UNIVERSITY OF ENGINEERING AND MANAGEMENT, KOLKATA
INSTITUTE OF ENGINEERING AND MANAGEMENT
DEPARTMENT OF BIOTECHNOLOGY
presents

BIOSPECTRUM'25

IN COLLABORATION WITH

FACULTY OF MEDICINE, "APOLLONIA"
UNIVERSITY OF IASI, ROMANIA

From 10th to 12th December 2025

ABSTRACT BOOK

International Conference on Biotechnology & Biological Sciences

10th to 12th December 2025

About BIOSPECTRUM 2025

The Department of Biotechnology at the University of Engineering and Management proudly announces **BIOSPECTRUM 2025**, the upcoming edition of our globally engaged **International Conference on Biotechnology and Biological Sciences**. Growing steadily in influence, the conference has established itself as a renowned scientific forum where pioneering researchers, academic visionaries, and industry innovators converge to exchange ideas, form strategic collaborations, and inspire the future of biotech-driven solutions. BIOSPECTRUM 2025 will be held from **10 to 12 December 2025**, opening a new milestone as the event is co-hosted with the **University of Iași, Romania**. Designed for broad scientific accessibility, the conference will support **hybrid participation**, welcoming delegates physically in Kolkata and virtually from research hubs around the world, ensuring a borderless platform for scientific discourse and discovery. The 3-day program will feature insightful keynote talks, peer-reviewed research presentations, theme-focused sessions, expert panel dialogues, and hands-on workshops, spanning critical areas such as **genome engineering, advanced biomedical science, sustainable bio-agricultural technologies, computational biology, and environmental biotechnology**. The agenda is crafted to foster both fundamental scientific depth and real-world impact. This year's themes spotlight breakthrough and future-shaping frontiers including N**ext-Gen Applications of Bioprocess Technology and Engineering**. Beyond a conventional academic conference, BIOSPECTRUM 2025 aims to be an energetic intersection of innovation and application—an ecosystem where new discoveries are shared, emerging tools are experienced, and forward-looking ideas take flight. Attendees will gain direct exposure to cutting-edge research, connect with distinguished global scientists, explore novel biotechnological paradigms, and contribute to transformative discussions that drive progress toward a sustainable and healthier future. BIOSPECTRUM 2025 is more than an event—it is a movement built on knowledge exchange, global partnerships, and the spirit of scientific advancement that continues to redefine how we interpret and transform the living world.

About the Department

Department of Biotechnology, University of Engineering and Management, Kolkata has framed the departmental syllabus and the curriculum to produce technically skilled engineers to compete with the growing pace. We have 30 sanctioned seats for B Tech in Biotechnology programme. Following the AICTE curriculum we give our students the opportunity of working in the lab under faculty mentor on the projects. We do have research scholars working under the supervision of the faculty members. Department organizes an international conference, Biospectrum, every year to provide students with opportunities to interact with academicians, researchers across the country and beyond. Department also brings out an international journal on a quarterly basis.

Undergraduate

B.Tech, the UG program offered by the department follows AICTE curriculum along with some added courses. Students get opportunities for a lot of extra and co-curricular activities. This helps them to be better employable by developing problem solving skills, life skills. The highlight of the syllabus is the practical knowledge that the students gain through working in the lab, internships, industrial visits.

Research / PhD program

The Laboratory of the Department of Biotechnology is well equipped with instruments to comply with research requirements. Research in the department is coordinated with faculty members where the students are directly and actively involved in projects and gain their knowledge of research through discussion with their mentors, departmental research seminars and interaction with scientists of national and international reputations is organized by the department on a regular basis. Department has projects and research scholars.

VISION AND MISSION OF THE DEPARTMENT

VISION

To evolve for global recognition with outcome-based teaching learning and be able to adapt with the advancements in the field of biotechnology.

MISSION

M1: To impart quality and value-based education to the students to make them socially responsible future leaders in the field of biotechnology.

M2: To inculcate an innovative teaching learning process to produce competent, creative engineers to thrive for excellence.

M3: To continuously upgrade the curriculum and infrastructure through periodic feedback from the stakeholders to equip the students with the advancements in biotechnology

PROGRAMME EDUCATIONAL OBJECTIVES (PEOs)

PEO 1: The program ensures that students have a strong foundation in the principles and practices of biotechnology, along with knowledge of science and mathematics.

PEO 2: The program will empower students with application-oriented domain knowledge and skills enabling them to emerge as capable and competent biotechnologists on a global scale.

PEO 3: The students will develop the ability to identify and analyze diverse biotechnology-related problems, employing lifelong learning and professional growth to devise sustainable solutions.

