protein, PAM constraint and off-target effects. To overcome these challenges naturally occurring Cas9 orthologs are being identified from the ever-increasing microbial genomic and metagenomic data. In this study we aim to identify novel Cas9 from in-house available floor metagenomes. A total of 2393 metagenomes were analysed for the presence of different CRISPR Cas systems. CRISPR Cas systems were abundantly present in these metagenomes including Class 1 and Class2 systems. Among all the CRISPR Cas systems present Cas9 proteins were selectively filtered. The potential Cas9 candidates were selected for further study on the basis of comparative phylogeny, completeness of the CRISPR-Cas locus and presence of domains and conserved catalytic residues required for Cas9 functionality. At last, the tracrRNA and Protospacer adjacent Motif (PAM) required (PAM) required for the activity of these Cas9 protein were predicted in silico. Over all this study provides a catalogue of Cas9 proteins which may be active nucleases with distinct properties and expand the available genome editing toolbox.

Poster Presentation

In Silico Mining of Biotic Stress-Responsive Gene Families in Plants: Comparative Analysis of Host Transcriptomic Responses to Viral Infections

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Abstract:

Plant viral infections remain a critical challenge to global agriculture, causing substantial yield and quality losses. Understanding the conserved and lineage-specific host responses to viral invasion is essential for guiding resistance breeding and biotechnological interventions. In this study, we conducted an in silico comparative meta-analysis of transcriptomic datasets from *Arabidopsis thaliana*, *Nicotiana benthamiana*, tomato (*Solanum lycopersicum*), and pepper (*Capsicum annuum*) challenged with diverse viral pathogens. By integrating multiple datasets, we identified consistently enriched gene families across hosts, highlighting shared antiviral mechanisms as well as species-specific adaptations. Our analysis confirmed the recurrent induction of pathogenesis-related (PR) genes, particularly PR1 and PR2, which are well-established markers of salicylic acid (SA)-mediated defense. Temporal data further supported a trend where early SA-dependent responses are followed by the activation of phenylpropanoid and secondary metabolism pathways, suggesting a sequential defense strategy. Transcription factor families, including WRKY, NAC, MYB, and ERF/AP2, were repeatedly upregulated across hosts, underlining their conserved role in transcriptional reprogramming during viral stress. NbWRKY40 and SlMYB4L are linked with enhancing the resistance against TMV and TYLCV, respectively. In addition, host-specific features were detected; *N. benthamiana* datasets showed enrichment of ribosomal and RNA processing factors, whereas tomato and pepper displayed stronger activation of MYB-regulated phenylpropanoid biosynthesis, consistent with their reported reliance on lignin and flavonoid production during defense. This study demonstrates the utility of secondary data mining and integrative transcriptomic analysis to uncover conserved antiviral defense modules and lineage-specific responses. The candidate genes and pathways identified here provide valuable targets for functional validation and can support strategies to engineer broad-spectrum resistance in crops.

Impact Of Plant Growth Promoting Rhizobacteria *Exiguobacterium acetylicum* RGK and *Enterobacter mori* RGK1 on Growth Parameters and Phytochemicals of *Asparagus racemosus*

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Abstract:

Rhizobacteria that promote plant growth (PGPR) are a wide range of soil bacteria that inhabit the rhizosphere of plants. In the present study, two plant growth-promoting bacterial strains were isolated from the rhizospheric soil of the Asparagus plant, namely Enterobacter mori RGK1 and Exiguobacterium acetylicum RGK, which can enhance plant growth. It was shown that both of these bacterial strains were able to synthesize exopolysaccharide, hydrogen cyanide (HCN), indole acetic acid and siderophores. These strains fix atmospheric nitrogen, solubilize phosphate, zinc and potassium. Additionally, has shown antibiotic susceptibility to antibiotics such as Amikacin, Netilin, Co-trimaxazole, Streptomycin, Furazolidone, Kanamycin, Nalidixic acid, Nitrofurantoin, Tobramycin, Oxytetracyclin, Chloramphenicol, Gentamycin and their ability to withstand salt concentration (NaCl) up to 5-6%. Treatment of Asparagus plantlets with separate and co-culture of both strains demonstrated a remarkable increase in physicochemical properties of soil, growth parameters and phytocompounds of Asparagus as compared to control. They improved the growth metrics of the plant such as shoot height, rhizome biomass, plant biomass as well as phenolic, flavonoid, saponin content and free-radical (DPPH) scavenging ability. As compared to the untreated plants, PGPR-treated plantlets showed higher amounts of secondary metabolites, primarily Diosgenin. The main focus is on the use of multiple microbial strains in a single formulation, an emerging trend in sustainable agriculture.

Poster Presentation

Isolation and Screening of Extremophilic Bacteria for Organophosphate Pesticide Degradation and Nutrient Solubilization from Himalayan Agroecosystems

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Abstract:

Organophosphate pesticide contamination is a growing concern in fragile Himalayan agroecosystems. In the present study, bacterial isolates were obtained from agricultural soils of the Northern Western Himalayas were screened on chlorpyriphos (1000 ppm) poisoned media. Out of these, 20 isolates exhibited measurable growth, with 5 showing superior tolerance and degradation ability. Biodegradation kinetics assays revealed that selected isolates degraded up to 73.33 per cent of chlorpyriphos (30 mg/L) within 07 days as confirmed by HPLC using the QuEChERS method. In addition to pesticide detoxification, the isolates were evaluated for mineral solubilization. Phosphate-solubilizing bacteria (e.g., PSB-6) released up to 6.83 µg P/ml broth at 20 °C, while potassium-solubilizing bacteria (e.g., KSB-10) mobilized 4.59 µg K/ml broth at 20 °C. Zinc- solubilizing strains (e.g., ZnSB-1) achieved a maximum of 8.9 µg Zn/ml broth under optimized conditions. Many isolates also expressed plant growth-promoting traits such as IAA production and siderophore activity. Molecular identification through 16S rRNA sequencing identified the efficient strains as *Stenotrophomonas maltophilia*, *Pseudomonas bubulae*, *Pseudomonas sp.* and *Pseudomonas orientalis*. The results demonstrate that extremophilic bacteria from diverse agro- climatic regions not only degrade hazardous organophosphate residues efficiently but also contribute to multi-nutrient solubilization. These multifunctional traits make them strong candidates for developing bio-input formulations aimed at pesticide remediation, nutrient mobilization, and sustainable crop productivity in challenging environments.

Production of Phytohormone by Pink Pigmented Facultative Methylotrophs

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Abstract:

The present study was conducted to investigate the potential of pink pigmented facultative methylotrophs (PPFMs) as PGPR, isolated from phyllosphere of rice by leaf imprinting method. The PPFM isolates were screened based on the effect on germination and seedling characters of rice. PPFM inoculation enhanced the germination, seedling length, and vigor index. Based on this study, three best isolates were selected for further studies. The selected PPFM isolates were screened based on their ability to produce plant growth hormones. IAA production ranged from 0.21 to 0.33 µg/mL of culture filtrate. Potent isolates could produce gibberellic acid in amounts ranging from 0.31 to 1.60 µg/mL of culture filtrate. The three isolates namely PPFM-1, PPFM-2 and PPFM-5 were characterized using morphological, biochemical, and molecular methods, revealed that selected isolates belonged to the genera *Methylorubrum aminovorans*, *Methylorubrum populi* and *Methylobacterium gregans*.

Poster Presentation

Aminoacyl-tRNA Synthetase: An Essential Target for Drug Discovery

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Abstract:

Aminoacyl-tRNA synthetases (ARSs) are essential enzymes responsible for feeding charged tRNAs into the protein synthesis machinery. Beyond this traditional function, these enzymes also play roles in several metabolic and signaling pathways important for cell viability. The active site of ARSs contains three subsites for substrates such as L-amino acid, ATP and 3'- end tRNA binding. Inhibition of these enzymes stops protein translation. In recent years, ARSs have been recognized as targets for drug discovery for the infectious and human diseases. The aminoacylation site inhibitors were classified based on their binding modes such as single, triple or multi-site, while the non-aminoacylation site inhibitors were grouped into editing, allosteric and non-translational functional site inhibitors. Over the past ten years, we have determined co-crystal structures of pathogenic parasitic ARS enzymes with inhibitory molecules and compared them with host and orthologous structures. Among the 20 aaRSs, phenylalanine-tRNA synthetase (FRS) has unique features as it consists of two subunits (α and β) and forms an (αβ)2 heterotetramer. The N-terminal domain of the α- subunit in apicomplexans and human FRS contains three DNA binding domains (DBDs), whereas the bacterial enzymes have a coiled-coil structure. Eukaryotic FRSs have an auxiliary pocket, while bacterial enzymes have an additional pocket below the substrate L-Phe site. There are three non-conserved residues in the auxiliary pocket between apicomplexans and human enzymes that determine the specificity of the inhibitor. Simultaneous targeting of subsites of prolyl-tRNA synthetase (PRS) enzymes using a cooperative ligand binding approach has recently been explored. Aminoacylation site inhibitors and their stereochemistry will be discussed in detail. This work is currently supported by grants from the Department of Biotechnology (PR32713) and the Indian Council of Medical Research (CAR-2024-000140).

Adansonia digitata (Baobab Tree): Ethnobotanical and Pharmacological Insights with a Focus on Traditional and Scientific Uses in Bulandshahr District, Uttar Pradesh, India

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Abstract:

Adansonia digitata L., commonly known as the African Baobab is a multipurpose tree of significant ethnomedicinal importance and has established a unique ethnobotanical niche in India, particularly in drier regions such as Uttar Pradesh, Madhya Pradesh, and Maharashtra. In Bulandshahr and neighbouring districts, the baobab is locally known as Gorakh Imli or Kalpvriksha; reflecting its mythological and medicinal stature. The tree is rare and often associated with sacred sites, such as the Parijaat tree in Barabanki district, which is protected and revered for its antiquity and supposed wish-fulfilling powers. Belonging to the Bombacaceae family, it has long been valued for its nutritional, therapeutic, and cultural roles. Recent studies highlight its antibacterial, antioxidant, anti-inflammatory, and hypoglycaemic properties, attributed to bioactive compounds such as flavonoids, tannins, saponins, and vitamin C. In Bulandshahr district of Uttar Pradesh, traditional healers and rural communities employ various parts of the tree leaves, bark, pulp, and seeds for remedies addressing fever, gastrointestinal disorders, microbial infections, and general debility. The present survey documents local knowledge systems while correlating them with contemporary pharmacological evidence. Previous studies suggest that aqueous and methanolic extracts of A. digitata leaves exhibit strong antimicrobial activity against pathogenic bacteria, alongside notable free-radical scavenging potential, thereby validating its role in combating oxidative stress-related ailments. This study underscores the urgent need to conserve Adansonia digitata, which faces ecological pressures, while promoting its integration into community health practices. By situating the research within Bulandshahr ethnobotanical landscape, the work bridges traditional wisdom and modern science, offering pathways for sustainable utilization and further clinical exploration. The outcomes hold promise for developing affordable, plant-based therapeutics that can strengthen rural healthcare resilience in India.

Poster Presentation

Virtual Screening and Evaluation of *Conzya sumatrensis* – Derived Compounds for Managing Cerumen Impaction

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Abstract:

The plants belonging to the Asteraceae family have many beneficial and harmful properties. *Conzya sumatrensis* is an herb, which has more medicinal qualities. The phytochemicals present can act therapeutically and help control secretions in the ear canal. In this specific research, more emphasis was given to the protein Q9J663 which is encoded by the gene ABCC11 and plays role in the synthesis of cerumen. The protein structure data were collected from the Uniprot database, and structure predictions were made using the AlphaFold predictor. The ADME profiles of the reported compounds were scanned using SwissADME tool. It also served the purpose of excluding compounds that proved to exhibit poor pharmacokinetic profile and thus narrowed down the study to compounds which exhibited good pharmacokinetic profile. Moreover, the active site of the Q9J663 was predicted by CASTp with a view of enhancing its accurate docking. Some molecular docking simulations were conducted to define the manner in which these phytochemical compounds would bind to the Q9J663 protein. Hence, the findings shown that some of the compounds isolated from *C. sumatrensis* exhibited considerable interaction with the Q9J663 protein; therefore, it is proved that the cited compounds could potentially block the activity of the ABCC11 gene. In conclusion, our study stresses the importance of natural sources like *C. sumatrensis* for searching novel solutions for treatment of ear wax and offering an understanding of some future avenues for the development of ear care products/therapeutic solutions.

Phytochemical Screening, Antibacterial Potential and Drug Likeliness Study of *Costus pictus*

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Abstract:

Plants produced certain novel natural compounds known as phytochemicals, which provided them evolutionary advantages such as promoting plant defence. This facilitated the interest in coordinating the plant phytochemicals to its therapeutic importance. Consumption of these plants played a vital role in prevention of diseases. *Costus pictus* was used in traditional medicine because of its diuretic, carminative and antiseptic properties. In this work, leaves extract of *Costus pictus* was prepared with three different solvents i.e., Acetone, Hot water and Ethanol. Phytochemicals and antibacterial activity of all extracts were performed. Among the three extracts, ethanol extract was found to be rich in biologically active compounds such as alkaloids, steroids, terpenoids, glycosides, carbohydrates, tannins, phenol, flavonoids, and proteins. The ethanol, acetone, and hot water extracts of *C. pictus* leaves were tested for their antibacterial activity by agar well diffusion method against *Bacillus cereus*, *Bacillus subtilis*, *Pseudomonas pneumoniae*, and *Pseudomonas aeruginosa* with Tetracycline (10 µg) as positive control and absolute solvents as negative control. The Zones of inhibition are recorded in millimetres. Acetone extract recorded the highest inhibition zone (15.6 mm) against *P. auregonisa* while less inhibition zone (10.8 mm) was observed against B. subtilis. Acetone extract of C. pictus leaves showed activity (15 mm) against *P. pnemoniae*, whereas (12.3 mm) against *B cereus*. Ethanol and Hot water extract of C. pictus leaf did not exhibit antibacterial activity against any of the tested pathogenic bacteria. The X-ray crystal structure of Insulin Receptor (IR3) of Homo sapiens with a resolution of 1.9 A° used. Through exploring literature data, ten phytoconstituents of *Costus pictus* was retrieved. It has been determined that 10 phytoconstituents have a drug-like molecular makeup and fall within the range where the Lipinski criterion is not violated. Their log P values are between the ranges of 1.36–8.91. All phytochemicals in terms of molecular weight, hydrogen bond acceptor, and hydrogen bond-donor, fall within the acceptable range. The admetSAR and ProTox servers evaluate pharmacokinetic parameters based on four criteria: absorption, distribution, metabolism, and excretion. The ADMET profiles of the phytoconstituents were within permissible bounds, indicating their efficacy as potential therapeutic candidates. All compounds showed good gastrointestinal absorption and presented moderate to high solubility. All the selected phytoconstituents are predicted to be not readily biodegradable but showed no carcinogenicity. The docking process was carried out using SwissDock. Docking findings for molecular targets IR, speculated that eight out of ten presumptive phytoconstituents displayed larger binding affinities. Since these are purely computational details, further in-silico comparative analyses should be performed to rule out all the in-silico possibilities for metabolism.

Bio-Fabrication of Mycelium-Based Composites for Circular Economy Applications

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Abstract:

The study is intended as an answer to an international crisis regarding plastic pollution, especially around single-use plastics, by reformulating a sustainable, biodegradable, and potentially edible cup and cutlery system using the *Agaricus bisporus* (white button mushroom). This mushroom exhibits properties like natural polymers (chitin and glucans) and nutrition, all of which were used to develop an environmentally friendly alternative. Three sample types were used in this study: Sample A (0%), Sample B (50%) and Sample C (100%). The development process was completed via microwave drying, milling, making dough, baking, and testing. The study showed that Agaricus bisporus has a promising and sustainable potential for use as material for a cup that is acceptable for eating food material. All samples compared well in regards to biodegradability, functional food safety, and shelf life, suggesting that mushroom-based cups show potential as a viable alternative to disposable single-use plastic alternatives to food packaging. The another study aims to the designing and manufacture of environmentally-friendly acoustic panels using agro-waste composites that are mycelium-based. The goal is to develop a sustainable alternative to synthetic sound absorbing materials. The main raw materials are paddy straw and sawdust, creating substrates with mycelium from the Pleurotus ostreatus (oyster mushroom) fungal species. The research clearly demonstrates that mycelium-based agro-waste composites represent an eco-friendly alternative to traditional synthetic acoustic panels. The resulting mycelium sawdust sandwich panels provided a good level of acoustic absorption especially in the mid-frequency range and is applicable for interior soundproofing applications. and the thermal conductivity performance of the mycelial sawdust sandwiched bio-composite panels was good. we believe the life cycle benefits to the environment achieved through composability and ability to mitigate agricultural wastes represents an overall benefit.

Global Transcriptomic Analysis of EhRrp44 Knockdown and Growth Stress Condition in *Entamoeba histolytica*

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Abstract:

Entamoeba histolytica, the causative agent of amoebiasis, affects approximately 50 million people worldwide and remains the third leading cause of parasitic death. While gene expression regulation has been explored in this parasite, the mechanisms governing RNA quality control and processing. Here, we present the first comprehensive characterization of EhRrp44, a crucial exosome component that provides both exo- and endo- ribonucleolytic activity essential for parasite survival. Through bioinformatic analysis, we identified two conserved functional PIN and RNB domains in EhRrp44: Structural modeling revealed significant conservation with homologs from S. cerevisiae (39% identity), H. sapiens (41%), and *T. brucei* (36%), with the RNB domain showing particularly high conservation across species. Intriguingly, subcellular localization studies revealed EhRrp44 maintains dual nuclear- cytoplasmic distribution under both normal and stress conditions, contrasting sharply with EhRrp6, that exits the nucleus during serum starvation. Western blot analysis showed approximately 1.4-fold reduction in EhRrp44 protein levels during serum starvation. Functional characterization through antisense-mediated knockdown revealed EhRrp44's critical role in cellular physiology. Down-regulation resulted in severe growth defects and markedly impaired erythrophagocytosis, a process essential for nutrient acquisition and pathogenicity. Transcriptomic profiling of knockdown cells identified 1554 differentially expressed genes, with significant dysregulation of phagocytosis-related proteins including EhCaBP6, EhCaBP3, EhARP2/3, and Rho1. Notably, 102 genes involved in ribosome biogenesis were affected, including helicases, kinases, and U3 snRNP components, underscoring EhRrp44's pivotal role in pre-rRNA processing. Pathway analysis revealed disruption of ubiquitin-mediated proteolysis and compensatory upregulation of EhRrp6 and Nob1, suggesting cellular attempts to maintain RNA homeostasis. The opposing expression patterns of 267 genes between EhRrp44 knockdown and serum starvation conditions highlight distinct regulatory networks. These findings establish EhRrp44 as a central regulator linking RNA metabolism to essential cellular processes in *E. histolytica*. The unique features of EhRrp44, including its stress-resistant dual localization and essential role in phagocytosis, present potential therapeutic targets for combating this devastating parasitic disease.

Scaffold/Antigen Based Mpox Vaccine Drives Coordinated Humoral and Cellular Response for Protection Against Lethal Vaccinia Virus

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Abstract:

The global spread of Mpox beyond endemic regions, alongside the emergence of the more virulent Clade Ib, underscores the urgent need for safe, broadly protective vaccines. To address the need for an optimal Mpox vaccine eliciting balanced humoral and cellular immunity against antigens from both intracellular mature virus (IMV) and extracellular enveloped virus (EEV) forms, we engineered an Mpox protein and developed it as a plug- and-play protein scaffold for a precise, stable, multi-antigen display platform, addressing limitations of conventional multi-antigen co-immunization challenges, with the feasibility to express and accommodate multiple antigens. Utilizing the engineered scaffold, we describe the generation of a bivalent vaccine candidate (BSP; Bivalent Scaffold Polyprotein expressing M1R and A35) with the dual targeting feature of humoral and cellular/cytotoxic T cell responses. The soluble BSP upon immunization in mice generates high-titer anti-MPXV antigen-specific humoral and balanced $CD8^+$ and $CD4^+$ Th1-type cellular responses, where the scaffold protein primarily promotes CTL responses. The scaffold, which is otherwise known to be essential for IEV egress, is characterized as an antigen, generating anti-MPXV humoral, cytotoxic T cell, and anti-VACV neutralizing responses. The alum-adjuvanted BSP provides protection against lethal respiratory infections challenged with neurotropic mice adapted to VACV and complete clearance of the virus from the brain. The overall modularity employed here provides insight towards a versatile, rapid substitution-compatible, structure-guided platform for next-generation orthopoxvirus vaccines addressing adaptation for future needs.