PEO 4: The students will be nurtured and developed as responsible engineers by inculcating the culture of values, ethics, integrity, leadership and social responsibility.

In the memory of our Founder Chancellor

Prof. Dr. Satyajit Chakrabarti

Message from the Chancellor

It gives me immense pleasure to write the foreword for the International Conference on Biotechnology and Biological Sciences, BIOSPECTRUM 2025. This international event brings together experts, researchers, academicians, students, and young scientists to share knowledge and innovations in biotechnology.

The theme of this year's conference, "Next-Gen Applications of Bioprocess Technology and Engineering" focuses on cutting-edge advancements in biotechnology. In recent years, biotechnology has moved far beyond laboratory research and has emerged as a transformative force in national economies and global policy. From AI-driven drug discovery and genome editing to bioeconomy expansion and climate-smart bioprocesses, the sector is undergoing a profound shift.

Biospectrum has always championed emerging ideas and served as a bridge between innovators and the world. This editorial highlights the voices, visions, and ventures that are propelling the biotech revolution forward.

May Biospectrum 2025 inspire our young scientists, researchers, and innovators to dream boldly, collaborate fearlessly, and innovate responsibly. Let this conference strengthen our shared vision for progress in biotechnology and the life sociences.

Banani Chakraborti

Prof. Dr. Banani Chakraborti

Chancellor

University of Engineering and Management, Kolkata

Message from the Vice Chancellor

It is a moment of pride and anticipation as we welcome you to BIOSPECTRUM 2025, our annual International Conference on Biotechnology, hosted at the UEM Kolkata campus. This year's event builds on our tradition of advancing knowledge and fostering collaboration across the life sciences.

Our Department of Biotechnology has worked tirelessly to create a platform that unites brilliant minds from fields like engineering, genetics, biochemistry, and microbiology. BIOSPECTRUM 2025 is designed to inspire meaningful dialogue, promote interdisciplinary research, and showcase pioneering breakthroughs in biotechnology. I am confident that this conference will provide stimulating discussions, valuable insights, and impactful collaborations that will drive innovation forward.

I am especially proud of the incredible work showcased in this conference publication, which captures the dedication of researchers working towards the betterment of society. My heartfelt congratulations to the organizing team for their commitment and efforts in bringing this event to life.

Prof. Dr. Sajal Dasgupta

Message from the Pro Vice Chancellor

It is a great honor to welcome you to BIOSPECTRUM 2025, our international conference on Biotechnology and Biological Sciences. This event highlights biotechnology's far-reaching impact across diverse fields—from medicine and agriculture to environmental sustainability and pharmaceuticals—touching nearly every aspect of human well-being.

This abstract book of BIOSPECTRUM 2025 brings together esteemed scientists and researchers from India and around the world, presenting groundbreaking advancements and pioneering research. I am proud to see the knowledge shared in this abstract book and deeply grateful to the researchers who have entrusted us with their work, reinforcing the success and reputation of this international conference.

I would like to extend my sincere thanks to the publishing houses for their valuable support in promoting BIOSPECTRUM 2025, helping us reach a broader audience. Additionally, I am grateful to our dedicated team of faculty and students, whose hard work and commitment have brought this journal to life.

Together, we have created a platform that celebrates innovation and fosters collaboration. My best wishes go to everyone involved for such an inspiring conference.

Satyajit Chakrabarti

Prof. Dr. Satyajit Chakrabarti

Acknowledgement

We, the organizing committee of Biospectrum, extend our heartfelt gratitude to everyone who contributed to the success of the conference. First and foremost, we are deeply grateful to our distinguished **Keynote speakers** and **Session chairs** for sharing their invaluable insights and expertise, enriching the discussions with their knowledge, and inspiring both professionals and students alike.

We extend our gratitude to **University of Iași, Romania** for being our esteemed collaborator. Their partnership and support have greatly enriched our event and we are truly thankful for their invaluable contribution.

We would also like to acknowledge the support of our publication partners, **Bioweb of Conference** whose generous contributions made this gathering possible.

Your commitment to advancing research and fostering collaboration in the life sciences sector has been instrumental in making Biospectrum a reality.

We are sincerely thankful to all the researchers who have trusted us and contributed to our conference to make it a successful one.

We extend our appreciation to each of the attendees for your participation and enthusiasm.

We are extremely thankful to the **Faculty members** of Department of Biotechnology for their support.

The **Research scholars and Student team** who worked tirelessly behind the scenes, we cannot thank you enough. Your dedication, professionalism, and attention to detail has ensured a seamless experience for all.

We hope Biospectrum has been a rewarding and inspiring experience for everyone involved.

Together, let us continue pushing the boundaries of science, innovation, and collaboration.

Thank you.

Prof. Dr. Susmita Mukherjee

On behalf of Biospectrum Organizing Committee

Committees

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- **Prof. Dr. Arun Bandyopadhyay**
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  Gujarat Former-Director CSIR-IICB

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CONTENTS

ORAL SESSION 3: PLANT BIOTECHNOLOGY

ORAL SESSION 4: ENVIRONMENTAL BIOTECHNOLOGY

ORAL SESSION 5: FOOD BIOTECHNOLOGY

29	202509074	Formulation and physiochemical characterization of fish skin (*Labeo rohita*) oil incorporated mayonnaise	31
30	202509022	Investigating Thermal Process-Induced Functional Changes in Little Millet: A RSM-based Comparative Insight	32
31	202509140	Genetic variability of Bowman Birk Inhibitor relation to total trypsin inhibitor activity in soybean with or without Kunitz trypsin inhibitor	33
DAY 2 (11TH DECEMBER 2025)			
KEYNOTE SPEAKERS			
32	**KEYNOTE ADDRESS 3 BY Dr. Gaurab Gangopadhyay** **Professor, Biological Sciences Bose Institute, Kolkata, India**		34
33	**KEYNOTE ADDRESS 4 BY Dr. Sulagna Basu** **Scientist G** **ICMR - National Institute for Research in Bacterial Infections, India**		35
34	**KEYNOTE ADDRESS 5 BY Dr. Swastika Paul** **Co-founder & Chief Scientific Officer at ExSURE, India**		36
ORAL SESSION 6: MEDICAL BIOTECHNOLOGY			
35	202509037	Phytoconstituents and HSP-70, the cancer biomarker: A molecular docking approach	37
36	202509009	Biofilms and Antimicrobial Resistance: A Hidden Driver in the One Health AMR Crisis	38
37	202509076	Whole-Genome Insights into High-Risk Escherichia coli Lineages Carrying OXA-48-like Carbapenemases: First Genomic Evidence of OXA-484 in India	39-40
38	202509129	Exploring Hematological Biomarkers through Data Mining for Multi-Disease Prediction	41
39	202509153	The Silent Epidemic: Chronic Arsenic Exposure and Carcinogenesis in the Gangetic Delta	42
40	202509158	Advances in Stem Cell and Regenerative Medicine for Overcoming Barriers in Tissue Repair and Organ Regeneration	43
41	202509160	A review of pharmacogenetic studies concerning genetics and treatment response in parkinson's disease	43A-43B

ORAL SESSION 7: MICROBIAL BIOTECHNOLOGY

ORAL SESSION 8: ENVIRONMENTAL BIOTECHNOLOGY II

SESSION 9: CONCEPTS OF LAW AND MANAGEMENT IN BIOTECHNOLOGY

POSTER SESSION 1: MEDICAL BIOTECHNOLOGY

POSTER SESSION 2: MEDICAL BIOTECHNOLOGY

POSTER SESSION 3:ENVIRONMENTAL AND PLANT BIOTECHNOLOGY

POSTER SESSION 4:ENVIRONMENTAL AND PLANT BIOTECHNOLOGY

International Conference on
Biotechnology & Biological Sciences

10th to 12th December 2025

Day 1: 10th December 2025

Keynote Speakers

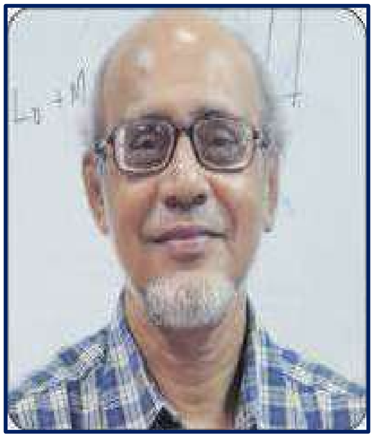
ABOUT SPEAKER

Dr. Arun Bandyopadhyay

Director - Gujarat Biotechnology University (Gujarat, India)

Dr. Arun Bandyopadhyay is currently the Director of Gujarat Biotechnology University, Gandhinagar — and prior to this he led CSIR-Indian Institute of Chemical Biology (IICB), Kolkata, where he served as a senior principal scientist and principal investigator. With more than 120 peer-reviewed publications, his research spans oxidative stress, mitochondrial dynamics, cell signalling, free radical biology, and biomarker discovery — establishing him as a leading expert in cell biology and physiology. Under his leadership at Gujarat Biotechnology University, he aims to steer the institution toward translational biotechnology, multi-omics research, and application-oriented life-science education, bridging fundamental research with real-world impact.