Poster Presentation

Structural and Biochemical Characterization Of Malarial Phenylalanine-tRNA Synthetase (FRS) Complexed with Novel Inhibitors

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Abstract:

Human malaria parasites are among the world's most challenging pathogens, with Plasmodium falciparum and Plasmodium vivax as primary causes of severe malaria. Rapidly evolving drug resistance in these parasites emphasizes the urgent need for new antimalarial treatments. Aminoacyl-tRNA synthetases (aaRS) are essential enzymes in protein synthesis and serve additional regulatory roles due to their cellular localization, nucleic acid binding, and protein-protein interactions. These versatile properties make aaRS enzymes particularly promising targets for antimalarial development. Our group is focused on creating structure-based inhibitors for parasitic aaRS enzymes to drive anti-parasitic drug discovery. We recently resolved the crystal structure of Phenylalanyl-tRNA synthetase (FRS) bound to a novel inhibitor that occupies the L-phe and auxiliary sites, extending through the ATP binding site of the enzyme. Notably, FRS enzymes are highly conserved across Plasmodium species, suggesting that a single chemical series could potentially target all five malaria-causing Plasmodium species. Our work lays a structural framework for designing novel derivatives against P. falciparum, P. vivax, and other parasitic pathogens with conserved sequences. This study presents the biochemical and biophysical characterization of FRS and its inhibitors, including enzyme inhibition and binding assays such as the Malachite Green and thermal shift assays.

Poster Presentation

Green Synthesis of Zinc Oxide and Titanium Dioxide Nanocomposites by Using *Saussurea obvallata* Extract, Characterization and Antibacterial Activity

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Abstract:

The biosynthesis of Zinc oxide and Titanium dioxide nanocomposites (ZnO/ TiO_2 NCs) has gained attention as a simple, sustainable, and cost-effective substitute for traditional physical and chemical methods. In the present study, *Saussurea obvallata*, a medicinal plant with clinically valuable flowers, was employed for the synthesis. The aqueous extract of its flowers functioned as a natural reducing and stabilizing agent, facilitating the conversion of zinc acetate and titanium oxide into ZnO/ TiO_2 Nanocomposites via a green synthetic route. The successful formation of nanocomposites was initially signaled by a visible color change and further verified through a characteristic absorption peak at 340 nm recorded by UV–visible spectroscopy. The morphology and particle size distribution of the synthesized nanocomposites were examined using transmission electron microscopy (TEM) and field emission scanning electron microscopy (FESEM). Fourier transform infrared (FTIR) analysis confirmed the involvement of phytochemicals in reduction and capping processes. Antibacterial properties were evaluated using the agar well diffusion method, while the minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) were determined through spread plate assays.

Poster Presentation

Assessment of Multidrug Resistance Profiles of *Pseudomonas spp.* from Environmental Samples

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Abstract:

Pseudomonas species, particularly *Pseudomonas aeruginosa*, are key members of the ESKAPE group of pathogens bacteria known for evading multiple classes of antibiotics. While clinical ESKAPE isolates have been extensively studied, environmental reservoirs such as contaminated soils and wastewater remain underexplored, despite their potential to harbor and disseminate resistance genes. The growing resistance to life-saving antimicrobial agents is alarmingly high and continues to rise, particularly in resource-constrained regions. These disparities emphasize the urgent need to strengthen health systems through infection prevention, early and accurate diagnosis, and equitable access to effective and affordable treatments. This study aimed to isolate Pseudomonas spp. from soil environments across Delhi and evaluate their multidrug resistance (MDR) profiles. Samples were collected from open drains, sewage-affected zones, and surrounding soils across multiple urban sites in Delhi. Bacterial isolates exhibiting characteristic Pseudomonas morphology were purified using selective and differential media and identified using Gram staining and biochemical tests like oxidase and catalase activity tests, and pigment production tests. Confirmed isolates were subjected to antimicrobial susceptibility testing (AST) via the Kirby-Bauer disc diffusion method against β-lactams, aminoglycosides, fluoroquinolones, and carbapenems, following CLSI guidelines. A considerable proportion of isolates exhibited resistance to three or more antibiotic classes, confirming MDR phenotypes after Antibiotic Susceptibility Testing. Resistance to beta-lactam cephalosporins and fluoroquinolones was frequent, while several isolates displayed reduced susceptibility to carbapenems, indicating possible efflux- or porin-related mechanisms. The detection of multidrug-resistant Pseudomonas spp. in Delhi's sewage and open-drain soils highlights the environmental expansion of the ESKAPE pathogens in the environment, which harbour multidrug resistance genes. These findings reinforce the need for continuous environmental surveillance and molecular characterization to mitigate the growing antimicrobial resistance threat at both community and clinical levels.

Poster Presentation

Synergistic Antibiofilm Activity of Cinnamon Essential Oil and Green Synthesised Silver Nanoparticles Against Selected MDR Foodborne Bacterial Pathogens

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Abstract:

The persistence of multidrug-resistant (MDR) biofilm-forming foodborne pathogens in mixed-species biofilms poses a major challenge to food safety and sanitation. This study evaluates the synergistic antibiofilm efficacy of cinnamon bark essential oil (CBEO) and green-synthesized silver nanoparticles (AgNPs) against mono- and dual-species biofilms formed by MDR *Salmonella enterica Typhimurium*, *Escherichia coli*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, and *Listeria monocytogenes* MTCC 657. Except for *L. monocytogenes*, all isolates were recovered from raw chicken samples. AgNPs were synthesized using *Piper cubeba* (Kababchini) aqueous extract and characterized by UV–Vis, FTIR, DLS, and SEM– EDX analyses. The minimum inhibitory concentrations (MICs) of CBEO and PC-AgNPs ranged from 0.039– 0.0781% (v/v) and 15.625–62.5 µg/mL, respectively, showing highest sensitivity in *S. aureus* and *S. enterica*, and lowest in *P. aeruginosa*. Checkerboard assays revealed fractional inhibitory concentration index (FICI) values between 0.132–0.914, indicating synergistic or additive interactions, with strong synergy (FICI ≤ 0.5) observed in several mixed cultures. Combined treatments (0.25× MIC of each agent) significantly inhibited biofilm formation (>60%) compared to individual agents. Confocal laser scanning microscopy (CLSM) showed a marked reduction in biofilm thickness, while SEM confirmed decreased cell aggregation, microcolony formation, and extracellular polymeric substance (EPS) production under combination treatment. These results demonstrate that CBEO and green-synthesized AgNPs exhibit strong synergistic antibiofilm potential at subinhibitory concentrations. The combined application offers a promising, sustainable, and natural nanomaterial-based strategy for controlling MDR biofilms in the food industry through antimicrobial coatings or sanitizing formulations.

Sub-MIC Colistin Impacts Morphology and Early Stages of Virulence in *Acinetobacter baumannii* KSK2

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Abstract:

Many a times, prescribed antibiotic concentrations fall below the desired in various body compartments. Evolutionary and medical implications of bacterial exposure to this low concentration of antibiotics (Sub-MIC) are mostly unexplored. At the present, most of the *Acinetobacter baumannii* nosocomial infections in India are resistant to most of the commonly prescribed antibiotics. The study investigated *A. baumannii* KSK2 response to sub-MIC levels of colistin, despite having a high MIC of 128 µg/ml. Sub-MIC colistin led to slowed growth, distorted cell morphology, and disrupted cell walls and membranes. Sub-MIC concentrations significantly increased biofilm production but invariable exopolysaccharide secretion. Lipid analysis showed changes in specific lipid species related to colistin resistance, stress, and virulence. When grown at Sub-MIC colistin *A. baumannii* KSK2 cells underwent stress, which triggered more biofilm synthesis, which is evident from the Microscopy, Biofilm and Exopolysaccharide quantification. The findings underscore the urgent need for a comprehensive understanding of these interactions to effectively address the challenges posed by antibiotic-resistant bacteria like *A. baumannii*. In-vitro virulence and resistance increase at Sub-MIC concentrations of antibiotic by enhancing the biofilm formation, polysaccharides production and altering lipid moieties. Sub-MIC concentrations of antibiotic present in environment, clinical settings and in different parts of human body may enhance the antibiotic resistance and virulence of bacteria by imparting the stress at even very low level.

Poster Presentation

Functional Role of Galectin-3 in Mediating EMT, Stemness, and Metastasis in Cigarette Smoke-induced Lung Cancer

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Abstract:

Cigarette smoking promotes aggressiveness and metastasis in lung cancer, which remains a leading cause of cancer-related death worldwide. Emerging evidence suggests that galectin-3, a β-galactoside lectin-binding protein, is elevated in smokers and could be associated with epithelial-to-mesenchymal transition (EMT), stemness, and metastasis, leading to tumour progression and therapy resistance. However, its functional role in cigarette smoke (CS) induced EMT and metastasis in lung adenocarcinoma is not well studied. This study aims to explore the functional role of galectin-3 in cigarette smoke extract (CSE)-induced EMT, stemness and metastasis in lung adenocarcinoma. A549 cells were exposed to CSE or exogenous galectin-3, and phenotypic assessments, including cell morphology, migration, invasion, and gene expression analysis by RT-PCR and western blotting, were performed to evaluate EMT, stemness, and metastasis markers. Secretion of galectin-3 in the extracellular vesicles (EVs) was analysed. Furthermore, an in- silico docking approach was employed to predict potential interacting partners relevant to EMT and metastasis in lung cancer. CSE exposure upregulated galectin-3 expression, reduced epithelial marker expression and enhanced mesenchymal marker expression (E-cadherin and N-Cadherin). Phenotypic assessment revealed increased migratory potential in CSE and gal-3-treated cells, which was inhibited by galectin-3 inhibitor, suggesting the role of galectin-3 in EMT and metastasis. Secretion of galectin-3 was detected via EVs, a non-classical pathway upon CSE induction of A549 cells. Furthermore, a molecular docking study identified a potential interaction between galectin-3 and EGFR, which may contribute to the exacerbation of EMT, stemness, and metastasis in lung tumour progression. The results from this study demonstrate that CSE upregulates galectin-3 expression and its secretion through EVs, which could interact with cell surface receptors and promote EMT stemness and metastasis in lung adenocarcinoma.

Poster Presentation

Microbial Synthesis of Zinc Oxide Nano Bioformulation and Its Applicability for Plant Growth Promotion

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Abstract:

Nanobioformualtions couple nanotechnology with biological agents for sustainable development. Total 15 bacterial isolates and 9 fungal isolates were obtained from rhizospheric soil and artificial pond soil. During primary screening for ZnO solubilization, 6 bacterial and 8 fungal isolates showed clear zones of zinc solubilization on ZnO-supplemented media followed by secondary screening, where quantitative estimation of ZnO solubilization was performed using atomic absorption spectroscopy (AAS). Heavy metal tolerance of different bacterial isolates was checked against different Zn metal precursors. The heavy metal tolerance for zinc sulfate was found maximum (62.5 µg/ml) for bacterial isolates Rb3, Rd2 and Rd3. Out of these isolates Rb3 showed significant ability for ZnO nanoparticle (colorless to milky white) synthesis. SPR (surface plasmon resonance) was (295 nm). The size of ZnO nanoparticle (50 nm) was checked by particle size distribution and zeta potential (-37 mv) was noted. Optimization of media component to maximize ZnO nanoparticle synthesis was carried out by OFAT method followed by PBD and CCD. Rb3 isolate showed maximum plant growth promoting activity as compared to control during seed germination (100%). Rhizosphere soil isolate Rb3 showed significant ability as a Nano biofertilizer. To check efficiency of this nano bioformulation, field experiment was carried out on watermelon, significant results were observed in watermelon plant.

Poster Presentation

Sustainable Edible Pigment Production Using Oleaginous Yeast

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Abstract:

The development of natural and sustainable edible pigments has gained increasing attention as a safer alternative to synthetic food colorants. This study focuses on the formulation of edible ink using natural pigments extracted from oleaginous yeast cultivated on fruit and vegetable waste collected from local mandis (vegetable markets), serving as a low-cost and nutrient-rich feedstock. Pigment-producing red yeast strains were cultivated on the pretreated waste hydrolysate to enhance pigment yield in an eco- friendly manner. The pigments were extracted using a solvent-based method, purified, and characterized spectroscopically to confirm their stability and chromatic properties. The extracted pigment was incorporated into a food-grade ink formulation using biodegradable carriers and stabilizers to achieve suitable viscosity, flow behavior, and adhesion for inkjet printing applications. The resulting edible ink exhibited strong colour intensity, good printability, and excellent compatibility with various food substrates. Stability analysis demonstrated that the ink maintained its colour integrity under different pH, temperature, and light conditions. The use of mandi waste as a fermentation substrate not only supports a circular bioeconomy approach by valorizing agro-waste into high-value products but also reinforces the development of non-toxic, environmentally friendly alternatives for food decoration and labelling. This research establishes yeast-derived pigments as promising candidates for next-generation natural edible ink formulations.

Poster Presentation

Design of a Multi-Epitope Vaccine using β-barrel Outer Membrane Proteins Identified in *Chlamydia trachomatis*

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Abstract:

Chlamydia trachomatis is an obligate intracellular Gram-negative pathogen that causes sexually transmitted infections (STIs) and trachoma. Current interventions are limited due to the widespread nature of asymptomatic infections, and the absence of a licensed vaccine exacerbates the challenge. In this study, we predicted outer membrane β-barrel (OMBB) proteins and designed a multi-epitope vaccine (MEV) construct using predicted proteins. We employed a consensus-based computational framework on the *C. trachomatis* D/UW-3/CX proteome and identified 17 OMBB proteins, including well-known Pmp family members and MOMP. Eight OMBB proteins were computationally characterized, showing significant structural homology with known outer membrane proteins from other bacteria. Sequence-based annotation tools were used to determine their putative functions. B-cell and T-cell epitopes were predicted from the selected proteins. The MEV construct was designed using four cytotoxic T lymphocyte (CTL) epitopes and 29 helper T lymphocyte (HTL) epitopes from six OMBB proteins, which were conserved across 106 C. trachomatis serovars. To enhance its immunogenicity, the vaccine construct was supplemented with the Cholera toxin B subunit and PADRE sequence at the N-terminus. The MEV construct, of length 780 amino acids, was predicted to be antigenic, non-allergenic, non-toxic, and soluble. Secondary structure analysis revealed 95% random coils. A three-dimensional structural model of the MEV was generated and subsequently validated. Molecular docking between MEV and toll-like receptor 4 (TLR4) revealed strong and stable binding interactions. The MEV-TLR4 complex was found to be structurally compact and stable using molecular dynamics simulation. Immune simulation of the MEV construct elicited a strong immune response. This study highlights OMBB proteins as promising immunogenic targets and presents a computationally designed MEV candidate for *C. trachomatis* infection.

Targeted Disruption of Nucleoside Diphosphate Kinase in *Leishmania donovani* Demonstrates its Role in Modulating Host Immunity and Parasite Persistence

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Abstract:

Leishmaniasis, a neglected tropical disease, triggers rapid activation of the host innate immune system. Innate immune cells, particularly mast cells and macrophages, are the first to encounter *Leishmania donovani*, and their response dictates whether the parasite is cleared or establishes intracellular persistence. A key survival mechanism of *L. donovani* is the secretion of Nucleoside Diphosphate Kinase (NDK), an enzyme predominantly expressed during the amastigote stage. While NDK traditionally functions in maintaining intracellular nucleotide pools through its phosphotransferase activity, it also modulates host immune responses by preventing host cell cytolysis, thereby facilitating parasite survival. To investigate the immunomodulatory functions of NDK, we generated an NDK-deficient *L. donovani* strain and evaluated its behavior in vitro using mast cell and macrophage co-culture systems. Functional assays, including measurements of parasite load, phagocytosis, host cell viability, and apoptosis, were conducted. The NDK-deficient parasites demonstrated enhanced early-stage growth and exhibited elongated flagella. Host cells internalized significantly higher numbers of mutant parasites compared to wild-type, indicating increased phagocytic uptake. However, the mutant showed increased intracellular killing than wild type parasite. Importantly, macrophages infected with NDK-deficient parasites displayed significantly elevated levels of apoptosis. Collectively, these findings highlight the crucial role of NDK in suppressing host cell death pathways, thereby promoting parasite persistence and immune evasion.

Poster Presentation

Silencing of the Meloidogyne incognita Effector Gene Mi-EP1 via dsRNA Feeding and Host-Delivered RNAi Suppresses Parasitism in Tomato and *Arabidopsis*

Alisha Guglani[1], Vishal Singh Somvanshi[2], Uma Rao[2], Arun Jagannath[1], Amar Kumar[1], Surekha Katiyar-Agarwal[3] and Manu Agarwal[1]

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Abstract:

The southern root-knot nematode (*Meloidogyne incognita*) is one of the most destructive plantparasitic nematodes (PPNs), causing global crop losses exceeding $80 billion annually. Its ability to parasitize over 2,000 plant species presents a significant challenge to global food security. In this study, we functionally characterized a candidate nematode effector gene, Mi-EP1, which is expressed 8.74-fold higher during the early J2 parasitic stage than in adult females. To evaluate its role in parasitism, J2-stage nematodes were transiently fed with double-stranded RNA (dsRNA) targeting Mi-EP1 and used to infect the roots of Adzuki bean (*Vigna angularis*) and tomato (*Solanum lycopersicum*). These pretreated nematodes exhibited significantly reduced infectivity compared to controls. Moreover, host-delivered RNA interference (RNAi) achieved via virus-induced gene silencing (VIGS) in tomato, using constructs designed to target the nematode Mi-EP1 gene, also led to suppressed parasitism. Additionally, transgenic lines of *Arabidopsis thaliana* expressing Mi-EP1-specific RNAi constructs showed marked reductions in nematode infection, including 26% fewer galls, 36% fewer females, 43% fewer egg masses, and up to a 68% reduction in the reproductive index. These findings confirm Mi-EP1 as a critical effector for nematode parasitism and validate it as a promising target for host-delivered RNAi-based resistance in crops. Further molecular analysis of Mi-EP1 and its interaction with host plant pathways will enhance our understanding of plant-nematode interactions and help in the development of durable resistance strategies.

Poster Presentation

Mapping and Quantifying Phosphate Starvation Regulated microRNA in Root Endophytic fungus *Serendipita indica* by RNA-Seq

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Abstract:

Serendipita indica (formerly *Piriformospora indica*) is a root endophytic basidiomycete belonging to the order Sebacinales, first described in 1998. It colonizes both monocot and dicot plants, enhancing growth, nutrient uptake, stress tolerance, and defense against pathogens. Unlike arbuscular mycorrhizal fungi, *S. indica* can be axenically cultured, making it a promising biofertilizer and bioprotector in sustainable agriculture. Its ~25.3 Mb genome encodes over 10,000 protein-coding genes involved in nutrient transport, metabolism, and stress responses. In the present work, we examined the effect of phosphate availability on *S. indica* microRNA transcriptomes. The fungus was cultured under high (1 mM) and low (10 µM) phosphate conditions, and total RNA was isolated on the 14th and 18th days of growth. High-quality RNA- seq libraries were generated and sequenced using Illumina NovaSeq 6000. Bioinformatics analyses revealed high-quality alignments (>95%) to the reference genome and identified differentially expressed genes (DEGs) under phosphate starvation. Comparative analyses demonstrated distinct expression profiles, with both upregulated and downregulated genes between phosphate-rich and phosphate-deprived conditions. Visualization through MA plots, heatmaps, PCA, and Venn diagrams confirmed these transcriptional changes. The study provides insights into the regulatory role of *S. indica* microRNAs in phosphate stress adaptation and lays the foundation for future investigations into splice isoforms, microRNA–gene interactions, and mechanisms by which S. indica supports plant physiology during nutrient deficiency. These findings highlight the potential of *S. indica* as a biofertilizer, probiotic, and biohardening agent in agriculture and environmental management. The study establishes a framework for further characterization of miRNA isoforms, target genes, and their role in enhancing plant resilience under nutrient-deficient environments.

EPTB in High-Burden Settings: A Study of Diagnostic Modalities and Disease Distribution

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Abstract:

In 2024, the WHO reported approximately 10.8 million cases of Tuberculosis, with 16% being Extrapulmonary tuberculosis (EPTB); accounting for a substantial proportion of TB cases in India and continues to pose diagnostic challenges due to its paucibacillary nature and diverse clinical spectrum. This prospective study aimed to assess the diagnostic yield and agreement between GeneXpert and liquid culture for MTB detection in EPTB samples. This study was conducted at Department of Translational Medicine, All India Institute of Medical Sciences (AIIMS), Bhopal, between August 2024 and October 2025. A total of 400 clinical specimens were recruited, of which 70 (17.5%) were extrapulmonary samples. Which were further processed using standardized diagnostic workflow. GeneXpert was performed followed by Mycobacteria Growth Indicator Tube (MGIT) culture system, and positive cultures were confirmed by MPT64 antigen detection test. Among 70 EPTB samples, cerebrospinal fluid (24) and pus (16) were most frequent, followed by ascitic fluid (8) and pleural fluid (6). Other specimens included LNA (4), FNAC (2), tissue (2), urine (2), and one each of abdominal fluid, biopsy, bone tissue, brain tissue, and psoas abscess. Of these, 25 were rifampicin-sensitive, 4 indeterminate, and 1 resistant. Additionally, 14 samples were positive by both GeneXpert and culture, 7 were culture-positive but GeneXpert-negative, and 7 were GeneXpert-positive but culture-negative, showing ~80% concordance. Although MGIT culture remains to be gold standard for MTB detection due to its higher sensitivity, GeneXpert demonstrated substantial diagnostic utility, particularly in paucibacillary specimens, where culture yield may be compromised due to low bacterial load or suboptimal sample processing conditions. The rapid turnaround time and ability to identify rifampicin resistance make CBNAAT a critical component in early case detection. The combined use of GeneXpert and culture enhances diagnostic accuracy and ensures reliable confirmation.