ABOUT SPEAKER



Dr. Partha P. Majumder

Distinguished Professor, John C. Martin Centre for Liver Research & Innovations
Emeritus Professor, Indian Statistical Institute, Kolkata
Adjunct Faculty Member, Indraprastha Institute of Information Technology Delhi

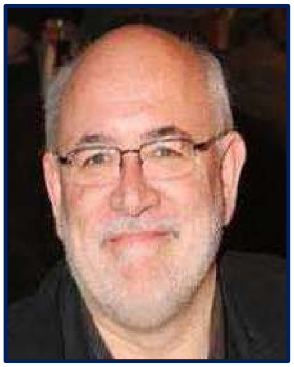
Dr. Partha P. Majumder is a National Science Chair (Scientific Excellence, Government of India) and Distinguished Professor at the John C. Martin Centre for Liver Research & Innovations, Kolkata, with a storied past as founder of the National Institute of Biomedical Genomics (NIBMG) and as Emeritus Professor of the Indian Statistical Institute (ISI), Kolkata.

Abstract

Cancer is a disease of the genome. For any type of cancer – lung cancer, oral cancer, cervical cancer, etc. – only rarely does one encounter families in which multiple family members are affected with cancer. In other words, familial cancers are rare. When a type of cancer runs in a family, it is usually caused by one or more heritable germline mutations that are transmitted over generations. Most cancers are sporadic – non-familial – in nature. The hallmark of cancer is uncontrolled growth of cells. Some DNA alterations in a normal cell provides a growth advantage to the cell, which then grows uncontrollably and abnormally to form a set of cells, called a clone, which forms a tumour. These DNA alterations occur mostly after an individual is born, and are called somatic alterations. If we consider the genome of a cancer cell as the "cancer genome," it is now clear that there is cellular evolution of the normal genome by somatic mutation and natural selection to the cancer genome.

In this talk, I shall explain the concept of evolution of cancers and the DNA changes involved in this evolutionary process. I shall then go on to describe our recent results on identifying the genomic and transcriptomic alterations that are associated with oral cancer, and the biology of the disease that can be gleaned from these findings.

ABOUT SPEAKER



Dr. Paul Williams

Emeritus Professor of Molecular Microbiology, Faculty of Medicine & Health Sciences,
University of Nottingham, UK

Dr. Paul Williams is Emeritus Professor of Molecular Microbiology at the University of Nottingham's Biodiscovery Institute (Faculty of Medicine & Health Sciences), UK. He is a globally respected authority on bacterial communication (Quorum sensing), biofilm formation and strategies for antimicrobial intervention — fields in which he has published over 400 research articles and patents, making him one of the most cited scientists in microbial signalling and virulence regulation.

Abstract

In bacterial pathogens such as *Pseudomonas aeruginosa* the expression of multiple virulence and biofilm development genes is often co-ordinately controlled at the transcriptional level by global regulatory systems incorporating quorum sensing (QS). The latter constitutes a cell-to-cell communication network that integrates information at the population level, co-ordinating the metabolic status of the cells with environmental cues. QS depends on the synthesis, secretion and perception of diffusible signalling molecules that enable pathogens to synchronize their behavior. QS signal molecules, although largely considered as effectors of QS-dependent gene expression are also emerging as multi-functional agents that impact on host-pathogen interactions and influence life, development and death in single and mixed microbial populations. QS is a potential antibacterial target in pathogens where strains carrying mutations in key QS genes exhibit highly attenuated pathogenicity in animal infection models Further indications that QS systems are active during human infections are emerging from clinical studies where QS signal molecules can been detected in patient body fluids. Since QS by definition depends on small molecule ligand/receptor interactions, it offers a direct pharmacological pathway to inhibitor development since the steric requirements for optimal ligand/receptor interactions means that antagonists can be readily obtained through structural modification of native agonists. In this context, advances in our understanding of the molecular and structural biology of 2-alkyl-4-quinolone (AQ)-dependent QS in *P. aeruginosa* have facilitated identification of multiple 'druggable' targets and small molecule inhibitors. In cystic fibrosis, the presence of AQs in plasma and urine correlates with clinical status highlighting their potential as biomarkers to aid diagnosis and assessment of the response to treatment.