Poster Presentation

Modulation of Amyloid-Sensitive Dye Behavior by PEG-Induced Macromolecular Crowding

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Abstract:

Macromolecular crowding profoundly influences biomolecular behavior, mimicking the dense cellular environment in vitro. While crowding agents such as ethylene glycol (EG) and polyethylene glycol (PEG) are widely employed to approximate physiological conditions during protein aggregation studies, their unintended interactions with analytical probes often go unrecognized. Commonly used amyloid-sensitive fluorescent and histological dyes like Thioflavin T (ThT), 8-anilinonaphthalene-1-sulfonic acid (ANS), and Congo red (CR) respond to such crowded environments in the absence of protein aggregates. Using spectroscopic and fluorescence- based assays, we examined the intrinsic optical properties of these dyes in varying concentrations of EG and PEG to elucidate potential non-specific interactions. Our results demonstrate that both EG and PEG alter the photophysical characteristics of these dyes, producing significant shifts in absorbance, emission intensity, and spectral maxima even in protein-free systems. For instance, ThT exhibited increased fluorescence in PEG-rich conditions, suggesting restricted dye mobility and altered solvent dynamics that can mimic amyloid binding signatures. Similarly, ANS and CR showed notable changes in their fluorescence and absorbance response respectively, likely arising from hydrophobic interactions or microviscosity effects induced by the crowding agents. These findings indicate that apparent increases in dye fluorescence or binding are not always reflective of genuine amyloid formation but may instead stem from dye and crowder associations. The study underscores the critical importance of incorporating appropriate blank and control experiments when employing fluorometric indicators to monitor protein aggregation under crowded conditions. Failure to account for these artefacts can lead to misinterpretation of aggregation kinetics, false-positive results, and erroneous mechanistic conclusions. We recommend rigorous pre-assessment of dye and crowder compatibility prior to experimental design to ensure that data obtained accurately reflect protein aggregation phenomena rather than dye-induced artefacts. This work highlights a pivotal yet often overlooked aspect of biophysical assay validation within crowded biochemical systems.

Poster Presentation

Understanding the Role of Different Domains in the Stability of Human Homologs of Guanylate Binding Proteins (GBPs)

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Abstract:

The guanylate binding proteins (GBPs) are interferon gamma-inducible large GTPases and play a significant role in innate immunity in the host body. These GTPases are characterized by the unique property of hydrolysing GTP to GMP, through the formation of GDP in two successive steps. Seven human homologs (hGBP1–hGBP7) are known to date, which share high sequence identity. Unlike small GTPases, hGBPs have evolved as multidomain proteins, where the conserved N-terminal globular domain possesses catalytic activity, but the extra C- terminal helical domain has a regulatory role in a few homologs. They are also known to form oligomeric assemblies during substrate binding and hydrolysis. In contrast to the small GTPases, like Ras, which are unstable in their nucleotide-free form, hGBPs are stable without substrates. In this study, we aim to investigate whether the helical domains of hGBPs contribute to protein stability, and to determine whether other domains play a role, and, whether substrate- induced oligomerisation influence the stability of the proteins. To explore this, we performed heat-induced denaturation studies on two closely related homologs, hGBP1 and hGBP2. Surprisingly, they exhibit considerable variation in structural stability. In both cases, overall stability is mainly contributed by the globular domain; however, in hGBP1, the helical domain stabilizes the full-length protein to some extent. On the other hand, in hGBP2, it essentially plays no role in providing overall stability, and the two domains unfold independently of each other. Our data further show that proteins become more stable in the presence of substrates, which is essentially mediated by their ability of forming oligomers upon substrate binding. However, these two proteins get stabilized to different extent. These findings indicate that the helical domain plays different roles in the stability of the two close hGBP homologs, which may have implications for the differences in their biological functions.

Poster Presentation

CTP Synthase as a Therapeutic Target Against Drug-Resistant Malaria

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Abstract:

India continues to face a substantial malaria burden, contributing the highest number of deaths in the Southeast Asia region. Despite sustained control and eradication efforts, the emergence and persistence of drug-resistant Plasmodium strains pose a major challenge. This highlights the urgent need to explore novel, under-characterized metabolic pathways for therapeutic intervention. Because Plasmodium parasites lack the ability to salvage pyrimidine nucleotides, they rely entirely on the de novo pyrimidine biosynthesis pathway, making enzymes within this pathway key vulnerabilities. In this context, our study identifies quercetin and its nanoparticle formulation, nano-quercetin, as promising inhibitors of Plasmodium falciparum CTP synthase (PfCTPS), a central enzyme responsible for CTP production. Recombinant PfCTPS was heterologously expressed in E. coli BL21 (DE3) and purified using Ni-NTA affinity purification yielded the expected ~100 kDa PfCTPS band. Immunofluorescence with PfCTPS-specific antibodies showed its cytoplasmic localization in parasites. Induced expression of PfCTPS in E. coli impaired bacterial growth, indicating toxicity from active enzyme, while quercetin or nano-quercetin treatment restored growth, confirming enzyme inhibition. MST analysis showed moderate quercetin binding (Kd = 83.9μM). In-vitro growth inhibition assays further demonstrated strong antimalarial activity of both quercetin and nano-quercetin. Together, these findings validate PfCTPS as an active, druggable enzyme and highlight its potential as a target to combat emerging malaria resistance.

Poster Presentation

DNA Damage Response Mediated by Rev1 Regulate Artemisinin Resistance in Malaria Parasite

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Abstract:

The global rise in Plasmodium falciparum malaria cases, combined with the rapid spread of artemisinin resistance, underscores the urgent need for new therapeutic strategies that address emerging antimicrobial resistance (AMR). In this context, our study investigates PfRev1, a key enzyme in the parasite's DNA damage tolerance pathway that enables survival under drug-induced stress. By facilitating translesion DNA synthesis, PfRev1 promotes mutagenesis, potentially accelerating the evolution of resistance to frontline antimalarial drugs such as artemisinin. This positions PfRev1 as not only a mediator of parasite survival but also a contributor to the broader challenge of AMR in malaria-endemic regions. We recombinantly expressed and purified the BRCT domain of PfRev1, confirming its stage-wide expression and dual cytoplasmic–nuclear localisations in P. falciparum. Functional complementation in yeast demonstrated that PfRev1 retains conserved roles in DNA repair and survival under artemisinin-induced damage. Importantly, Bractoppin a known human Rev1 inhibitor exhibited potent antimalarial activity in vitro and in vivo, without detectable cytotoxicity, indicating its potential to selectively target parasite DNA repair pathways. By disrupting PfRev1 function, this work highlights a promising strategy to limit mutagenic repair processes that drive artemisinin resistance, thereby contributing to global efforts to combat antimicrobial resistance.

Poster Presentation

Lysine Peptide Dendrons: A Self-Adjuvating Nanoplatform for Potent MSP3 and SARS-CoV-2 RBD Subunit Vaccines

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Abstract:

subunit vaccines are safe, but suffer from poor immunogenicity due to inefficient antigen delivery and typically require potent external adjuvants highlighting the need for novel delivery platforms. We developed cationic lysine peptide dendrons as a novel, self-adjuvating delivery system for the protein antigens delivery that gives a robust immune response against malarial pfMSP3 and COVID-19 spike RBD antigens. Recombinant His-tagged PfMSP3 (37kDa) and SARS-CoV-2 RBD (26 kDa) were expressed in E. coli, purified by Ni-NTA, and confirmed by SDS-PAGE and western blot. Dendrons were synthesized, NMR-characterized, and shown to be non-cytotoxic in HepG cell lines. Biophysical characterization of dendron–antigen complexes using DLS, AFM, and TEM revealed uniform nanoscale particles. Binding affinities were determined by surface plasmon resonance (SPR) and microscale thermophoresis (MST), with the strongest interactions observed for dendron (K D ≈ 4.9 μM for RBD; 481 nM for MSP3). In BALB/c mice, dendron-formulated MSP3 and RBD elicited high IgG titers (≥1:10,000), strong Th1 cytokines (IFN-γ >500 pg/mL, TNF-α >300pg/mL), and balanced Th2 responses. ADCI assays demonstrated that antibodies elicited by the MSP3-dendron vaccine effectively cooperated with human monocytes to inhibit Plasmodium growth in vitro, confirming a key mechanism of protection, also blocking the parasite entry in RBCs by Invasion assay using antisera. Thus, strong performance of dendron-formulated MSP3 and SARS-CoV-2 RBD antigens establishes peptide dendrons as a versatile, self-adjuvating delivery platform for subunit vaccines, paving the way for next-generation vaccines with efficient antigen delivery, immune activation, without any side- effects against diverse pathogens developing resistance.

Poster Presentation

Cyanobacteria Driven Modulation of Macrophage Polarization and Immune Activation

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Abstract:

Cyanobacteria represent a rich reservoir of bioactive secondary metabolites with established antioxidant, anticancer, and antimicrobial properties; however, their immunomodulatory potential remains inadequately investigated. In the present study, cyanobacterial strains were isolated, morphologically characterized, and taxonomically validated via 16S rRNA sequencing. Methanolic extracts were biochemically profiled using UV–Visible spectroscopy, fluorescence analysis, and GC-MS, confirming the presence of multiple high-value metabolites. To assess their immunological effects, THP-1 macrophages were exposed to these extracts, and macrophage activation and polarization were evaluated by qPCR. Treatment with cyanobacterial extracts resulted in a marked upregulation ($p< 0.05$) of classical M1-associated markers including TNF-α, IL-8, IL-1β, and CXCL10, accompanied by a reduction ($p< 0.05$) in alternatively activated M2 markers such as Stab1, TGF-β, CD163, and CD206. Notably, TLR-2 inhibition significantly attenuated pro-inflammatory cytokine expression, indicating that the immunostimulatory signaling is partially dependent on TLR-2 activation. Furthermore, gold-based nanoformulations of cyanobacterial extracts developed to improve stability and performance retained the M1-polarizing activity observed with crude extracts. Collectively, the findings demonstrate that bioactive constituents of locally isolated cyanobacteria and their nanoformulations robustly promote innate immune activation and skew macrophage polarization toward a pro-inflammatory M1 phenotype. This work highlights the immunostimulatory relevance of Indian cyanobacterial isolates and positions them as promising candidates for nutraceutical, therapeutic, and immune- modulatory applications, warranting deeper mechanistic investigation.

Poster Presentation

Studies on Nitrogen-Driven Modulation of Phycobiliproteins in Different Cyanobacterial Strains

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Abstract:

Phycobiliproteins are brightly fluorescent, water soluble pigment-protein complexes that serve as major antenna molecules in cyanobacteria. Besides their role in light harvesting, these pigments exhibit notable antioxidant, anticancer and anti-inflammatory activities, making them valuable compounds for nutraceutical, biomedical and diagnostic applications. For such applications, obtaining phycobiliproteins with high purity and yield is crucial, necessitating the importance of refining extraction strategies. In this study, various cyanobacterial strains were grown in BG-11 medium supplemented with different nitrogen concentrations to evaluate how nitrogen availability influences pigment biosynthesis. Pigment extraction was carried out using phosphate buffer, aided by repeated freeze-thawing and gentle sonication to ensure effective cell disruption. UV-Visible spectroscopy analysis revealed characteristic absorption peaks at 620 nm, 652 nm and 562nm corresponding to C-phycocyanin, allophycocyanin and phycoerythrin respectively, confirming successful pigment extraction and enabling quantitative comparison between treatments. Variation in nitrogen levels significantly affected phycobiliprotein accumulation, with some species exhibiting enhanced pigment content under specific nitrogen conditions. The optimized cultivation and extraction protocol improved pigment recovery, resulting in satisfactory yields of phycobiliproteins suitable for therapeutic and biomedical applications.

Poster Presentation

Development of Multiepitope Peptide Vaccine Using SPy_2191 Protein Conjugated with TLR2 Agonist Against Group A Streptococcal Infections

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Abstract:

Group A *Streptococcus* (GAS), also termed *Streptococcus pyogenes,* is a human-specific, host-adapted, Gram-positive, catalase (CAT)-negative pathogen with characteristic β-hemolysis. It has more than 220 reported emm serotypes. Globally, GAS is estimated to cause 1.78 million new cases and 517,000 deaths annually in low- and middle-income countries. Infection with *Streptococcus* pyogenes results in a broad spectrum of clinical manifestations, from asymptomatic colonisation to common conditions (pharyngitis, scarlet fever, and impetigo) and diseases that cause high mortality (invasive disease and rheumatic heart disease). Group A streptococcal (GAS) infections have been attracting increasing attention, as many countries were overwhelmed by a rapid surge of invasive GAS (iGAS) infections in late 2022 and 2023 after an overall low incidence during the years of the COVID-19 pandemic. Therefore, the development of licensed GAS vaccines is crucial. This was one of the high-priority recommendations made by the WHO's Strategic Advisory Group of Experts on Immunization in 2023. However, owing to serotype diversity, antigenic variation, and the potential for autoimmune sequelae that GAS causes, the development of GAS vaccines has for decades been a challenge for researchers. Major impediments in GAS vaccine development involves high genetic diversity of antigen targets, lack of relevant animal models, cross-reaction of antibody with antigen resulting autoimmune disorders (RHD and ARF). Recent study published by our lab (Sanduja et al., 2020) showed that SPy_2191 protein is conserved across GAS serotypes (98%) of developed and developing countries, inhibit adherence as well as invasion, surface exposed. Further, SPy_2191 was found to be significantly protective with 88% survival rate against Indian serotypes. SPy_2191 elicit bactericidal antibodies against prevalent GAS serotypes of India. We propose to develop multi-epitopic peptide vaccine from suitable T cell and B cell epitopes of SPy_2191 using bioinformatic analysis and conjugate with Toll like receptor 2 agonist with alum as a 3rd generation vaccine formulation against *S. pyogenes* that can elicit more specific robust cellular and humoral immune responses in the host with least side effects.

NMR Based Plasma Metabolomic Profiling Reveals Altered Metabolites Associated with HIV-Infected ART Responsive and Failure Subjects

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Abstract:

According to UNAIDS report, 40.8 million people were living with HIV and 1.3 million became newly infected by the end of 2024, making HIV infection still a major worldwide health concern. With the introduction of antiretroviral therapy (ART), HIV has been reduced from a deadly illness to a chronic, treatable condition; nonetheless, many people still experience immunological dysfunction and metabolic abnormalities even after viral suppression. The current study aimed to elucidate differences in the metabolic profile of HIV- infected ART responsive and failure subjects compared to healthy controls (HCs).We used an untargeted approach through 1 H Nuclear Magnetic Resonance (NMR) spectroscopy to perform metabolomic profiling of plasma samples from 19 HIV infected patients [ART responders (n = 11), ART failures (n = 8), treatment naive (n = 10)], and 14 HCs. Multivariate and univariate analyses were performed to identify the differential gut metabolites associated. ART failure patients showed greater metabolic perturbation than either HIV-infected group, with 18 metabolites significantly altered compared to 17 in ART responders and 14 in treatment naïve patients, relative to HCs (adjusted $p<0.05$). Each group of HIV infected subjects displayed distinct metabolic profiles, yet several metabolites were commonly altered across all the groups, including dimethylglycine, tyrosine, histidine, 3-hydroxybutyrate, trimethylamine, glutamate and pyruvate. In the combined HIV positive versus controls, the most discriminatory metabolites were dimethylglycine, pyruvate, glutamate, trimethylamine, tyrosine and 3-HB (AUC $\geq$ 0.80). Overall, these findings offer insights into the plasma metabolome of HIV-infected patients in India and highlight for the first time the metabolic disruptions associated with HIV-infected ART responsive and failure subjects.

Poster Presentation

Identification of a Lytic Transglycosylase as a Potential Antibacterial Target in Group A *Streptococcus*

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Abstract:

Lytic transglycosylases (Ltgs) are key enzymes involved in peptidoglycan metabolism and bacterial cell division. Although extensively studied as antibacterial targets in Gram-negative bacteria due to their functional redundancy, their potential in Gram-positive pathogens remains largely unexplored. Group A *Streptococcus (*GAS), a major human pathogen, causes a spectrum of diseases ranging from mild infections such as acute pharyngitis and impetigo to severe invasive conditions, including necrotizing fasciitis. Rising antibiotic resistance in GAS driven by excessive and inappropriate antibiotic use necessitates the identification of new therapeutic targets. The GAS genome encodes a protein, SPy_2191, predicted to contain a lysozyme-like domain characteristic of Ltgs. These enzymes catalyze the intramolecular transacetylation that cleaves the glycosidic bond between N-acetylmuramic acid and N-acetylglucosamine, producing a 1,6-anhydromuramoyl residue and contributing to peptidoglycan remodeling. Using bioinformatic analyses, we identified putative ligand-binding cavities within SPy_2191 and evaluated their suitability for inhibitor design. Targeting Ltg activity has also disrupted cell wall remodeling, thereby impairing bacterial growth and division. This work provides a framework for the rational design of small-molecule inhibitors against GAS Ltgs. Such inhibitors have the potential to serve as alternative therapeutics to traditional antibiotics, offering a promising strategy to combat antibiotic resistance in Gram-positive bacteria.

Poster Presentation

Expression and Detergent Solubilization of the High-Affinity Iron Transporter PiFTR from the Root Endophyte *Piriformospora indica*

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Abstract:

Iron (Fe) is an essential micronutrient for plant growth, yet its poor solubility in soil frequently limits bioavailability, leading to Fe deficiency in crops and, consequently, in human populations. *Piriformospora indica*, a root-colonizing endophytic fungus, has been shown to enhance Fe acquisition in plants. A high-affinity Fe transporter (PiFTR) from *P. indica* was previously identified and functionally characterized, establishing its critical role in Fe uptake and delivery during plant–fungal symbiosis. In the present study, we focused on the heterologous expression and detergent solubilization of PiFTR as a foundation for future purification and mechanistic investigations. The PiFTR coding sequence was cloned into the dual-host compatible 83nu vector containing an N-terminal FLAG tag, a C-terminal His tag, and a galactose-inducible promoter. The construct was expressed in the Saccharomyces cerevisiae (DSY5) strain. Membrane fractions from induced and uninduced cultures were analyzed by western blotting with anti-FLAG and anti-His antibodies, confirming successful expression and membrane localization of PiFTR under induction conditions. To identify suitable solubilization conditions, two detergents n-dodecyl-β-D-maltoside (DDM) and lauryl maltose neopentyl glycol (LMNG) were evaluated at concentrations of 0, 10, and 25 mM. DDM efficiently solubilized PiFTR at both 10 and 25 mM, while LMNG supported solubilization only at 10 mM. These results provide optimized conditions for PiFTR stabilization in detergent micelles and form the basis for downstream purification strategies. This work represents the first successful heterologous expression and solubilization of PiFTR, establishing a platform for subsequent purification and structural-functional analyses that will deepen our understanding of fungal-mediated Fe acquisition in plant symbiosis.

Poster Presentation

Study of *Piper longum* Derived Phytochemicals and Their Derivatives as Antimicrobial and Anti-Inflammatory Agents

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Abstract:

Antibiotic resistance has emerged as a serious global concern, necessitating the urgent development of innovative antibacterial drugs derived from natural sources. *Piper longum* L., a medicinal plant utilised in Ayurveda, is thought to possess bioactive compounds having therapeutic properties. In this work, a crude extract from *Piper longum* fruits was macerated and tested for antibacterial activity against both Gram-positive and Gram-negative bacteria. The findings indicated substantial antibacterial activity, indicating the presence of active chemicals. To identify them, the extract underwent preparative high-performance liquid chromatography (HPLC), with distinct fractions recovered based on retention time. Each fraction was then tested for antibacterial activity using the agar well diffusion method. Surprisingly, not all fractions exhibited activity; nonetheless, some demonstrated significant inhibition against Gram-positive and Gram-negative bacteria. Further investigation of their mode of action was carried out using a live/dead bacterial cell staining assay, which revealed disruption of bacterial membrane integrity. These findings suggest that *Piper longum* contains phytochemicals with substantial antibacterial activity, emphasising its potential as a source of natural antibacterial agents. Furthermore, I aim to identify which compound is responsible for the antibacterial activity by performing LC-MS analysis.

In Vitro Assessment of Antimicrobial Activity of *Ventilago maderaspatana* Gaertner Stem Bark Extracts

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Abstract:

Background: *Ventilago maderaspatana* Gaertner is a climbing shrub of Rhamnaceae family commonly known as Rakthavalli and Dinesavalli in Sanskrit, Pitti in Hindi and Red creeper in English. It has medicinal properties and found in Western & Eastern Ghats of India and widely distributed in Sri Lanka, Myanmar and Java. Its Stem bark and Roots are used traditionally and in many Ayurvedic medications to treat various skin diseases. This study aims to evaluate the antimicrobial activity of *Ventilago maderaspatana* Gaertner Stem Bark Extracts. Stem Bark extract of *Ventilago maderaspatana* Gaertner was obtained from successive extraction from Hexane, Ethyl acetate, Acetone and Methanol by Soxhlet extraction, which was evaluated in-vitro against Gram Positive (*Staphylococcus aureus* ATCC 25923), Gram Negative (*Escherichia coli* ATCC 25922) and Yeast (*Candida albicans* ATCC 24433) by agar well diffusion method. It is found that 10µl of 100mg/ml Hexane, Acetone, Ethyl acetate, and Methanol extract of *Ventilago maderaspatana* stem bark is effective against *S. aureus*, with zone of inhibition 6mm, 12mm, 9mm and 13mm respectively. Acetone extract shown activity against *C. albicans* with 14mm zone of inhibition. Gentamycine disc (17µl/disc) for bacteria and Fluconazole disc (25µl) for C. albicans were used as a Positive control shown 26mm & 17mm zone of inhibition. DMSO was used as negative control, not shown any activity against *S. aureus*, *E. coli* and *C. albicans*. None of the extract shown activity against *E. coli*. *Ventilago maderaspatana* Gaertner Stem Bark extract shown antimicrobial activity against *S. aureus* and *C. albicans*.

In Vitro Assessment of Antibacterial Activity of *Tribulus terrestris Linn.* Methanolic Seed Extract

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Abstract:

Background: *T. terrestris* is a traditional medicinal plant. It is related with zygophyllaceae family. Its Hindi name is Gokshura or Gokharu. It is found in tropical, subtropical and warm temperature region worldwide. It grows as a weed in dry, sandy soils, agricultural field and wastelands. Gokshura used in Ayurvedic medicine as a diuretic and also used for other kidney related disease. Its role is also mentioned in Ayurvedic text like Charak Samhita & Sushrut Samhita for UTI infection, dysuria, cystitis. In Ayurveda Gokshura helps maintain the balance of Vatta, Pitta and Kapha. This study aims to evaluate the antibacterial activity of methanolic seed extract of *Tribulus terrestris* Linn. against gram positive cocci (*S. aureus* ATCC 25923). Shade dried seed of *T. terrestris* grind to form powder and dissolve in 20gram/100ml methanol for extraction by maceration method. The solution shakes at 100-150 rpm for 72 hrs on rotary shaker. Filter the solution and concentrate the supernatant at 65ºC for 24 hrs in water bath. 100mg extract dissolved in 1ml DMSO which was evaluated in vitro against gram positive (*Staphylococcus aureus*) by agar well diffusion method. It is found that 50µl, 75µl and 100µl methanolic seed extract of *T. terrestris* is effective against *S. aureus* ATCC 25923 with zones of inhibition of 3 mm, 5 mm, and 8 mm respectively. Gentamycin was used as a positive control with 18mm zone of inhibition, DMSO used as a negative control showing no any activity against *S. aureus*. *T. terrestris* methanolic seed extract shown antibacterial activity against *S. aureus* significantly.

Poster Presentation

Development of a Photo-Activated, Implantable and Retrievable NP-Coated Chip for Targeted Eradication of Deep-Tissue UTI Infections Using Photothermal Therapy

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Abstract:

Urinary tract infections (UTIs), predominantly caused by uropathogenic *Escherichia coli* (UPEC), represent one of the most common bacterial infections worldwide, affecting more than 150 million individuals annually. A severe manifestation, termed deep-tissue UTI, extends beyond the superficial urinary tract to involve organs such as the kidneys and prostate. Despite antibiotic therapy, relapse occurs in 30–50% of cases, and the growing resistance of UPEC to last-resort antibiotics, including carbapenems and colistin, poses a critical clinical challenge. Nanomaterial-based photothermal therapy has recently emerged as a promising strategy due to its ease of application, potent antibacterial activity, and reduced risk of resistance development. In this study, we developed an implantable and retrievable chip designed for photothermal ablation of *E. coli* upon near-infrared (NIR) irradiation. The chip exhibited a broadened absorption spectrum spanning UV-Vis to NIR-I and NIR-II regions, with a plasmonic peak near 750 nm and strong absorption up to 1500 nm, enabling deep-tissue penetration. Thermal imaging confirmed rapid and reversible localized heating, generating transient hyperthermia. This thermal effect, coupled with the intracellular production of reactive oxygen species (ROS), resulted in effective bacterial suppression and significant disruption of mature biofilms. Biocompatibility was validated using the chorioallantoic membrane model, where the chip supported vascularization and angiogenesis. In vivo studies on wound healing and dermal infections demonstrated accelerated tissue repair and improved infection control, as evidenced by histological restoration of the epithelial barrier and expression of key regenerative biomarkers. In a UTI model, the system successfully eliminated GFP-tagged *E. coli* within 48 hours of implantation and irradiation, as confirmed by IVIS imaging and bacterial culture of tissues and body fluids. Collectively, these findings highlight the photo-responsive chip as a promising alternative for targeted eradication of deep-seated bacterial infections and promotion of host tissue repair.

Antimicrobial Peptides (Amps) Mediated Membrane Targeted Approach against Methicillin Resistant *Staphylococcus Aureus* (MRSA) Infections

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Abstract:

Bacteria, with their relatively simple unicellular structure and capacity for rapid genetic evolution, can swiftly develop resistance to antibiotics. To combat these resistance mechanisms, targeting the bacterial membrane has emerged as an effective strategy. Antimicrobial Peptides (AMPs) are emerging as promising alternative to conventional antibiotics by targeting anionic bacterial membrane via electrostatic and hydrophobic interaction. Venoms, a rich source of bioactive peptides present promising avenues for drug discovery and development. Latarcins, a class of seven AMPs isolated from the venom of ant spider *L.tarabaevi*, exhibit notable biological activities including antimicrobial and anticancer effects. Our ongoing research focuses the assessment of therapeutic efficiency and the mechanism of membrane interaction of Latarcins. Our preliminary results revealed that Latarcins exhibited broad-spectrum antimicrobial activity against gram-positive and negative bacterial and fungal pathogens, with Latarcin2a showing the highest efficacy. Flow cytometry analysis using PI dye confirmed nearly 50% membrane disruption in treated MRSA cells. Time kill kinetics demonstrated rapid bacterial killing, with all active Latarcins inducing bacterial death within 30 minutes, notably Ltc2a achieving a 1-log reduction in MRSA cell population within 5 minutes. Interestingly, checkerboard assay revealed that Oxacillin and Ltc2a showed synergetic effects with FIC value of 0.25 by reducing the oxacillin MIC to 1 µg/mL. Structure Illumination Microscopy (SIM) imaging of Ltc2a treated MRSA cells stained with Nile red showed that the organization of phospholipids is altered confirmed by the accumulation of Nile red dye on the one side of the membrane in treated samples. Further, the efficiency of treatment for the higher order structures having higher infection risk such as on biofilms, intracellular infections will be evaluated. This combinational approach along with the inherent antibacterial potential of AMPs seems to be a promising strategy to resensitize the MRSA cells to conventional beta lactams with lesser chance of inducing resistance evolution.

Poster Presentation

Identification of Some Potential Chemopreventive Agents and to Investigate their Efficacy in Cancer Cells

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Abstract:

Chemoprevention needs identification of compounds that possess the potential to suppress initiation or growth of tumors. In this study, we evaluated the chemopreventive potential of Acumapimod, BAM 15, and 7-Methoxyisoflavone (7-MIF). We tested their ability to suppress cell proliferation in three different cancer cell lines: HCT116, MCF-7, and A549. As we previously identified Monoamine Oxidase A (MAO-A) as a potential therapeutic target for cancer aggressiveness, we checked the effect of these compounds on MAO-A expression/ activity as well as on cell proliferation in all those cell lines. Our results demonstrated the efficacy of Acumapimod in controlling MAO-A- mediated cancer progression. On the other hand, BAM 15 markedly increased the expression of p21 and p53 in all three cell lines while inhibiting proliferation, suggesting that tumor suppressor-mediated apoptotic pathways were activated. Interestingly, BAM 15 had no effect on MAO-A expression/ activity, suggesting that its effect on proliferation is independent of MAO-A. In A549 and MCF-7 cells, 7-MIF exhibited strong antiproliferative activity, which caused MAO-A, BAX, and P21 upregulation whereas BCL2 downregulation in MCF-7 and A549 cells. These findings thus indicate the mechanistic actions of 7-MIF in regulating cell survival and apoptosis. Collectively, these results demonstrate that 7-MIF, BAM 15, and Acumapimod modulate various molecular pathways, such as tumor suppressor activation, apoptotic regulation, and suppression of MAO-A expression/activity, to produce unique anticancer effects. The importance of focusing on a variety of cellular mechanisms in cancer treatment and prevention is highlighted by this study, which also offers insightful information about their potential as chemopreventive agents.

Poster Presentation

Phytochemical Diversity and Extract Protocols Impart Differential Anti-Cancer Potentiality to Tridax procumbens Silver Nanoparticles Prepared from Leaves Collected from Pan-India

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Abstract:

Cancer is a major public health problem worldwide. According to GLOBOCAN 2022, 19,976,499 cases of cancer were reported in the year 2022. Nanoparticles due to their profound implications explored as; Vehicle in drug delivery, as antimicrobial agents, and cancer therapy. *Tridax procumbens* is a widely distributed plant thriving across tropical, subtropical, and mild temperate regions worldwide. It holds a prominent place in traditional medicine systems of India, Africa, and the Americas, where it has been extensively used to treat wounds, cancer, skin infections, diarrhoea, and various respiratory and gastrointestinal ailments, often serving as a natural antiseptic. In this study we synthesized *Tridax procumbens* silver nanoparticles (TNP s) from leaves of *Tridax procumbens* collected from 15 differect sites of India. Synthesis of TNPs confirmed by UV-Visible spectroscopy showing maximum absorbance between 410nm to 435nm of all 15 TNPs. Size of TNPs were confirmed by TEM. FTIR analysis showing 6 major peaks from 15 different TNPs; out them 3 peaks observed in all 15 TNPs that are representing O-H streching, N-H bending and M-O streching. HRLC-MS analysis was done to find out the phytochemical profile of TNPs. Total 38 different compounds were found from 15 TNPs out of them 15 compounds were documented for anti-cancer activity. Cytotoxicity of TNPs on cancerous cells were checked using MTT assay, wound healing assay and anti-oxidant assay. The localization assay was employed to examine the target site of TNPs within cancerous cells. TNPs significantly inhibit cancerous cells prolifiration. The IC50 values from MTT assay of all 15 TNPs ranged from 6.93 µg/ml to 49.87 µg/ml for A549 (non-small cell lung carcinoma) and from 1.31 µg/ml to 16.43 µg/ml for A431 (human epidermal melanoma) cell lines.

Poster Presentation

Exploring Enzymatic Degradation of Plasticizers: Insights from Functional and In Silico Studies

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Abstract:

Plastic pollution, particularly from phthalate acid esters, is a major environmental concern due to its persistence and toxicity. In the present study, three previously characterized bacterial strains were explored for degradation of plasticizers, in particular phthalate esters. Through genome mining, nearly 18 genes associated with degradation of widely used plastics like polybutylene adipate terephthalate (PBAT), polyethylene terephthalate (PET), polyurethane (PU) and nylon were identified. Phylogenetic diversity analysis of alpha/beta hydrolases and carboxylesterase/lipase enzymes was carried out using protein sequences. The analysis suggested the occurrence of highly conserved domains. Further, homology modelling of PETase enzymes retrieved from the genomes was carried out. Protein ligand interactions of PETases from the three strains with four selected ligands benzyl butyl phthalate (BBP), bisphenol A (BPA), diisobutyl phthalate (DIBP), and terephthalic acid (TPA) were studied. Finally, to assess the phthalate degradation potential, the bacteria were exposed to a mixture of phthalates containing BBP, BPA, DIBP, and TPA. The lysate of the exposed cells was used to determine carboxylesterase activity, which revealed an enhanced activity compared to the unexposed control cells. The findings, integrating genomic potential, computational modelling, and functional assays, indicate viable bacterial candidates for plastic waste bioremediation.

Non-Albicans Candida Predominance in Candidemia Enzymatic Activity and Antifungal Susceptibility Analysis in a North Indian Cohort

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Abstract:

Candidemia, a leading cause of invasive fungal infections, is increasingly driven by non-albicans Candida (NAC) species, with rising antifungal resistance posing significant challenges, especially for immunocompromised patients. This study explores the virulence characteristics and antifungal susceptibility profiles of *Candida* species isolated from bloodstream infections in Varanasi, India, to inform targeted therapeutic strategies. From August 2022 to August 2025, 515 *Candida* isolates from blood cultures at Sir Sunderlal Hospital, Banaras Hindu University, were studied. Species were identified using phenotypic (Gram staining, Hi-chrome Candida agar, Cornmeal agar, Germ tube assay) and genotypic (RFLP, MALDI-TOF MS) methods. Virulence factors (phospholipase, proteinase, esterase, haemolysin) were assessed via standardized assays. Antifungal susceptibility to eight agents (amphotericin B, fluconazole, voriconazole, itraconazole, posaconazole, caspofungin, micafungin, anidulafungin) was tested per CLSI M27-A3 guidelines. NAC species dominated (83.88%, n=432), with *C. utilis* (30.6%) and *C. tropicalis* (29.5%) being the most prevalent, compared to C. albicans (16.11%, n=83). C. albicans exhibited the highest virulence, with 85.5% showing very strong phospholipase activity, 78.31% proteinase, 90.36% esterase, and 96.38% haemolysin activity. Among NAC species, *C. orthopsilosis, C. parapsilosis, and C. guilliermondii* displayed notable proteinase and haemolysin activities, while *C. rugosa and C. guilliermondii* lacked phospholipase activity. Antifungal susceptibility varied widely: *C. albicans* showed high susceptibility to azoles (e.g., 89.15% for fluconazole) and echinocandins (>98%), whereas C. auris exhibited significant resistance to fluconazole (88.88%) and amphotericin B (29.62%). *C. glabrata* and *C. parapsilosis* were highly susceptible to azoles and echinocandins, while *C. rugosa* and *C. pelliculosa* showed reduced azole sensitivity. The predominance of NAC species, particularly *C. utilis* and *C. tropicalis*, coupled with the heightened virulence and resistance of *C. auris*, highlights the critical need for species-specific antifungal strategies. Continuous monitoring of enzymatic profiles and resistance patterns is vital to optimize candidemia management and improve patient outcomes.

Poster Presentation

A Marine Endophytic Bacillus subtilis Strain Exhibiting Multifunctional Plant Probiotic Traits for Sustainable Agriculture

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Abstract:

Marine ecosystems harbor diverse microorganisms with unique metabolic capabilities, but their role in promoting plant growth remains largely unexplored. In the present study, a marine endophytic bacterium was isolated from a macroalga, *Ulva lactuca*, and was subsequently identified as *Bacillus subtilis* ULB16 through 16S rRNA gene sequencing. The strain demonstrated multiple plant growth-promoting traits, including indole-3-acetic acid production, inorganic phosphate solubilization, and nitrogen-fixing ability, indicating its diazotrophic potential. These attributes highlight the isolated endophyte's prospect to stimulate plant development under nutrient-limited conditions. Further, Bacillus subtilis ULB16 significantly improved seed germination percentage, root and shoot elongation, and overall seedling vigor under stress conditions. Collectively, these findings highlight Bacillus subtilis ULB16 as a multifunctional marine endophyte with strong potential as a sustainable bioinoculant to enhance crop productivity and resilience in saline and nutrient-deficient agroecosystems. To our knowledge, this is the first report demonstrating a marine endophytic bacterium as a promising candidate for plant probiotic applications.

Exophiala spinifera CSF123: A Novel Source of Biosurfactant Molecules with Biotechnological Potential and Applications

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Abstract:

Microorganisms, including bacteria and fungi, produce biosurfactants, which are surface-active, biodegradable, and eco-friendly molecules analogous to chemical surfactants. While bacterial biosurfactants are well studied, fungal counterparts, particularly from filamentous Ascomycota, remain less explored yet hold great potential. Their structural diversity, stability, and non-toxic nature make them attractive alternatives to synthetic surfactants. Owing to their antibacterial, antifungal, and anticancer properties, fungal biosurfactants are valuable for applications in environmental remediation, pharmaceuticals, cosmetics, and the food industry. The present study focuses on the isolation, structural and functional characterization of two biosurfactant molecules from a fungus obtained from a cashew oil-contaminated soil. The biosurfactants from the fungal strain, named *Exophiala spinifera* CSF123, exhibited strong anti- quorum sensing activity against *Chromobacterium violaceum*. The HPLC-purified molecules also possess antibacterial activity against both wild-type and methicillin-resistant *Staphylococcus aureus* (MRSA), highlighting their pharmaceutical potential. In addition, they showed remarkable dye-removal efficiency against Congo red, malachite green, methylene blue and crystal violet, demonstrating their suitability for environmental bioremediation applications. Structural characterization of the molecules was carried out using elemental analysis, UV-visible spectroscopy, and mass spectrometry. From the mass spectra, the neutral masses of the molecules were determined to be 414 Da and 428 Da. Elemental analysis revealed a remarkably low carbon content of 28.54% and 16.54%, respectively, indicating unique structural composition and distinguishing the biosurfactant molecules produced by *Exophiala spinifera* CSF123 from typical classes of biosurfactants. Overall, *Exophiala spinifera* CSF123 represents a novel and potent source of multifunctional biosurfactants with antimicrobial and dye-removal activities, highlighting its transformative potential in biotechnological, environmental, and pharmaceutical applications.

Poster Presentation

Insights into the Characteristics and Bioactivity of Encapsulated Native Orange Oil using Maltodextrin and Salai Gum

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Abstract:

The present study focuses on the encapsulation of *Citrus reticulata* (Nagpur orange) essential oil using maltodextrin and native *Boswellia serrata* (Salai) gum as natural wall materials. Encapsulation was performed by the spray-drying technique following high-speed homogenization of oil-in-water emulsions at varying ratios: (i) 15 mL oil + 25 g maltodextrin + 85 mL distilled water, (ii) 25 mL oil + 25 g maltodextrin + 75 mL distilled water, and (iii) 25 mL oil + 25 g maltodextrin + 2 g Salai gum + 75 mL distilled water. The microencapsulated powders were characterized for physicochemical parameters including moisture content, bulk and tapped densities, particle density, porosity, flowability, cohesiveness, water dispersibility, and hygroscopicity. Phytochemical and bioactive properties were assessed through total phenolic, flavonoid, and surface phenolic content analyses, along with antioxidant assays (DPPH, ABTS, and FRAP). Preliminary observations revealed that incorporation of Salai gum improved powder flowability and dispersibility, indicating better retention of bioactive components. Antioxidant assays demonstrated concentration-dependent radical scavenging potential, while antibacterial activity (against *E. coli* and *S. aureus*) and antifungal activity (against *R. solani* and *A. niger*) highlighted the functional efficacy of the encapsulated formulations. Scanning electron microscopy (SEM) will be performed to confirm particle morphology and structural integrity. The study emphasizes the potential of using native gums and essential oils in developing natural, stable, and bioactive encapsulated systems for food, pharmaceutical, and agricultural applications.

Advancing Proton Pump Dynamics for Improved Proton Transport and Energy Conversion Efficiency in Algae

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Abstract:

Enhancing proton transport efficiency in algae is a key strategy to improve photosynthetic energy conversion and bioenergy generation. Proton pumps located in the thylakoid and plasma membranes regulate the proton motive force essential for ATP synthesis and electron transfer. This study presents multifaceted approaches to advance proton pump dynamics in algal cells through integrated genetic, biochemical, and environmental optimization. In the current study, media modifications and environmental factors were explored to induce proton transport responses for increased photovoltaic yield or biohydrogen generation. The change in pH, metal ions, nutrient limitation, and photoperiod manipulations caused an increased transport of protons. Mass optimization for the isolated Scenedesmus sp. from mixed algal culture was obtained (3.9×10^6 cells/ml in 100 ml and 19.5×10^6 cells/ml in 500 ml), with pigment extraction values of chlorophyll a (6.31 µg/ml) and chlorophyll b (8.08 µg/ml). The initial day cell concentration in the medium was 1.6×10^6 cells/ml, which gradually increased over 10 to 12 days. The metal cofactors in the photoelectrodes further enhanced voltage generation and overall energy conversion efficiency. These findings highlight the potential of targeted biochemical and environmental modulation of proton pumps for scaling sustainable algal bioenergy systems and improving integrated bioelectrochemical applications.

Genetic Polymorphisms in ABCA1 (Rs2230806 and Rs141420090) Gene and their Association with the Risk of Type2 Diabetes and CAD: A Case Control Study

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Abstract:

Type 2 Diabetes Mellitus (T2DM) and Coronary Artery Disease (CAD) are complex, multifactorial conditions that share common genetic and metabolic mechanisms. The ATP- binding cassette transporter A1 (ABCA1) gene is essential for the metabolism of cholesterol efflux and high-density lipoproteins (HDL) and, for maintaining glucose and lipid homeostasis. Genetic variations in ABCA1 may affect insulin sensitivity and lipid transport, which in turn may affect susceptibility to T2DM and CAD. This study aims to determine the association of the ABCA1 gene polymorphisms rs2230806 and rs141420090 to the risk of T2DM and CAD in the population of Haryana state. A case control study was conducted including clinically diagnosed T2DM patients, CAD patients, T2DM with CAD patients and healthy controls. Genomic DNA was isolated from peripheral blood samples, and genotyping was performed using PCR-RFLP followed by agarose gel electrophoresis. Allelic and genotypic frequencies were compared using chi-square analysis, and odds ratios (OR) with 95% confidence intervals (CI) were calculated to assess disease association. Lipid profiles and fasting glucose levels were also evaluated to correlate genotypic variations with biochemical parameters. This study examined T2DM, CAD, and T2DM+CAD patients with healthy controls, making sure that age was matched correctly between groups no discernible changes were found. A statistically significant difference in allelic distribution (G vs A) was observed between healthy subjects and T2DM patients of rs2230806. However, there is no statistically significant differences were observed in allelic distributions (A vs C) between healthy subjects and T2DM patients of rs141420090. The current study suggests that the ABCA1 mutation rs2230806 may work as a risk factor for the development of type 2 diabetes and type 2 diabetes with CAD. Furthermore, the variant rs141420090 was found to not be a risk factor for the development of T2DM, CAD, or T2DM with CAD. More large-scale research are still needed to validate the results because of the sample size's poor power.

Unlocking Antifungal Potential of *Bacillus chitosanase*: A Sustainable and Unexplored Solution to Fungal Pathogens

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Abstract:

The global rise in severe, antifungal-resistant fungal infections, including post-COVID-19 aspergillosis and mucormycosis, necessitates novel control strategies. This study investigates the broad-spectrum antagonistic potential of *Bacillus velezensis* against a series of significant fungal pathogens: *Rhizopus oryzae*, *Rhizomucor pusillus*, *Mucor circinelloides*, *Apophysomyces elegans* and *Fusarium fujikuroi*. Antifungal activity of the cell-free supernatant of *B. velezensis* was characterized using cross-streak and poison food assays, with centrifugal ultra-filtration, heat and enzyme sensitivity tests confirming the bioactive agent was a heat-labile enzyme. Enzymatic profiling identified this molecule as a chitosanase. Microscopic examination of chitosanase effect showed a pronounced structural alteration in fungal spores and hyphae, suggesting degradation of the chitosan layer and compromise of cell wall integrity. Chitosanase production was optimized through a one-variable-at-a-time approach followed by Plackett–Burman screening and response surface methodology (RSM). The resulting statistically significant RSM model yielded a 94% increase in chitosanase yield. To our knowledge, this is the first comprehensive study detailing the broad-spectrum antifungal activity of a chitosanase from *B. velezensis*, encompassing screening, characterization and optimization. These findings position this enzyme as a promising, sustainable biocontrol tool for managing fungal diseases in both clinical and agricultural sectors.

Exploring the Role of ABCA1 Gene Polymorphisms (Rs2066718 and Rs138271089) in the Pathogenesis of Type 2 Diabetes Mellitus (T2DM), Coronary Artery Disease (CAD) and T2DM with CAD Patients

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Abstract:

The ATP-binding cassette transporter A1 (ABCA1) gene is pivotal in cholesterol efflux and high-density lipoprotein (HDL) synthesis, affecting vulnerability to metabolic and cardiovascular disorders. Single nucleotide polymorphisms (SNPs) in ABCA1, including rs2066718 and rs138271089, are posited to influence disease risk and phenotypes in type 2 diabetic mellitus (T2DM), coronary artery disease (CAD) and their comorbidity. This study sought to examine the genotypic and allelic distribution of ABCA1 SNPs among healthy controls, T2DM, CAD and T2DM with CAD patients, as well as to evaluate their correlation with disease state. ABCA1 SNPs (rs2066718, rs138271089) were genotyped via PCR-RFLP utilising HpyCH4V and Nt.CviPII restriction enzymes, with statistical analysis conducted using chi-square tests, odds ratios and Hardy-Weinberg equilibrium assessments. For SNP rs2066718, the GA genotype was most prevalent, whereas the GG and AA genotypes exhibited lower prevalence. The allelic distribution (G vs. A) exhibited no significant difference between healthy controls and T2DM patients ($p = 0.456$); however, a highly significant difference was noted between controls and CAD patients ($p = 0.002$). Similar for SNP rs138271089, the heterozygous CG genotype was the most prevalent, whereas the CC and GG genotypes were less frequent. The allelic frequencies of C and G exhibited no significant differences among healthy controls, T2DM, CAD, or CAD+T2DM groups. Resultant rs2066718 of ABCA1 gene serves as a potential genetic marker for vulnerability to coronary artery disease, although rs138271089 does not show such associations.

Population Based Analysis of ABCA1 Variants (Rs9282543 and Rs187652566) and their Correlation with Coronary Artery Disease (CAD) and Type 2 Diabetes mellitus (T2DM)

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Abstract:

Type 2 diabetes mellitus (T2DM) and coronary artery disease (CAD) are among the most common metabolic disorders globally, frequently co-occurring due to overlapping genetic and environmental risk factors. The ATP-binding cassette transporter A1 (ABCA1) gene is crucial for reverse cholesterol transport (RCT) and lipid metabolism, affecting insulin sensitivity and cardiovascular risk. Four groups healthy controls, T2DM patients, CAD patients and CAD+T2DM patients were genotyped for ABCA1 rs187652566 and rs9282543 via PCR- RFLP using HpyCH4V and HphI restriction enzymes respectively. Allelic and genotypic frequencies, along with Hardy-Weinberg equilibrium, were evaluated. Statistical analysis was conducted utilizing chi-square tests and odds ratios (OR) accompanied with 95% confidence intervals (CI). For rs9282543, no significant differences in allelic distributions (A versus G) were observed among controls and T2DM (p=0.974), CAD (p=0.107) and T2DM + CAD (p=0.24) cohorts. For rs187652566, a significant difference in allele distribution (C vs A) was identified between healthy individuals and CAD subjects ($\chi^2 = 12.916$, OR = 0.554 [95% CI: 0.400–0.765], p = 0.001), although no significant difference was detected for T2DM and T2DM+CAD subjects. These findings indicate that particular ABCA1 variations may affect lipid metabolism and play a role in the etiology of CAD in the examined population.

Association of ABCA1 Gene Polymorphism (Rs145105484) with T2DM and CAD

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Abstract:

The transmembrane protein ATP-binding cassette transporter A1 (ABCA1), which is extensively expressed in several tissues, is one of the numerous proteins involved in maintaining cholesterol homeostasis. As the initial stage of reverse cholesterol transport (RCT), one of its primary roles is the efflux of intracellular free cholesterol and phospholipids across the plasma membrane to combine with apolipoproteins, primarily apolipoprotein A-I (Apo A-I), to form nascent high- density lipoprotein-cholesterol (HDL-C) particles. A case control study was conducted including clinically diagnosed T2DM patients, CAD patients, T2DM with CAD patients and healthy controls and their association with ABCA1 gene polymorphism. Total 640 subjects were taken. Genomic DNA was isolated. The selected SNP (rs145105484) was amplified through PCR (product size 174bp) and analyzed using the restriction fragment length polymorphism (RFLP) technique. The digested products were visualized by agarose gel electrophoresis. Statistical analysis was performed using the chi-square test, odds ratio (OR), and 95% confidence interval (CI) to determine disease association. The heterozygous TG genotype constituted largest genotype (52% in healthy subjects, 53.3% in T2DM, 55.3% in CAD and 57.3% in CAD+T2DM patients) followed by homozygous genotype TT (36% in healthy subjects, 30% in T2DM, 31.3% in CAD and 30.6% in CAD +T2DM and homozygous mutated genotype GG (12% in healthy subjects,16.6% in T2DM, 13.3% in CAD and 12% in CAD +T2DM. Statistical analysis of genotyping and allelic frequencies revealed no significant association between rs145105484 polymorphism and any of the disease groups.

Occurrence of G Allele at Rs1800976 of ABCA1 Gene in North Indian Population (Haryana) Confers Increased Susceptibility to Atherosclerotic Complications in Diabetic Individuals

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Abstract:

Type 2 diabetes mellitus (T2DM) increases the risk of coronary artery disease (CAD) due to shared metabolic and genetic factors. The ATP-binding cassette transporter A1 (ABCA1) gene mediates cellular lipid export and contributes to atheroprotection. Variants in this gene can therefore affect lipid transport pathways leading to cardiometabolic susceptibility. The current study aims to investigate the association of ABCA1 polymorphisms (rs1800977 and rs1800976) with T2DM, CAD and T2DM+CAD in the population of Haryana state. A case control study of 600 participants (150 controls, 150 T2DM, 150 CAD and 150 T2DM+CAD) was conducted. Biochemical parameters were measured enzymatically and genotyping was performed by PCR–RFLP. Associations were analyzed using chi-square tests and odds ratios with Bonferroni correction. SNP rs1800977 showed no significant association with disease risk but was linked to improved lipid and blood pressure profiles among CAD and T2DM+CAD patients. ABCA1 variant rs1800976 exhibited a strong association with CAD and T2DM+CAD ($p < 0.05$), with the G allele conferring increased susceptibility to atherosclerotic complications (OR ≈ 3.1). Thus, ABCA1 rs1800976 variant may serve as a genetic marker for CAD risk in diabetic individuals, while rs1800977 appears to influence lipid metabolism. Larger multi-ethnic studies and functional evaluations are required to validate these finding.

Poster Presentation

Synthesis, Purification, Characterization and Biological Activity of Novel Angiotensin Converting Enzyme Inhibitor Peg- 2-Thienyl-Alanine-Ornithine-Proline (Pegylated Top) for Hypertension

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Abstract:

Hypertension is a major global risk factor for cardiovascular disease, necessitating the development of safer and more effective treatments. While angiotensin-converting enzyme (ACE) inhibitors are widely used, traditional agents often exhibit limited bioavailability, rapid clearance, and adverse side effects. In this study, we report the synthesis, purification, and characterization of a novel PEGylated tripeptide, PEG-2-Thienyl-Alanine-Ornithine-Proline (PEGylated TOP), designed as an innovative ACE inhibitor. The compound was synthesized using solid-phase peptide synthesis with targeted PEGylation to enhance pharmacokinetic stability. High-purity PEGylated TOP was obtained via preparative HPLC and confirmed by MALDI-ToF mass spectrometry. Circular dichroism and dynamic light scattering analyses confirmed structural integrity and successful PEG conjugation. PEGylated TOP represents a promising therapeutic candidate for hypertension, combining rational peptide design and PEG-based drug delivery to improve efficacy and safety.

Poster Presentation

Genetic Association of ABCA1 Polymorphism with Type2 Diabetes and Coronary Artery Diseases in North Indian Population

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Abstract:

ATP-binding cassette transporter 1 (ABCA1) is a trans-membrane protein responsible for the efflux of cholesterol and phospholipids across the cell membrane. Mutations in ABCA1 are a major genetic contributor to genetic risk factor for Type 2 Diabetes mellitus (T2DM), Coronary Artery Diseases (CAD) and T2DM with CAD. The present investigation was carried in the rs2066715 and rs2230808 polymorphisms in ABCA1 gene and find out its associations with the risk of T2DM, CAD and T2DM with CAD on the chromosome 9p21 and ABCA1 in a North Indian population. A total of 600 (150 healthy individuals, 150 T2DM patients, 150 CAD patients and 150 T2DM with CAD patients) aged above 35 years of either gender from different zones of Haryana or North Indian State were included in the study. The presence of these SNPs was then checked by using PCR-RFLP and the associations were analyzed using chi- square test and odd ratios with Bonferroni correction. The polymorphism at position R1587K in ABCA1 gene was significantly associated with development of T2DM, CAD and CAD + T2DM ($p = 0.016$, $p = 0.001$). Our study suggested that TA+AA genotype of SNP rs2230808 is strongly associated with alterations in lipid metabolism and may confer increased risk for T2DM, CAD, and T2DM + CAD both. But significant association could not be observed between V825I variant of ABCA1 gene and diseases risk.

Poster Presentation

Addressing the Genomic Limitations in Gerbera for Functional Genomics

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Abstract:

Gerbera is an economically important plant with vibrant and wide range of colors. Despite its significance in global cut market, molecular research for trait improvement in Gerbera is lagging. Also, Gerbera has limited gene sequences available in public domain. For this reason, the utility of advanced cutting-edge technology in Gerbera is still infancy. In contrast, genomic resources are available for many ornamental plants that have facilitated the identification of genes regulating ornamental traits such as flower color, floral pattern, and fragrance. This has strengthened the cutting edged molecular research in other ornamental plants. To address this gap in genetic resources in Gerbera, we performed whole genome sequencing of the Indian variety Gerbera hybrida 'Him-Aabha' developed at CSIR-IHBT, Palampur, using Oxford Nanopore Technologies. Exploiting this data an attempt has been made to explore molecular mechanism underlying the changes in the flower color of Gerbera. CSIR-NBRI, Lucknow, maintains multiple Gerbera genotypes, including Toro Rosso (red), Sorrono (yellow), Bubblegum (pink), Pavitra (orange), and Casa Blanca (white). In this study, virus-induced gene silencing (VIGS) was attempted in Toro Rosso and Bubblegum to assess preliminary effects of targeted gene silencing. Additionally, an efficient regeneration and transformation protocol was established in Toro Rosso. A 544 bp guide RNA (gRNA) cassette was successfully developed in the pKSE401 vector for CRISPR-based genome editing. These results provide proof-of-concept for functional genomics in Gerbera and open avenues for dissecting the molecular mechanisms underlying flower color regulation in the Asteraceae family. The knowledge gained will support targeted manipulation of Gerbera flower color, strengthening India's floriculture sector and enhancing farmer profitability.

Degradation of Imidacloprid and its Metabolite Imidacloprid Olefin by Fungal Isolate *Penicillium Oxalicum* and its Applicability for Soil Bioremediation

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Abstract:

All over the world, due to the overuse of chemical pesticides soil gets polluted and fertility of the soil decreases day by day. Imidacloprid is a nicotinoid pesticide, which is very toxic and shows detrimental effects to human beings like blindness, nausea etc. Half-life of Imidacloprid is 26-229 days, its metabolite Imidacloprid olefin also shows harmful effects. Enrichment was carried by Indigenously fabricated columns. Total 30 fungal isolates were isolated from imidacloprid contaminated soil and pesticide tolerance was checked by gradient plate technique and MIC (Minimum inhibitory concentration), fungal isolated I4 showed maximum tolerance up to 1,00,000 mg/L concentration of Imidacloprid. Degradation kinetics study was observed, as compared to other isolates, fungal isolate I4 *Penicillium oxalicum* showed maximum degradation of Imidacloprid (100 mg/L) and its toxic metabolite imidacloprid olefin in 72 and 96 h respectively. Growth kinetics study of 3 maximum Imidacloprid degrading fungal isolates was also studied, *Penicillium oxalicum* showed maximum growth (dry weight) in presence of Imidacloprid. Degradation was carried out in acclimatized condition, in absence of carbon maximum degradation (100%) degradation was observed. Toxicity of Imidacloprid was studied by seed germination assay allium cepa assay which proves that no toxic metabolite is present in biodegraded media, mitotic index was higher (18.52%) in presence of biodegraded media. According to optimization study like OFAT, statistical analysis Plackett-Burman Design (PBD) and Central composite design (CCD), three factors potassium chloride (0.2 g/L), sucrose (30 g/L) and inoculum size (0.7 ml) were significant (p value<0.05) which were responsible for maximum degradation. After optimization, 100% degradation of Imidacloprid and its toxic metabolite imidacloprid olefin was occurred in 42 and 72 h respectively. Metabolite imidacloprid olefin (m/z 253.59) was detected by GC-MS and LC-MS analysis. Degradation pathway was proposed for degradation of Imidacloprid in to imidacloprid olefin. Field assay was performed in which production of cabbage get increased in presence of fungal isolate I4 and it also improves soil properties through bioremediation process. Biodegradation process which is used in research study is economical, ecofriendly and versatile.

Exploring the Structural Basis of Octamer Formation in *H. pylori* 26695 N-Carbamoylputrescine Amidase (CPA)

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Abstract:

Helicobacter pylori is a major human gastric pathogen associated with chronic gastritis and gastric cancer. Amidst the increasing challenge of antimicrobial resistance, identifying alternative therapeutics has become essential. Polyamines are absolutely indispensable for the growth and survival of plants and bacteria. Thus, N-carbamoylputrescine amidase (CPA), an intermediate enzyme in the polyamine biosynthesis pathway, could be a promising target for new therapeutics, because it is absent in humans. CPA is a nitrilase family enzyme, and nitrilases fold into a spiral-shaped multimeric assembly. Although some structural studies of these nitrilases are available, limited information is available that describes the importance of multimerisation in protein function. Previous data suggest that *H. Pylori* 26695 CPA exists as an octamer, and mutations in specific residues at the interface lead to the formation of inactive dimers. This indicates that additional interface(s) may play a role in the multimerisation. To explore these residues, we examined the available structures of CPA homologs. The octameric Medicago truncatula CPA, with 40% sequence similarity to *H. pylori* CPA, was used to generate *H. pylori* 26695 CPA structure. Our study reveals several critical interfacial interactions involved in the formation of an active CPA. Mutations of these residues significantly reduce both catalytic activity and thermal stability. Additionally, a Glu residue, near the interface, appears to play a crucial role in substrate binding, underscoring a close relationship between its catalytic function and oligomeric state. Together, our studies indicate that three different interfaces mediate the formation of an octamer. Mapping these key residues provides a framework for designing inhibitors that may disrupt oligomerisation. Such an approach holds promise for developing novel therapeutics against *H. pylori* in the era of rising antibiotic resistance.

Poster Presentation

Characterization of Sesquiterpene Synthase Gene(S) for the Over-Production of High Value Compounds from *Pelargonium Graveolens* (L.)

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Abstract:

Pelargonium graveolens (rose-scented geranium) is an important aromatic plant due to its high value essential oils which contains geraniol, citrinellol and linalool and various low abundance sesquiterpenes. Sesquiterpenes are valued for their therapeutic properties and serve as key ingredients for aroma and pharma industries. The transcriptomic data uncovered the identification of several novel sesquiterpene synthase genes for their characterization and potent specialized metabolites. However, these commercially important compounds are produced in very low amount in plants. In order to full fill the growing demand of these sesquiterpenes in in the flavor, fragrance and pharmaceutical industries, a development of sustainable heterologous production in microbial system (*E. Coli*) is required. To address this, we identified some novel sesquiterpene synthase from the transcriptome data of the *P. graveolens*. To analyze invitro enzyme activities, the ORFs exhibiting signature terpene synthase motifs were cloned in to pET-28b (+) bacterial expression vector for the expression with a C-terminal His6 tag. Recombinant PgTPS protein were expressed in *E. Coli* BL-21 Codon plus strain with IPTG induction. Soluble protein fraction was confirmed by SDS-PAGE. For the production of the identified sesquiterpene synthase genes in high amount, we have also optimized the codon of these genes for bacterial system and co-transformed in synthetic FPP producing bacteria. The novel compounds will be extracted from the bacterial cultures for co-transformed genes using hexane. These hexane extracts will be analyzed and validated using GC-MS and NMR. The present investigation will lead to the high production of commercially important, high value, novel sesquiterpenes.

Poster Presentation

Structural and Functional Insights into the Uncoupling of Phosphate Transport and Signaling in the High-Affinity Transporter PiPT of *Piriformospora indica*

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Abstract:

The high-affinity phosphate transporter PiPT from *Piriformospora indica* is homologous to the *Saccharomyces cerevisiae* transporter Pho84. PiPT was heterologously expressed in a Pho84-deficient yeast strain to investigate structure–function determinants. Using the crystal structure as a reference, eleven non-conserved residues located within the cytosolic tunnel, predicted proton-release pathway, and phosphate-binding region were subjected to mutagenesis. Several variants exhibited markedly reduced activity, including an approximately three-fold increase in Km. Structural modeling indicated that specific substitutions obstruct the phosphate-binding pocket. These findings demonstrate that phosphate transport and downstream signaling can be functionally uncoupled in PiPT, consistent with observations for Pho84.

Poster Presentation

Fluoroquinolones: Mechanism, Prevalence of Drug Resistance and New Development

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Abstract:

Fluoroquinolones are synthetic broad-spectrum antibiotics valued for their excellent oral absorption, pharmacokinetic profile, and potent activity against a wide range of pathogens. Their mechanism of action involves inhibition of the essential bacterial enzymes DNA gyrase and topoisomerase IV (primarily gyrA, gyrB, parC and parE which encode them) thereby impairing DNA replication and transcription which leads to irreversible DNA damage. However, the extensive and often inappropriate use of these agents in both human healthcare and veterinary practice has driven a rapid rise in resistance. Multiple mechanisms contribute to this phenomenon, including chromosomal mutations within quinolone resistance– determining regions, overexpression of efflux pumps, reduced outer membrane permeability, and plasmid-mediated resistance genes such as qnr genes (e.g., qnrA, qnrB, qnrS). These adaptations frequently act together, leading to cross-resistance among fluoroquinolone derivatives. Global surveillance reports indicate alarming resistance levels in pathogens such as *Escherichia coli, Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Neisseria gonorrhoeae*, *Mycobacterium tuberculosis* etc. The clinical consequences of this situation include treatment failure, limited therapeutic options and higher mortality rates. This review integrates mechanistic insights, resistance patterns, and epidemiological data, emphasizing the importance of antimicrobial stewardship, improved diagnostics, and development of innovative therapies to safeguard the efficacy of fluoroquinolones.

Microbial-Derived Compounds as Antibiofilm Agents against *Pseudomonas aeruginosa* NG4

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Abstract:

Pseudomonas aeruginosa, a Gram-negative opportunistic pathogen, is renowned for its capacity to form robust biofilms, which significantly enhance its resistance to conventional antibiotics and host immune responses. Infections associated with *P. aeruginosa* biofilms present a substantial clinical challenge, particularly in patients with cystic fibrosis, burn wounds, and those with implanted medical devices. Recently, microbial-derived compounds have emerged as promising alternatives to synthetic antibiofilm agents due to their natural origin, structural diversity, and environmental friendliness. The impact of Oleic acid (OA) and Indole-3-butyric acid (IBA) on Pseudomonas aeruginosa biofilm formation was evaluated at concentrations of 5-100 µg/mL in DMSO. OA showed significant biofilm inhibition at 5 µg/mL (35%) and 50 µg/mL (47%), with the strongest effect at 50 µg/mL. In contrast, IBA showed little to no inhibition at lower doses and only a slight effect (13.3%) at 100 µg/mL. Indole inhibited biofilm growth by 22.85% at 100 µg/L. Indole Acetic Acid (IAA) reduced it by 10.75% at 20 µg/L and 8.87% at 200 µg/L. At higher concentrations, both Indole and IAA reduced planktonic growth compared to the control. Treatment with these compounds likely limited the bacteria's ability to move freely, showing reduced swimming activity. The reduced biofilm formation suggests that the compounds may have inhibited the bacteria's ability to spread across surfaces through swarming. Confocal imaging would demonstrate a decrease in both the thickness and surface area of biofilms in treated samples when compared to the control group. Overall, OA was effective than IBA, with 50 µg/mL as the optimal concentration for biofilm inhibition. These compounds operate through multiple mechanisms, including the inhibition of initial cell attachment, interference with quorum-sensing pathways, disruption of extracellular polymeric substances (EPS), and induction of oxidative stress leading to biofilm dispersal. Investigating microbial-derived antibiofilm agents offers a sustainable and innovative approach to combating multidrug-resistant *P. aeruginosa* infections. Further exploration of the combined study on microbial-derived compounds along with antibiotics may be explored to inhibit biofilm linked to infection caused by *P. aeruginosa*.

Traditional Knowledge-based Phyto-pharmacological exploration of *Curcuma caesia Roxb*

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Abstract:

Introduction *Curcuma caesia*, a popular folklore medicine used by traditional healers of North-East India for the treatment of various diseases, including cancer. Hence, the present study aimed to investigate the phytochemicals, network pharmacology, antioxidant, and anti-proliferative efficacy using the Acetone (CcAc) and hydroalcoholic (CcHA) extracts of *Curcuma caesia*. Methods: Phytochemical profiling of CcAc and CcHA was established using Agilent-6500 series Q- TOF. Cytotoxicity efficacy was investigated on Human cancer cells (HeLa, KBM-5, HCT-116 and U266) using MTT Reduction and live/dead assay. The antioxidant potentials were studied by in-vitro assays. The distinct yet overlapping pathways targeted by their bioactive compounds were annotated using various tools, including SWISS ADME, ToxPred, Swiss Target Prediction, and STITCH. Specific network associations were constructed using Cytoscape software. The cancer-related disease genes were obtained from the OMIM and Genecards. Results: CcAc and CcHA have significantly ($p<0.001$) inhibited the proliferation of KBM-5, HCT-116, and HeLa cells in the MTT assay. The extracts also induced apoptosis as indicated by cleavage of PARP and an increase in dead cells. The CcAc caused down-regulation of cell survival and metastatic proteins, indicating its anticancer potential. LCMS/MS analysis revealed the presence of 77 phyto-constituents in CcAc and 71 in CcHA. A total of 50,000 cancer genes were obtained from the OMIM and Genecards, and 826 target genes from the Swiss Target prediction, of which 821(1.6 %) were common genes. The Human cell line genes expression, top ten genes identified by cytohubba network (BCL2L1, ACTB, BCL2, PARP1, PIK3CA and CXCR4), annotation and corroborate the bioactive compounds obtained from the *C. caesia* affecting the cancer survival, apoptosis, cAMP signalling, and neuroactive-ligand receptor interactions. The present investigation justified the claim of folklore healers for *C. caesia* as an anti-tumour agent and CcAc and CcHA is identified as an excellent source of anti-tumour agent for the future.

Poster Presentation

CRISPR- Based Gene Editing for Crop Improvement, Current Progress and Future Prospectus

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Abstract:

Traditional breeding methods based on hybridization and selection are limited by long breeding cycles and unpredictable outcomes, making them inadequate for meeting modern agricultural demands and future food security challenges. Recent advances in next-generation sequencing have generated extensive genomic data, enabling the development of targeted genome-editing tools such as ZFNs and CRISPR/Cas. These technologies have opened a new era of precise, efficient crop improvement. This review provides an overview of current plant genome-editing techniques, with emphasis on the CRISPR/Cas system, and highlights their present applications and future potential in crop biology.

Micropropagation for Conservation and Sustainable Uses of Floriculture Crops

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Abstract:

Micropropagation has emerged as a vital tool for the conservation and sustainable utilization of floriculture crops. Many ornamental species face challenges such as habitat loss, overexploitation, low seed viability, and slow conventional propagation rates. Tissue culture-based micropropagation offers a rapid, reliable, and disease-free method for mass multiplication of elite genotypes, ensuring the preservation of valuable and rare floricultural germplasm. Through techniques such as shoot tip culture, somatic embryogenesis, and organogenesis, micropropagation enables year-round production and uniform quality planting material while reducing pressure on natural populations. Additionally, it supports sustainable floriculture by facilitating large-scale propagation of high-demand ornamental varieties, improving floral traits, and enhancing stress tolerance. This review highlights the role of micropropagation in ex situ conservation and its contribution to environmentally responsible and economically viable floriculture production.

Poster Presentation

Evaluation of Antibody Response and Viral Titer of Human Coronavirus 229E in Mice Based on Route of Infection

Navya Chauhan[1], Sakshi Nautiyal[1], Dileep Verma[1], Shushma Mithani[1], Chandan Kumar Verma[1], Rimpy Sherawat[1], Sonia Chourdhary[1], Satendra[1], Vikas[1], Shailendra Mani[1]✉

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Abstract:

Human coronavirus 229E (HCoV-229E) is a seasonal alphacoronavirus that generally causes common cold symptoms but may lead to severe respiratory illness in elderly and immunocompromised individuals. Although it is clinically significant, suitable small-animal models to study its infection and immune response are scarce. Understanding host immunity against HCoV-229E is important for guiding vaccine development and antiviral strategies. This work explored how different routes of infection influence antibody production and viral distribution in BALB/c mice. Twenty-four male mice were assigned to four groups: intranasal, intraperitoneal, intramuscular, and a mock control. Animals were observed for seven days, with body weight recorded regularly. Serum samples collected on days 0, 3, and 7 were examined using Luminex bead-based IgG assays and microneutralization tests. Lung and spleen tissues were processed for viral RNA detection by qPCR, and were analyzed histologically. All exposed groups developed measurable antibody responses by day 7. The intraperitoneal route produced the most pronounced humoral response, with high neutralizing antibody titres (up to 1:80). By contrast, intranasal and intramuscular groups showed lower titres (around 1:20). Viral RNA was not detectable in lung tissues, indicating restricted replication or rapid clearance, consistent with the absence of the human receptor in mice. Importantly, none of the infected animals exhibited weight loss or severe clinical signs, suggesting minimal pathogenicity in immunocompetent BALB/c mice. These findings demonstrate that the route of infection strongly modulates antibody responses to HCoV-229E in mice. While wild-type animals may not sustain robust viral replication, they can serve as a useful model for immunogenicity studies. Insights from this work may support future strategies for vaccine delivery and therapeutic evaluation against both endemic and emerging coronaviruses.

Poster Presentation

Targeting Lytic transglycosylase for Antibacterial Interventions in Group A *Streptococcus*

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Abstract:

Lytic transglycosylases (Ltgs) are key enzymes involved in peptidoglycan metabolism and bacterial cell division. Although extensively studied as antibacterial targets in Gram-negative bacteria due to their functional redundancy, their potential in Gram-positive pathogens remains largely unexplored. Group A *Streptococcus* (GAS), a major human pathogen, causes a spectrum of diseases ranging from mild infections such as acute pharyngitis and impetigo to severe invasive conditions, including necrotizing fasciitis. Rising antibiotic resistance in GAS driven by excessive and inappropriate antibiotic use necessitates the identification of new therapeutic targets. The GAS genome encodes a protein, SPy_2191, predicted to contain a lysozyme-like domain characteristic of Ltgs. These enzymes catalyze the intramolecular transacetylation that cleaves the glycosidic bond between N-acetylmuramic acid and N-acetylglucosamine, producing a 1,6-anhydromuramoyl residue and contributing to peptidoglycan remodeling. Using bioinformatic analyses, we identified putative ligand-binding cavities within SPy_2191 and evaluated their suitability for inhibitor design. Targeting Ltg activity has also disrupted cell wall remodeling, thereby impairing bacterial growth and division. This work provides a framework for the rational design of small-molecule inhibitors against GAS Ltgs. Such inhibitors have the potential to serve as alternative therapeutics to traditional antibiotics, offering a promising strategy to combat antibiotic resistance in Gram-positive bacteria.

Deciphering How Environmental Pollutants Drive Antibiotic Selective Pressure in *S. aureus*

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Abstract:

India confronts a critical antimicrobial resistance (AMR) crisis, with *Staphylococcus aureus* resistance rates reaching 37-41% nationally. Beyond clinical antibiotic overuse, a largely overlooked driver emerges from environmental pollution—particularly pharmaceutical effluent from India's position as the world's leading drug manufacturer. Our review synthesizes evidence showing how heavy metals, sub-inhibitory antibiotic residues, and co-contaminants from hospitals and agriculture create selective pressures that favour antibiotic-resistant *S. aureus* populations. Pharmaceutical manufacturing units discharge ciprofloxacin at concentrations exceeding 28 mg/L into waterways, yet many of these environments harbour antibiotic-resistant bacteria at pollutant levels below bacterial killing thresholds but above those needed for resistance selection. Heavy metals co-select for antibiotic resistance through shared efflux pumps and linked resistance genes, while sub-inhibitory antibiotic exposures trigger stress responses that simultaneously enhance both drug resistance and virulence. Hospital wastewater and municipal treatment plants amplify this effect, releasing biofilm- forming, multidrug-resistant *S. aureus* into rivers and agricultural water sources. Livestock antimicrobial use further contaminates the environment through manure, with resistant *S. aureus* detected in 40-69% of milk samples across Indian states. These converging pollution pathways explain why India's resistance rates remain alarmingly high despite antimicrobial stewardship efforts. Understanding how environmental stressors activate resistance mechanisms particularly through mobile genetic elements and stress-response pathways reveals that conventional antibiotic control alone is insufficient. Regulating pharmaceutical effluent at source, upgrading wastewater infrastructure, and restricting agricultural antimicrobials represent complementary strategies essential for reversing India's AMR trajectory. This perspective reframes antibiotic resistance not merely as a clinical problem but as an environmental one, requiring urgent regulatory and infrastructural intervention.

Poster Presentation

Comparative Evaluation of Phage Delivery through Chitosan Nanoparticles and Biochar for Antibacterial Efficacy

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Abstract:

The rapid and unpredictable rise in antimicrobial resistance has created an urgent need for effective and practical substitution to traditional antibiotics, opening a new possibility of treating microbial infections with bacteriophages. These viruses are gaining renewed attention as safe, highly specific and environmental friendly alternatives. However, the success of clinically using these viruses depends on stability, controlled release and targeted delivery. Existing literature studies two recent carrier systems, chitosan nanoparticles (CS-NPs) and biochar independently for antibacterial activity. However, the gap lies in comparative evaluation between the two. Therefore, this study aims to compare CS-NPs and biochar for the encapsulation and targeted delivery of bacteriophages to evaluate their antibacterial efficacy. Chitosan obtained by N-acetylation of chitin is a biodegradable, toxicity free and muco-adhesive polycationic polysaccharide. Phage encapsulation with CS- NPs enhance phage stability and controlled release, thus improving bactericidal action. Biochar is a carbonaceous porous material that functions as an effective phage-adsorbing substrate. Due to its high surface area, functional groups and ability of generating reactive oxygen species, it contributes to antibacterial and anti-biofilm activity with minimal cytotoxicity. Bacteriophage loaded CS-NPs will be synthesized using the ion gelation technique, whereas the bacteriophage immobilized biochar will be prepared by incubating biochar with bacteriophage suspension under agitation at 30°C for 2 hours. The comparative outcomes of this study will provide insights into the suitability and efficiency of each carrier system for phage stabilization and delivery. These findings will lay the groundwork for developing optimized or hybrid delivery strategies aimed at enhancing the therapeutic potential of bacteriophages against bacterial infections.

Poster Presentation

Biosynthesis of Copper Nanoparticles Using *Vitex negundo* Leaf Extract: A Promising Antibiofilm Strategy against Pathogenic Bacteria

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Abstract:

The rise of microbial resistance and persistent biofilm-associated infections has intensified the demand for eco-friendly antimicrobial alternatives. In this study, copper nanoparticles (CuNps) were green synthesized sustainable method using the aqueous leaf extract of *Vitex negundo* a medicinal plant renowned for its antimicrobial and antioxidant properties. Phytochemicals such as flavonoids, alkaloids, and phenolics in the extract acted as natural reducing and stabilizing agents, facilitating nanoparticle formation, which was visually indicated by a color change and confirmed by UV-Vis spectroscopy. Comprehensive characterization using FTIR, XRD, SEM, and TEM revealed that the CuNps were crystalline, predominantly spherical, and ranged in size from 20–50 nm. Antibacterial testing demonstrated effective activity against both Gram-positive and Gram- negative bacteria. Notably, the CuNps exhibited potent antibiofilm activity against *Staphylococcus aureus* and *Pseudomonas aeruginosa*, as assessed via crystal violet staining. The antibiofilm effect was dose-dependent and significantly stronger than that of the plant extract alone, suggesting a synergistic interaction between copper ions and plant-derived phytochemicals. This green synthesis approach not only aligns with environmental sustainability but also offers enhanced antimicrobial and antibiofilm efficacy. The biosynthesized CuNps show strong potential for application in medical and industrial settings particularly in preventing biofilm formation on biomedical devices and contact surfaces. Future directions will focus on elucidating the underlying mechanisms and developing CuNps-based antimicrobial coatings.

Poster Presentation

Indian Spices: Natural Allies against Antibiotic Resistance

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Abstract:

Antibiotic resistance has become a growing global concern due to the excessive and indiscriminate use of antibiotics which has led to the spread of antibiotic resistance genes (ARGs) in the environment. In this study, water sample was collected from a source near the hospital. The samples were cultured on plates containing antibiotics to select the pathogenic bacterial strains. The antimicrobial properties of some commonly used Indian spices were evaluated against these resistant strains. Anti-inflammatory properties of spices were also checked in which bay leaf showed promising results. This study highlights the potential of natural spices as complementary or alternative agents in the fight against antibiotic resistance.

Poster Presentation

Ribulose-5-Phosphate Epimerase as Novel Predictor for Glioma Prognosis

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Abstract:

Sugar plays a vital role in the proliferation of cancerous cells, mainly through enhanced glycolysis: a pivotal pathway in cellular energy production. Relevant prognosis of cancer patients helps in better management of the diseases. To identify novel genes which could predict glioma prognosis (LGG and GBM), we analyzed the glycolysis pathway and its associated genes in detail. A total of 200 glycolysis-related genes were obtained from the GSEA MSigDB database. Differential gene expression between normal and cancerous cells was examined using the GEPIA database. The overall survival (OS) and disease-free survival (DFS) for respective genes were obtained from TCGA, CGGA and REMBRANDT datasets. Online platforms which provide relevant do it by yourself analysis such as GEPIA, GlioVis, UALCAN, Xena were used to assess the clinical relevance of these genes. Out of the 200 genes, 86 showed a statistically significant difference in expression between tumor and normal samples, suggesting their potential involvement in cancer progression. Among these, we identified Ribulose-5-phosphate epimerase (RPE) as a novel gene of interest which was able to predict prognosis. The data revealed that RPE expression was linked with cancer prognosis. This indicates that RPE might play an important role in the glioma and could serve as a potential prognosis marker. Our analysis suggests that altered RPE expression may contribute to metabolic reprogramming in glioma and could act as a predictive marker for tumor grade and patient prognosis. Further functional and molecular studies are necessary to elucidate the accurate role of RPE in glioma metabolism.

Poster Presentation

Uroporphyrinogen III Synthase and Uroporphyrinogen Decarboxylase as Novel Prognostic Markers in Lower-Grade Glioma

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Abstract:

Fatty acid metabolism plays a crucial role in cancer cell proliferation and survival by supporting energy production and membrane biosynthesis. Accurate prognostic assessment of cancer patients facilitates improved disease management. To identify genes with prognostic potential in glioma (LGG and GBM), we investigated the fatty acid metabolism pathway and its associated genes. A total of 159 genes from the hallmark fatty acid metabolism gene set in the GSEA MSigDB database were screened. Differential gene expression between normal and glioma tissues was evaluated using the GEPIA platform. Overall survival (OS) and disease- free survival (DFS) analyses were performed using data from the TCGA, CGGA, and REMBRANDT datasets. Publicly available online tools enabling independent analysis, including GEPIA, GlioVis, UALCAN, and UCSC Xena, were utilized to evaluate the clinical significance of the identified genes. Among the 159 genes analyzed, 33 exhibited statistically significant dysregulation in expression between tumor and normal tissues, indicating their possible involvement in gliomagenesis. Among these, Uroporphyrinogen III synthase (UROS) and Uroporphyrinogen decarboxylase (UROD) emerged as novel genes of interest with significant prognostic potential in LGG. Expression of both genes correlated significantly with patient survival, highlighting their potential roles in LGG progression. UROD expression correlated with poor prognostic outcomes, whereas UROS expression correlated with favorable prognosis, reflecting their contrasting functional implications in LGG. These findings suggest that dysregulated expression of UROS and UROD may modulate metabolic adaptation in LGG and could serve as novel prognostic biomarkers of tumor grade and patient survival. Further functional and molecular studies are required to clarify the precise roles of UROS and UROD in lower-grade glioma metabolism.

Poster Presentation

Isolation and Screening of Polyketide-Producing Microbes from Soil Samples

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Abstract:

Polyketides are a large group of secondary metabolites that possess great pharmaceutical properties, especially as antibiotics, antifungals, and anticancer drugs. This study focuses to screen and isolate soil microbes that produce polyketide substances. Soil samples were obtained from a dumping ground in a local area, an environment with rich microbial diversity due to the presence of organic wastes. The cultures were serially diluted and plated on LB agar and Starch Casein Agar (SCA) and incubated at 37 ºC for 48 h. 14 morphologically different colonies were isolated, purified and stored in 20% glycerol stocks for subsequent analysis. These stored strains were then revived, and tested for antibiotic sensitivity on Mueller-Hinton agar (MHA) plates. Inhibition zones, as seen, suggested that a number of isolates are sensitive against respective antibiotics. To verify the Polyketide biosynthetic potential of these isolated strains, further study is being carried out.

Poster Presentation

Isolation and Screening of Plant Probiotics from Paddy Rhizosphere Soils of Haryana

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Abstract:

The rhizosphere soil is home to beneficial microorganisms called plant growth-promoting rhizobacteria (PGPR), also known as plant probiotics. These organisms play a pivotal role in providing sustainable and eco-friendly ways to improve plant growth and productivity. The objective of this study is to isolate and characterize the plant probiotic microorganisms from the paddy rhizosphere soils of Haryana and assessing their plant growth promoting properties. Seventeen bacterial and fungal isolates were obtained through serial dilution of soil and plating methods. The isolates were screened for various plant growth promoting properties like nitrogen fixation, IAA production, siderophore production, phosphate solubilization, salt tolerance and heavy metal. Five potential isolates: 4 bacteria and 1 fungi, showing desirable properties, were selected for further study. These isolates were applied to barley seeds before planting to evaluate their effectiveness in promoting the growth of plant and nutrient uptake. As compared to control, an improvement in plant height was attained with the probiotic coated seeds, with one isolate AB12, indicating its superior potential in plant growth promotion. This study highlights the significance of harnessing the potential of native plant probiotics for sustainable agriculture to enhance crop productivity and reduce reliance on chemical fertilizers.

Poster Presentation

Assessment of Copper Resistance in Bacteria Isolated from Garden Soil and Yamuna Water

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Abstract:

Copper, an essential micronutrient, becomes toxic when its accumulation in the environment exceeds critical threshold levels, predominantly driven by anthropogenic activities. The accumulation of this heavy metal poses a considerable threat to both terrestrial and aquatic ecosystems. The primary objective of our study is to successfully isolate copper (CuSO4.5H2O) tolerant bacteria from two distinct ecological matrices: garden soil (terrestrial) and the Yamuna River (aquatic), and to subsequently evaluate their potential for bioremediation. The microbes were isolated from both samples using Nutrient Agar and Luria Bertani agar plates. Thereafter, the Maximum Tolerance Limit of bacterial isolates to copper was determined by assaying their growth under varying concentrations of copper in NA and LB agar media. The maximum tolerance limit for the bacterial isolates from the soil sample was found to be 800 µg/mL of Cu, while for the water sample, the tolerance limit was observed to be 1000 µg/mL of Cu. Comparative morphological analysis of the isolates (Gram staining and Spore staining) revealed Gram-negative rods of varying length and width. Subsequently, their biochemical properties (IMViC, Nitrate reduction assay, Urease reduction test and Triple Sugar Iron test) were also analysed, followed by analysis of antimicrobial resistance profiles of the isolates with the help of the Kirby-Bauer disk diffusion test. This study effectively demonstrates the successful isolation of highly copper-tolerant bacteria from soil and water samples that can be utilised effectively for bioremediation of copper pollution, providing an environmentally sustainable and economical approach. Future research will endeavour to study the uptake of copper by the selected isolates and visualise their localisation within the cells.

Poster Presentation

Microplastics and Their Multisystem Health Effects: A Growing Threat to Human Well-being

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Abstract:

Microplastics, defined as plastic particles smaller than 5 mm, have emerged as pervasive environmental pollutants with growing implications for human health. These particles originate from the degradation of larger plastics and are increasingly detected in food, water, and air, facilitating human exposure through ingestion and inhalation. Once internalized, microplastics can translocate across biological barriers, distributing to vital organs and triggering inflammatory and oxidative stress responses. Evidence suggests that chronic exposure may disrupt multiple physiological systems, including the gastrointestinal, cardiovascular, reproductive, and nervous systems. In the gut, microplastics alter microbiota composition and impair nutrient absorption. Cardiovascular studies indicate potential endothelial damage and increased risk of thrombosis. Reproductive toxicity, manifested as hormonal imbalance and reduced fertility, has been observed in both animal and cell-based models. Moreover, neurobehavioral changes linked to neuroinflammation highlight possible implications for brain health. Despite these findings, the precise mechanisms of microplastic toxicity in humans remain under investigation. This study synthesizes recent insights into the pathways and systemic effects of microplastic exposure, emphasizing the urgent need for standardized risk assessment and global mitigation strategies. Understanding their multisystem impact is crucial to safeguarding public health and informing sustainable environmental policies.

Poster Presentation

Comprehensive Water Quality Assessment by Combining Microbial and Physico-Chemical Evaluation

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Abstract:

The contamination of various water sources leads to a significant public health risk; it requires comprehensive monitoring that comprises both chemical and biological safety measures. The dependency on complex and costly laboratory techniques restricts assessment of water sources, which is the main issue addressed. In this research, various water samples from different sources were evaluated. Most Probable Number (MPN) was used as a quantitative indicator of faecal contamination. Gram Staining was used for confirmation of Gram-negative, pink colour rods. The Eijkman test at 45°C was used to confirm thermotolerant faecal coliforms, and positive samples were isolated on Eosin Methylene Blue (EMB) plates to observe a metallic green sheen, which indicates the presence of *E. coli* bacteria. Further biochemical test (IMViC) was done on the isolated culture. The standard titrimetric and calorimetric methods were used in physico-chemical analysis to measure the following parameters, such as pH, hardness of water ($Ca^{2+}$and Mg^{2+}), chloride content, residual chlorine, and fluoride (F^-). As per the results, raw water samples showed high MPN indices, which indicates severe faecal contamination confirmed by the Eijkman test. Based on physico-chemical tests, several samples showed high levels of fluoride that were higher than the permissible limit (1mg/L), which affects infrastructure and health. MPN and physico-chemical analysis of water samples tested in our research highlights the presence of coliforms and faecal coliforms in supply water and natural resources, which is a serious health concern and poses a significant health risk to local communities. There is an urgent need for stringent regulatory measures and the development of sustainable and cost-effective bioremediation techniques and water treatment techniques for elimination of contaminants and hazardous substances from water.

Poster Presentation

Evaluating the Impact of Common Mouthwashes on the Cell Wall Integrity of *Candida albicans*

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Abstract:

Candida albicans, is a dimorphic opportunistic fungal pathogen causing oral, vaginal, and systemic candidiasis, particularly in immunocompromised individuals. Currently available antifungal drugs act by disrupting ergosterol biosynthesis, an essential component of fungal cell membranes. However, the growing incidence of drug-resistant Candida strains has made treatment increasingly challenging, highlighting the need for alternative or complementary preventive approaches. The current project aims to evaluate and compare the antifungal efficacy of commercially available mouthwashes against *C. albicans*, focusing on their potential role as prophylactic agents in oral candidiasis. Various types of mouthwashes will be tested to evaluate their effects on fungal growth and, more importantly, on cell wall integrity. Disruption of the fungal cell wall is a crucial indicator of antifungal action, as it directly affects the organism's survival and pathogenicity. The findings may help highlight easily accessible and cost-effective oral hygiene products that could contribute to the prevention of oral candidiasis. Overall, this study aims to provide a better understanding of how routine mouthwash use might serve as a simple yet effective strategy for reducing Candida-associated oral infections.

Evaluation of the Effect of Commonly Used Mouthwashes on the Filamentation Pattern of *Candida albicans*

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Abstract:

Candida albicans, is a dimorphic opportunistic fungal pathogen causing oral, vaginal and systemic candidiasis, especially when the immune system is weakened or the normal microbial balance is disrupted. The formation of yeast to hyphae is a morphological transition or filamentation pattern. Currently available drugs majorly target ergosterol biosynthesis, but emergence of drug-resistant strains is a serious concern. The current project aims to evaluate and compare the efficacy of commercially available mouthwashes in the market against oral candidiasis. Action of various kinds of mouthwashes would be evaluated as potential prophylactic agents for their effect on growth, filamentation and cell wall integrity. Since mouthwashes are widely used as part of routine oral hygiene, evaluating their antifungal potential provides a practical approach to reducing the colonization and virulence of *Candida albicans*. This study seeks to assess the antifungal potential of mouthwash formulations containing different active ingredients, such as chlorhexidine, alcohol and herbal extracts.

Poster Presentation

Computational Insights into the Antifungal Efficacy of Common Mouthwashes against *Candida albicans*: An In-silico Preventive Approach

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Abstract:

Oral candidiasis is a common opportunistic fungal infection of the oral cavity, primarily caused by *Candida albicans*. This dimorphic fungus exhibits yeast-to-hyphal transition, adhesion to mucosal surfaces, and biofilm formation, contributing to its virulence and persistence. The infection is prevalent among immunocompromised individuals and those with poor oral hygiene. Increasing antifungal resistance and side effects of conventional treatments necessitate safer and more effective alternatives. This study evaluates the antifungal potential of commonly used mouthwashes as prophylactic agents against *C. albicans*. Formulations containing chlorhexidine, povidone-iodine, alcohol, and herbal extracts were analyzed through molecular docking using SwissDock to determine their binding affinities with key virulence proteins such as Als3, Hwp1, and Sap2 are responsible for adhesion, filamentation, and tissue invasion. Pharmacokinetic and drug-likeness properties were further assessed using SwissADME and SwissParam tools. Docking results revealed that chlorhexidine and povidone-iodine showed the highest binding affinities with Als3 and Hwp1, indicating potential inhibition of fungal adhesion and hyphal growth. All compounds exhibited favorable ADMET profiles. Overall, this in-silico study suggests that chlorhexidine and povidone-iodine possess significant antifungal potential against C. albicans and could serve as preventive agents against oral candidiasis, warranting further experimental validation.

Poster Presentation

Beyond Fresh Breath: Unveiling the Antifungal Efficacy of Mouthwashes against *Candida albicans* growth

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Abstract:

Candida albicans is a dimorphic opportunistic fungal pathogen responsible for causing oral, vaginal, and systemic candidiasis. Currently available antifungal drugs mainly target ergosterol biosynthesis, however, the increasing emergence of drug-resistant strains has become a serious concern. This has created a need to explore alternative antifungal approaches for the effective management of candidiasis. The current study aims to evaluate and compare the efficacy of commonly used mouthwashes as potential prophylactic agents for their effect on the growth kinetics of the *Candida albicans*. The findings aim to highlight the inhibitory potential of different mouthwash formulations and contribute to a better understanding of their preventive role in controlling oral candidiasis. Overall, this study seeks to provide insights about the relevance of mouthwashes in reducing the risk of oral candidiasis.

Poster Presentation

Antibiotics and Their Effect on Gut Microbiome

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Abstract:

Antibiotics are widely used to treat bacterial infections, but their impact on the human gut microbiome has become a growing concern. The gut microbiome is a diverse community of beneficial microorganisms that help in digestion, vitamin production, and immune regulation. However, when antibiotics are taken, they not only kill harmful bacteria but also destroy beneficial microbes that maintain gut balance. This disturbance, known as dysbiosis, can lead to digestive problems, reduced immunity, and an increased risk of infections such as Clostridium difficile. This project explores how different classes of antibiotics affect gut microbial diversity, the time required for recovery after antibiotic use, and the role of probiotics and diet in restoring balance. Understanding these effects is essential for promoting responsible antibiotic use and maintaining long-term gut health. The study highlights that while antibiotics are lifesaving, their misuse or overuse can significantly disrupt the natural ecosystem of the human gut.

Poster Presentation

A Comprehensive Study of Bacterial Cellulose and its Applications in Biomedical and Healthcare

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Abstract:

Bacterial Cellulose (BC) is biocompatible and highly pure exclusive biomaterial obtained from several species of bacteria by fermentation. Bacterial species produce cellulose pellicles in response to the external environment factors including UV radiation as gel-like substance at the air-liquid interface of batch culture. BC is structurally similar to the plant cellulose but it attained high degree of purity due to exclusion of hemicellulose, pectin and lignin. Moreover, remarkable physical and chemical properties, high crystalline structure, water holding capacity, high tensile strength, nontoxicity, substantial biocompatibility etc. makes BC an attractive biomaterial used for several biomedical and healthcare applications. Recent studies showed its diverse use in regenerative medicine, wound management, cardiovascular systems, ophthalmic scaffold and contact lenses, artificial skeleton and tissue grafting, drug delivery and potential antibacterial and anticancer agent. The high water holding capacity and porous structure help to maintain moist environment at wound which makes it ideal for dressing material. It also acts as physical barrier which help to reduce the pain and protect from microbial infection. BC possesses a significant bioengineering potential for addressing ophthalmic diseases. It enhances the proliferation of the retinal pigment epithelium (RPE), corneal stromal cells and keratinocytes. Further, BC membranes are effectively employed in sophisticated drug delivery systems, enabling the controlled release of therapeutic agents, such as anti-inflammatory and antimicrobial compounds, directly to target site. Reports indicate that Bacterial Cellulose (BC) is an excellent material for creating artificial blood vessels to replace atherosclerotic coronaries. Its high moldability and mechanical properties, which closely match those of small-diameter natural vessels, make it ideal for this use. This study aims to compile most recent development in the biomedical and healthcare applications of bacterial cellulose.

Poster Presentation

Strain-Specific Topical Probiotics: A Smart and Targeted Biotherapeutic Approach for Cancer

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Abstract:

Cancer remains one of the leading causes of mortality worldwide, and despite advancements in chemotherapy, radiotherapy, and immunotherapy, these conventional treatments often pose challenges due to systemic toxicity, drug resistance, and relapse. In this context, probiotics traditionally known for their gut health benefits have emerged as promising biotherapeutic agents with notable anti-cancer properties. Recent studies highlight the potential of probiotics, applied directly to topical tumor sites, as a safe, localized, and targeted approach for treating solid tumors such as cervical, colorectal, breast, and skin cancers. These probiotics exert multi-faceted anti-cancer effects through apoptosis induction, modulation of immune responses, suppression of inflammatory mediators, inhibition of angiogenesis, and remodeling of the tumor microenvironment. Crucially, strain specificity plays a decisive role in determining therapeutic outcomes. Even closely related strains within the same species exhibit distinct anti-cancer profiles, varying in their ability to adhere to cancer cells, regulate key oncogenic pathways, and produce bioactive metabolites such as exopolysaccharides, bacteriocins, and short-chain fatty acids. Mechanistic analyses reveal strain-dependent modulation of tumor-related genes including BAX, BCL-2, CASP3, PTEN, MMP-2, and VEGFA, alongside activation of immune mediators such as IFN-γ and IL-12. Genetic and preclinical studies further demonstrate that certain engineered or naturally hypoxia-responsive strains like Lactococcus lactis can selectively colonize tumor tissues and enhance therapeutic delivery without inducing toxicity. In vitro and in vivo models, including 3D tumor spheroids, confirm that probiotic supernatants can penetrate hypoxic tumor cores, suppress NF-κB signaling, and selectively induce apoptosis in cancer cells while sparing normal tissues. Collectively, these findings underscore the potential of strain-specific topical probiotic therapy as a novel, low-toxicity, and precision-oriented strategy in oncology. This study aims to elucidate the phenotypic and genomic mechanisms underlying these strain-specific effects to advance the rational design of probiotic-based interventions for solid tumors.

Poster Presentation

Exploring the Functional and Health-Promoting Potential of Kanji: A Traditional Indian Fermented Beverage

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Abstract:

Ancient Indian fermented beverages have long been integral to regional food practices and cultural traditions; however, their potential influence on gut microbiome modulation and systemic health remains largely underexplored. Among these beverages, Kanji traditionally prepared from black carrots and beetroots is recognized as a culturally rooted, non-dairy probiotic drink. It contains indigenous lactic acid bacteria (LAB) such as *Pediococcus acidilactici* and *Lactobacillus plantarum*, along with various bioactive compounds including phenolic acids, flavonoids, anthocyanins, and vitamin precursors that contribute to its diverse microbial ecosystem. Collectively, these probiotic and bioactive components confer multiple health benefits, including antimicrobial protection, antioxidant defense, and metabolic regulation through cholesterol assimilation. They also exhibit immunomodulatory potential along the gut-brain and gut-liver axes, thereby promoting overall host health and homeostasis. In the present study, probiotic strains were isolated from homemade beetroot Kanji and subsequently characterized for their probiotic attributes, including Gram staining, morphological observation, and biochemical testing (catalase, indole, methyl red, and Voges Proskauer tests). Additionally, the survival of the isolates was evaluated under simulated gastric fluid (SGF) and simulated intestinal fluid (SIF) conditions to assess their functional stability in gut-like environments. Future work will focus on the molecular identification of promising isolates for potential incorporation into functional food formulations.

Poster Presentation

Microbial Diversity and Health Risk Assessment of Airborne Communities in the Bhalswa Legacy Landfill, Delhi

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Abstract:

Legacy landfills represent complex and dynamic microbial habitats shaped by years of organic decomposition, chemical leaching, and anthropogenic activity. Old landfill sites of Bhalswa are characterized by long-term organic, inorganic and possibly biological waste accumulation that offer a unique ecological niche supporting diverse and often unexpected microbial populations. In this study, passive sampling from the excavation site was analysed to explore the microbial diversity of this extreme environment. Cultivation on enriched media enabled the isolation of even fastidious organisms, while differential media such as EMB agar, MSA, PDA and cetrimide agar helped in differentiating organisms on the first instance. The 16S rRNA gene sequencing resulted in identification of obtained isolates. The data further gave insights into the phylogenetic relationships among microbes reflecting the evolutionary interplay of successfully surviving microbes. Preliminary observations suggest the coexistence of both environmental and opportunistic bacterial species. This work contributes to a broader understanding of microbial diversity in legacy landfill ecosystem and gives information about microbial interplay in this extreme environment. Landfill, being present within the human community serves as a reservoir of unpredictable, yet challenging outcomes yielding health risk assessment.

Poster Presentation

Analysis of End-Lip-Amy Enzymes Obtained from *Thermomyces Lanuginosus* Strains Using Gene Network and their Utilization in Cellulose Nanofibril and Biofuel Production from Biowaste

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Abstract:

The present research work aims to explore the genomic and functional landscape of *Thermomyces lanuginosus* enzymes with industrial relevance, specifically endoglucanase, lipase, and amylase (end-lip-amy). In the present work, we propose a systems biology-based approach to analyse the gene co-expression network of *T. lanuginosus* using Weighted Gene Co-expression Network Analysis (WGCNA) and associated bioinformatics tools. The study will identify key modules and hub genes linked to enzyme regulation and secretion efficiency. The transcriptomic analysis will help in revealing the gene regulation occurring in *T. lanuginosus* VAPS24 and *T. lanuginosus* VAPS25. The gene network analysis will help in understanding the co-expression and upregulation of genes, which may be beneficial for further strain improvement. The activity of enzymes may also increase after the construction of enzyme complexes or the introduction of directional mutations, following the determination of the 3D structures of enzymes within the consortium. This will reduce the time of production and the action of individual enzymes. The consortia/chimeric enzymes can be utilized for deinking of multiple types of wastepaper (laser-printed, magazine, newspaper) and degradation of lignocellulosic waste, as compared to individual enzymes. The QM/MM simulation will help in finding the catalytic pathways of enzymes in the consortium. This will also help in finding the interaction of enzymes in the consortium. The insights gained from this study are expected to facilitate the rational engineering of *T. lanuginosus* strains for improved enzyme yields and to enhance their applicability in the sustainable production of cellulose nanofibrils and biofuels from biowaste. This integrative approach will contribute to advancing fungal biotechnology and biowaste valorisation strategies for a circular bioeconomy.

Poster Presentation

Analytical Tools and Omics Technologies in Food Microbiology

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Abstract:

Modern food safety management relies on accurate detection, monitoring and prevention of microbial hazards throughout the food supply chain. Advancements in analytical tools and omics technologies have significantly transformed the field of food microbiology, enabling more precise detection, identification, and characterization of microbial communities in food systems. Rapid molecular techniques such as PCR, qPCR, LAMP and immunoassays offer improved sensitively and specificity and are increasingly used for supplementing traditional culture-based methods. Spectroscopic and chromatographic tools such as MALDI-TOF MS, HPLC, and GC/LC - MS further augment microbial identification and detection & quantification of microbial toxins. Recently, omics technologies - including genomics, metagenomics, transcriptomics, proteomics, and metabolomics - are increasingly contributing to food safety by providing comprehensive insights into microbial activity in food systems. They are valuable tools in optimization of fermentation and food processing. Whole genome sequencing (WGS) is now widely employed for pathogen detection in outbreak investigation and antimicrobial resistance analysis, while metagenomic approaches offer the advantage of studying microbial communities in foods without the need to culture them. Transcriptomic and proteomic studies reveal microbial responses under stress and spoilage, contributing to a better understanding of spoilage and fermentation processes. Integrated approaches utilizing some of these tools combined with bioinformatics and machine learning, are being developed to support predictive microbiology that can be used for risk assessment in food safety and quality control. Collectively, analytical and omics tools have tremendous application in foodborne outbreak investigations, antimicrobial resistance surveillance and quality control and shelf-life prediction.

Functional Characterization of *Priestia filamentosa* for Biocontrol of Tomato Pathogens and Nutritional Enhancement: Insights from CLSM, SEM, and GC-MS Analysis

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Abstract:

Tomato (*Solanum lycopersicum*), an important horticultural crop grown worldwide, is valued for its substantial economic and nutritional value. Tomato fruits play a significant role in human health due to variable yet significant nutritional compounds. Tomato is highly susceptible to fungal diseases that reduce yield and affect quality. Among pathogens, *Sclerotinia sclerotiorum* causes stem rot or fruit rot in tomato, which can be managed by fungicides. The emergence of resistance and consumer safety are major concerns that require urgent attention. Realizing this, *Priestia filamentosa*, a plant beneficial bacterium, was recovered from wheat rhizosphere and evaluated for biocontrol efficacy against *S. sclerotiorum* and its consequential impact on the nutritional quality of tomato fruit. In planta, pathogen-challenged plants treated with *P. filamentosa* significantly reduced disease severity, improved plant growth, and fruit yield over controls. Confocal Laser Scanning Microscopy (CLSM) and Scanning Electron Microscopy (SEM) images of antagonist-treated plants revealed a reduction in tissue damage and pathogen colonization, confirming the biocontrol efficacy of the bacterium. GC-MS analysis of fruits harvested from *P. filamentosa* inoculated plants revealed 33 bioactive compounds, such as sugars, organic acids, amino acids, and vitamins, underscoring the enhanced nutritional value. This study suggests that *P. filamentosa* holds great promise as a sustainable biocontrol agent with the added benefits of a quality-enhancing agent.

Poster Presentation

Discovery of Glycosome Biogenesis Inhibitors in *Leishmania donovani* via Computational Screening and Experimental Validation

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Abstract:

Visceral leishmaniasis (VL) is caused by *Leishmania donovani* and *L. infantum*, which are transmitted through the bite of the sandfly vector. Most VL cases occur in Eastern Africa, South America, and the Indian subcontinent. Glycosomes, peroxisome-related organelles present in kinetoplasts, are considered an energy hub for the parasite and play a pivotal role in cellular metabolism. Several glycolytic enzymes and their metabolic pathways are compartmentalized inside these specialized organelles. The biogenesis and integral functioning of glycosomes rely on the interaction between two key proteins, PEX3 and PEX19. Targeting this interaction represents a promising strategy for therapeutic intervention against VL. Using the Glide of Schrödinger, this study employed over analyticon natural compound drug library (n = 6996) and an FDA-approved drug library (n = 3597) for docking against *Leishmania donovani* PEX3 and PEX19. The XP docking with the Analyticon natural product library yielded docking scores ranging from –11.5 to –6.3 for PEX3 and PEX19, while docking with the FDA-approved drug library produced scores between –8.4 and –5.6, and with the PEX3-PEX19 complex is from -9.2 to -4 kcal/mol. These potential drugs were then subjected to pharmacokinetic ADMET analysis using QikProp, and binding free energy was estimated. This rigorous computational analysis allowed us to shortlist the most promising candidates, strong binders with therapeutic properties. The five top-ranked compounds-complex with PEX proteins were evaluated for microscopic interaction by performing molecular dynamics and validated in vitro against promastigotes of *Leishmania donovani*, in comparison to reference drug miltefosine (IC_{50}-2.7µM). The top-performing inhibitors were also found to be safe when evaluated for cytotoxicity using the J774A.1 murine macrophage cell line model. This experiment helps us to identify a potential inhibitor targeting glycosome biogenesis of Leishmania and gives us a positive hope for developing antileishmanial drugs.

Poster Presentation

CAR-T Manufacturing: From Patient to Product

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Abstract:

Chimeric Antigen Receptor T-cell (CAR-T) therapy is a personalized cancer treatment where a patient's own T cells are genetically engineered to recognize and kill cancer cells. Although CAR-T therapies have shown remarkable success in blood cancers, their effectiveness depends heavily on a complex and time-sensitive manufacturing process. CAR-T manufacturing involves multiple steps from patient cell collection to genetic modification, expansion, and final product release each of which influences therapy cost, quality, and clinical outcomes. Understanding this workflow is essential to improving accessibility and safety. The CAR-T manufacturing process begins with leukapheresis, where T cells are collected from the patient's blood. These cells are then purified and activated using specific cytokines or beads to stimulate proliferation. Next, the T cells are genetically modified using viral vectors (typically lentiviral or retroviral) to introduce the CAR gene. The engineered cells are expanded in bioreactors until sufficient numbers are obtained for therapy. After expansion, the cells undergo quality-control testing (sterility, viability, transduction efficiency) and are cryopreserved. Finally, the CAR-T product is transported back to the clinical center for infusion into the patient. Despite its success, CAR-T manufacturing faces significant challenges. Autologous CAR-T production is individualized, making the process slow, expensive, and logistically complex. Variability in patient health and T-cell quality often affects final product consistency. The reliance on viral vectors adds cost and regulatory hurdles, while stringent quality-control requirements can cause delays. Additionally, maintaining sterility and cell viability during transport and storage remains a major bottleneck. Efforts to overcome these issues include adopting automated closed-system bioreactors, using non- viral gene-editing methods such as CRISPR, and developing allogeneic "off-the-shelf" CAR-T products from healthy donors. Advancements in manufacturing technologies have improved the efficiency and reliability of CAR-T production, but significant challenges remain. Automation, standardized processes, and allogeneic cell therapies show promising results in reducing manufacturing time, lowering costs, and increasing broader patient access. Continued innovation in gene-editing and scalable bioprocessing is expected to further streamline the manufacturing pipeline and enhance the clinical success of CAR-T therapy.

Lab Grown Meat and Sustainable Food Tech: Innovating Meat without Killing the Innocent Animals

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Abstract:

Global demand for meat is rising rapidly, which causes suffering and slaughtering of millions of animals also traditional farming contributes to greenhouse gas emission, deforestation, water consumption and wastage. Lab-grown or culture meat offers a revolutionary solution by producing real meat directly from animal cells, eliminating the need for killing innocent animals. Lab-grown meat is produced through cellular agriculture, beginning with the extraction of a small sample of animal cells, typically muscle stem cells, from a living animal. These cells are placed in a nutrient-rich growth medium that supports proliferation. The growing cells are then guided to differentiate into muscle tissue within bioreactors, where environmental conditions such as temperature, pH, and oxygen levels are tightly controlled. Scaffold structures are often used to mimic natural muscle alignment, enabling the development of textures like traditional meat. It can be engineered to have healthier fat profiles (more omega-3s, less saturated fat) also helps to prevent foodborne pathogens (like *E. coli* and *Salmonella*). Lab-grown meat represents a revolution in food technology by combining biotechnology, sustainability, and ethics. It promises to feed the world without harming animals, reducing environmental impact, and providing safe, nutritious meat for the growing global population. Compared to conventional livestock farming, lab-grown meat has the potential to drastically reduce carbon emissions, antibiotic use, and habitat destruction. Lab-grown meat represents a transformative step toward a more sustainable and compassionate food system. As technology matures, cultured meat may redefine how humanity meets nutritional demand without compromising animal welfare or planetary health. This is more than innovation and kindness. This is the beginning of a world where no innocent animal gets killed for us to live. Eat with empathy: Meat that doesn't hurt.

Poster Presentation

Sustainable β-Glucan Biosynthesis from Oleaginous Yeast Cultivated on Mandi Waste

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Abstract:

The increasing demand for sustainable bioactive compounds has driven interest in utilizing agro-industrial residues as low-cost substrates. This study investigates the cultivation of oleaginous yeast using mandi (vegetable market) waste hydrolysate to enhance the production of β-glucan, a high-value polysaccharide with known immunomodulatory, nutraceutical, and pharmaceutical applications. The waste biomass was processed through hydrolysis to obtain a nutrient-rich medium, providing an economical carbon source for yeast growth. Selected oleaginous yeast strains were cultivated under optimized conditions to maximize both biomass and β-glucan yield. Growth kinetics, substrate utilization, pH variation, and β-glucan extraction efficiency were evaluated. Preliminary findings indicate that mandi waste hydrolysate supports robust yeast proliferation and significant β-glucan accumulation, demonstrating its potential as a cost-effective and eco-friendly alternative to conventional synthetic media. This approach not only valorizes organic waste but also supports circular bioeconomy goals by integrating waste management with bioproduct synthesis. Further optimization could enhance industrial-scale feasibility for β-glucan extraction from oleaginous yeast grown on waste-derived substrates.

Poster Presentation

Unveiling the Anticancer Potential of Gut Microbiota-Derived p-Cresyl Sulfate on Colon Cancer

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Abstract:

In recent decades, several reports have highlighted gut metabolites with anticancer activity and potential roles in immunotherapy. p-Cresyl sulfate (pCS) is a gut-derived metabolite produced from the microbial metabolism of tyrosine and phenylalanine in the colon. However, its potential as an anticancer agent remains unexplored. In this study, we evaluated the selective anticancer properties of pCS on colon cancer cells. Treatment of HCT116 adenocarcinoma cells and normal colon epithelial cells (CCD 841) with pCS led to a decrease in cell proliferation, cell viability, and ATP content. Colon cancer cells exhibited an 18.2% increase in apoptosis compared to control. pCS demonstrated selective anticancer activity, exerting less toxic effects on normal colon cells compared to cancer cells. Following pCS treatment, cell morphology was distorted, cell numbers decreased, intracellular vesicle formation occurred, and cells detached and floated in the medium. pCS triggered significant oxidative stress through ROS production, leading to DNA damage, cell membrane disruption, and lactate dehydrogenase (LDH) release. Epithelial barrier integrity in monolayers was compromised, as evidenced by reduced transepithelial electrical resistance (TEER) values, decreased colony-forming ability, an increased BAX/Bcl-2 ratio, and elevated LDH release. Additionally, cell cycle progression was arrested at the S phase, ultimately resulting in cell death. In silico docking studies further supported these observations, showing strong interactions of pCS with HDAC6, tubulin, and PARP-1 proteins, suggesting epigenetic modulation and cytoskeletal disruption as additional mechanisms of action. These findings establish p-cresyl sulfate (pCS) as a promising metabolite with selective anticancer potential against colon cancer cells.

Poster Presentation

Stress, Mitochondrial Dysfunction, Metabolomics mRNA Vaccine Technology beyond COVID-19

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Abstract:

mRNA vaccine technology, first highlighted during the COVID-19 pandemic, is increasingly recognized as a flexible platform with broad applications in global health. Unlike conventional vaccines, mRNA-based vaccines introduce a synthetic genetic blueprint that lets cells within a host make certain antigens, thus eliciting protective immune responses without requiring live pathogens. This technology has the potential for rapid development, very high safety, and ease of adaptation toward infectious disease prevention, cancer treatment, and even autoimmune and rare genetic disorders management. The design of mRNA vaccines includes targeting an antigen of interest and encoding its sequence into a modified mRNA molecule. These mRNA sequences are encapsulated in LNPs for protection and to facilitate cellular delivery. Intramuscular injection allows entry of LNPs into host cells, where the mRNA is translated into antigenic proteins. Processed antigens are then presented via both MHC pathways, stimulating both humoral and cellular immune responses. To date, various new formats include self-amplifying mRNA, circular mRNA, and organ-targeted LNPs that are continuously being developed for improved stability, potency, and tissue specificity. Beyond COVID-19, various applications of mRNA technology are now moving into several therapeutic areas. For infectious diseases, advanced clinical trials are underway for mRNA-based vaccines against influenza, HIV, RSV, CMV, Zika, and malaria. In oncology, promising responses have been observed from personalized cancer vaccines encoding tumor-specific neoantigens by stimulating cytotoxic T-cell responses and lowering disease recurrence. The tolerogenic mRNA vaccines are also under investigation in autoimmune diseases such as multiple sclerosis and type 1 diabetes through induction of regulatory T-cell responses. mRNA platforms are also tested for the purposes of protein replacement in genetic disorders and allergy desensitization. Despite these advances, challenges such as mRNA instability, cold-chain dependence, and improved delivery systems remain to be resolved. Recent studies have shown that mRNA vaccines hold great potential beyond pandemic response. A trial of personalized mRNA cancer vaccines for melanoma conducted in 2023-2024 reported improved survival and reduced recurrence when used in combination with immunotherapy. mRNA influenza vaccines that target conserved antigen regions are currently in Phase II trials and exhibit strong cross-strain immunity. Self-amplifying mRNA vaccines against Zika and CMV have exhibited robust antibody and T-cell responses at much lower doses. Emerging research into circular mRNA demonstrates enhanced stability and prolonged protein expression, opening pathways toward the treatment of chronic diseases. Overall, current studies confirm that mRNA vaccines represent a powerful, adaptable platform positioned favourably to shape the future of vaccinology and precision medicine.

In Vitro Evaluation of Anti-Obesity Potential of Aqueous Extracts of Fenugreek and Fennel Seeds

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Abstract:

Obesity, a global metabolic epidemic characterized by excessive adipose fat accumulation, significantly elevates the risk of severe comorbidities like Type 2 diabetes and cardiovascular disease. Current pharmacological and surgical interventions often carry considerable side effects, highlighting an urgent need for safer, cost-effective, and natural alternatives. Traditional Indian medicine frequently employs fenugreek (*Trigonella foenumgraecum*) and fennel (*Foeniculum vulgare*) seeds for weight management, a practice attributed to their rich content of bioactive compounds, including saponins, polyphenols, and dietary fiber. However, scientific validation of the anti-obesity potential of their aqueous extracts, particularly those prepared under traditional soaking conditions, remains limited. This study aimed to biochemically validate the anti-obesity potential of aqueous extracts of fenugreek and fennel seeds, focusing on key therapeutic targets for fat and cholesterol absorption. Aqueous extracts were prepared by standardizing variables such as seed concentration (5g/100ml and 10g/100ml), soaking duration (4 to 24 hours), and temperature to mimic and optimize the traditional home preparation method. The anti-obesity efficacy was then assessed in vitro using standard methods for Enzyme Inhibitory Assays, specifically targeting: 1) Pancreatic Lipase Inhibition 2) Cholesterol Esterase Inhibition 3) HMG-CoA Reductase Inhibition The study also determined the Total Phenol and Flavonoid Content and evaluated Antioxidant Activity (e.g., DPPH assay) to find the correlation between these phytochemical properties and the observed anti-obesity effects. The IC50 values of the extracts were calculated and compared to standard anti-obesity drugs (e.g., Orlistat). Furthermore, the research investigated the potential synergistic or antagonistic effects when fenugreek and fennel extracts were combined. Preliminary results are expected to scientifically substantiate the traditional use of these seeds, providing a mechanistic basis for their anti-obesity action through the inhibition of key fat-metabolizing enzymes and alleviation of oxidative stress. This research supports the development of fenugreek and fennel aqueous extracts as promising, readily available, and side-effect-free nutraceutical interventions for the prevention and management of obesity.

Effect of Sprouting Time on Phytochemical Levels of *Trigonella Foenumgraecum* (Fenugreek) Seeds

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Abstract:

Trigonella foenumgraecum (Fenugreek) seeds have been studied for their diverse therapeutic benefits. It is one of the main Indian spices that is commonly found in Indian households and is called “methi”. Fenugreek is an herb from the Fabaceae (Leguminosae) family that is widely cultivated in regions such as India, Egypt, and Mediterranean countries, mainly for its seeds. Its seeds provide bioactive compounds, like galactomannans, flavonoids, coumarins, saponins, alkaloids, and essential oils, which carry out various pharmacological activities. Fenugreek has been reported to have anticarcinogenic, anti-microbial, antifungal, hypocholestrolemic, antidiabetic, antioxidant and immunologic properties. Fenugreek has been reported to regulate the levels of blood sugar, lipids and hormones, thereby balancing the body’s metabolic and physiological profile. It showed antimicrobial and antifungal properties against MDR (Multi- drug resistant) and XDR (Extensively drug resistant) strains. In the present study, the extract of fenugreek seed sprouts has been tested for its qualitative estimation of phytochemicals. Concentration of tannins increased with sprouting time and gave maximum precipitate at 4th day, decreased a little from 6th day and became stagnant till 10th day. Similarly, concentration of flavanoids was observed to be maximum on 4-6th day of sprouting. Concentration of saponins was observed from 2-4th day of sprouting. Quantitative tests for phenols revealed that the absorbance was maximum on 4th day. These results show that much concentration of phytochemicals were produced from 4th day of sprouting. Since the concentration of phytochemicals that are integral to the phyto-immune system, possessing significant biological activities and potential health benefits and other constituents is expected to be very high during the sprouting period, sprouts have been used. The correlation of sprouting time with the antibacterial property of seeds would be done for further analysis.

A Comprehensive Pipeline for Biological Data Analysis: Integrating Web-Scraped and Custom Data for AI-Driven Trend Identification

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Abstract:

This proposed work outlines a data science pipeline designed for the collection, integration, and analysis of biological and environmental datasets. The system gathers data from governmental websites using both web scraping methods and custom-developed tools, while also accepting experimental or observational data from independent sources. Core stages include data preprocessing, cleaning, and standardization to accommodate variability across heterogeneous datasets. A variety of cutting-edge AI techniques, such as cloud-based platforms and locally optimized models created for biological domains and sustainable development goals, are used in the analytical component. These models can identify trends, find domain-specific patterns, and produce explanatory analytics. Although data collection and basic analysis are successfully automated by the existing system, its modular design enables the installation of new capabilities for more complex analyses and automated report production. This pipeline may facilitate improved pattern recognition, comparative analysis, and predictive evaluation for environmental and biological patterns as development advances. The workflow's adaptability makes it appropriate for a variety of uses, from identifying new trends impacting sustainability to real-time environmental monitoring. This work shows how data science and AI-driven approaches may be used to turn diverse, unprocessed datasets into biological sciences insights that can be put to use in variety of places.

Poster Presentation

Yogurt and Gut Microbiota: Linking Conceptual Insights with Functional Characterization of Probiotic Strains

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Abstract:

Probiotics, prebiotics, and postbiotics play a vital role in sustaining gut microbial harmony and enhancing host physiological resilience. Among various functional foods, yogurt stands out as a fermented dairy product rich in beneficial lactic acid bacteria, particularly *Lactobacillus*, *Bifidobacterium*, and *Streptococcus thermophilus*. Extensive research highlights that regular yogurt consumption improves digestive efficiency, lactose utilization, immune modulation, and short-chain fatty acid production, thereby contributing to overall gastrointestinal (GI) well-being. Findings from population studies and clinical interventions further indicate that yogurt functions as a transient yet effective modulator of gut microbiota, providing metabolic and digestive benefits without causing permanent microbial shifts. As part of our ongoing dissertation work, probiotic strains are being isolated from commercially available yogurt samples for detailed morphological and biochemical characterization, functional evaluation, and assessment under simulated gastric fluid (SGF) and simulated intestinal fluid (SIF) conditions. These isolates are further examined for milk coagulation activity, antioxidant potential, cholesterol assimilation, and shelf-life study of the sample. Future work will emphasize molecular identification and genomic sequencing of the most promising isolates to identify resilient candidates for future functional food applications.

Exploring Postbiotic Potential in Traditional Fermented Products: A Microbiological and Functional Perspective

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Abstract:

Idli batter is a traditional South Indian fermented food prepared from a mixture of ground rice and black gram. The natural fermentation process, typically carried out overnight at ambient temperature, is mediated by microorganisms such as *Lactobacillus* species and yeasts. These microbes produce lactic acid and carbon dioxide, resulting in a soft, spongy, and mildly sour batter. Fermentation not only enhances the texture and flavor but also improves the nutritional quality by increasing digestibility and the bioavailability of essential nutrients, making idli a wholesome and health-promoting food. In the present study, lactic acid bacteria (LAB) were isolated from idli batter samples collected from local vendors. The isolates were characterized for probiotic attributes using standard microbiological tests, including Gram staining, catalase, Voges–Proskauer, indole, and methyl red assays. Additionally, the survivability of the isolates was evaluated under simulated gastric fluid (SGF) and simulated intestinal fluid (SIF) conditions to assess their tolerance to low pH and bile concentrations. Furthermore, molecular identification of the promising isolates will be conducted to confirm their probiotic identity. These strains may serve as potential candidates for the development of traditional fermented functional foods upon confirmation of their probiotic efficacy.

Identification of RbpA-RNAP Interaction Inhibiting Molecules to Curb Infections of Anti-Microbially Resistant Non-tuberculous Mycobacteria and *Mycobacterium tuberculosis*

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Abstract:

Antimicrobial resistance (AMR) has emerged as one of the most pressing issues of the century. In 2019, bacterial AMR alone was responsible for about 4.95 million global deaths. Recognizing the critical role of tuberculosis in the AMR crisis, 7 of 40 research topics prioritized under WHO's Global Research Agenda for Antimicrobial Resistance in Human Health (June 2023) specifically addressed multidrug-resistant tuberculosis (MDR-TB). Beyond MDR-TB, non-tuberculous mycobacteria (NTMs) have been reported to complicate lung infections, invasive procedures, and care for immunocompromised individuals, posing urgent need for effective intervention to combat increasing mycobacterial infections and resistance. In the present study, we investigated the mycobacterial genomes and RNA polymerase-binding protein A (RbpA), a highly conserved transcription factor essential for mycobacterial survival. Literature evidence indicates that the stabilising interaction between RbpA and RNA polymerase (RNAP) is a key non-mutational resistance mechanism responsible for rifampicin tolerance central to drug-resistant TB and NTM infections. Drawing from this, we screened 4500 small bioactive molecules to assess their potential to disrupt the interaction between RbpA and RNAP to overcome rifampicin tolerance and resistance. Using in-silico approaches, the molecules were docked in the central core domain (CD) of RbpA for optimal RNAP contact. An integrated computational pipeline combining docking, interaction profiling, ADMET assessment, MMGBSA scoring, and molecular dynamics (MD) simulations, was used to evaluate the molecules. This enabled identification of 12 drug-like compounds demonstrating good docking and MMGBSA scores, nuclear membrane permeability, favourable pharmacokinetics, stable interactions, advantageous residue movements, and stable MD trajectories. The top leads demonstrated strong potential to counter rifampicin tolerance in *M. tuberculosis* and non-tuberculous mycobacterial infections by competitively disrupting RbpA-RNAP interaction stability, while also reducing protein-protein interactions by inducing minor conformational changes. These findings provide a foundation for subsequent in-vitro and in-vivo validation, advancing the development of novel anti-mycobacterial therapeutics.

Poster Presentation

Identification and Characterization of Plant Growth Promoting Rhizobacteria from Rice Rhizosphere Capable of Redirecting Root Architecture and Enhancing Plant Growth

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Abstract:

The vigor of a plant's above-ground growth is fundamentally relied on its below-ground root system. This vital connection occurs in the rhizosphere, the dynamic zone of complex interplay between plant roots and the surrounding soil microbial communities. Plants actively recruit these beneficial microorganisms via root exudates, leading to colonization of the root surface and internal tissues. Many of these recruited microbes are Plant Growth-Promoting Rhizobacteria (PGPR). PGPR enhance plant growth through various mechanisms like biological nitrogen fixation, nutrient solubilization, phytohormone production, and disease suppression. For the past decade, the production of exogenous auxin (Indole-3-acetic acid) by PGPR has been considered as one of the most important PGP attributes, directly contributing to improving the host root system for better resource utilization. However, in our current study, we observed a crucial finding: that non-auxin producing bacteria can also profoundly alter the host root architecture and promote plant growth. We first performed acclimatization in insoluble inorganic phosphate media (NBRIP) to screen bacterial isolates from rice rhizospheric soil, with a high potential for phosphate solubilization. Potent isolates were then selected based on other PGP attributes, including nitrogen fixation, potassium solubilization, and ammonia production, with a varied ability for exogenous auxin production. We successfully identified a specific non-auxin producing bacterial isolate, *Pantoea dispersa* PB11, which was highly effective in improving root architecture and promoting overall plant growth. Co-inoculation of PB11 with *Arabidopsis* was found to effectively suppress primary root growth while simultaneously promoting lateral root density. We further investigated that PB11 modulates the root architecture by negatively regulating the auxin abundance in the primary root and enhancing the expression of key regulators of lateral root development. Therefore, our findings suggesting that beneficial rhizospheric isolates can alter the physiology and growth of the plant by exploiting partially different mechanisms, rather than solely relying on exogenous auxin production.

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