International Conference on
Biotechnology & Biological Sciences

10th to 12th December 2025

Day 1: 10th December 2025

Oral Presentations

DAY 1

10TH DECEMBER 2025

ORAL SESSION 1

Use of AI and ML in Biotechnology

Paper Code: 202509062

Comparative Performance of Next-Gen YOLO Models for Leaf Health Classification in Ornamental Species

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ABSTRACT

Automated plant disease detection has become an essential application of deep learning, supporting early diagnosis and effective crops and ornamental plant management. Recent advancements in the You Only Look Once (YOLO) family of object detection models have improved both accuracy and efficiency, making them suitable for real-time deployment. This paper presents a comparative analysis of YOLOv8, YOLOv9, and YOLOv11 for classifying diseased and healthy leaves of Ixora and Bougainvillea, two widely grown ornamental species. A curated dataset of annotated leaf images covering multiple disease conditions was used to train and evaluate the models under consistent experimental settings. Performance was assessed using mean Average Precision (mAP), precision, recall, F1-score, and inference speed (FPS). Results indicate that YOLOv11 achieves the highest detection accuracy, especially in capturing subtle disease patterns, while YOLOv8 and YOLOv9 demonstrate competitive performance with faster inference, making them preferable for resource-limited applications. The findings highlight practical trade-offs between accuracy and efficiency across YOLO versions, offering valuable insights for real-world deployment. By extending research beyond staple crops to ornamental plants, this work underscores the broader applicability of AI-driven disease detection and establishes a benchmark for evaluating next generation YOLO architectures in horticulture.

Keywords: YOLOv8, YOLOv9, YOLOv11, Leaf disease detection, Ixora and Bougainvillea, Deep learning, Comparative analysis.

Paper Code: 202509020

A Comparative Classification Framework Using PCA and Modified PCA with Ensemble and Kernel-Based Learning Models for Mangrove Feature Analysis

Arpita Saha Chowdhury, Dr. Keya De Mukhopadhyay

Abstract

Dimensionality reduction plays a critical role in satellite-based environmental monitoring, particularly when working with high-dimensional multi-temporal datasets. This study presents an integrated classification framework combining Principal Component Analysis (PCA) and a modified PCA strategy with multiple machine-learning classifiers to evaluate mangrove ecosystem characteristics derived from the AnnualMGF dataset. The feature cube, comprising 35 spectral-temporal variables, was transformed using PCA to reduce redundancy while preserving key variance. The performance of five widely used classifiers—Random Forest (RF), Light Gradient Boosting Machine (LightGBM), Extreme Gradient Boosting (XGBoost), Support Vector Machine (SVM), and K-Nearest Neighbors (KNN)—was systematically assessed on PCA-transformed features.Model evaluation employed accuracy metrics, confusion matrix analysis, and visual diagnostics, including PCA explained variance plots and two-dimensional scatter representations of the reduced feature space. Random Forest and LightGBM demonstrated superior robustness across the reduced-dimensional domain, while XGBoost yielded competitive performance with enhanced sensitivity to class variability. Feature importance analysis derived from the Random Forest classifier further revealed the relative contributions of principal components toward discriminative capability. Comparative results highlight the effectiveness of PCA and modified PCA in enhancing computational efficiency without compromising classification quality.The proposed framework provides a reproducible, scalable, and computationally efficient pipeline for environmental monitoring tasks that involve large spatial datasets. This study demonstrates that combining dimensionality-reduction techniques with ensemble learning models significantly improves classification accuracy, strengthens interpretability, and enables comprehensive performance diagnostics suitable for remote sensing applications.

Paper Code: 202509123

A decision support machine learning tool for environmental bioremediation as water safety in India

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Abstract

Ensuring access to the safe drinking water is a major public-health challenge across many parts of India, as water is contaminated due to chemical contamination or inadequate treatment. Routine laboratory experiments yield reliable but very slow and costly process. In this work, we present a simple and interpretable machine learning framework that uses commonly measured physicochemical parameters to predict the potability of drinking water and offer decision support for bioremediation planning. This study utilizes a publicly available dataset showing some important parameters such as pH, turbidity, total dissolved solids, conductivity, chloramines, and trihalomethanes. These were followed by systematic preprocessing and exploratory analysis, and multiple models were evaluated; the ensemble methods provided robust and stable performance. Feature-importance patterns and SHAP-based explanations assist the identification of the parameters most responsible for non-potability, thus linking such insight to either an appropriate biological or ecological treatment. This approach demonstrates how lightweight Artificial Intelligence tools may supplement traditional monitoring practices and aid in targeted remediation initiatives in resource-constrained environments.

Keywords: Water potability, Machine Learning, Physiochemical indicator, Environmental bioremediation, Decision support system.

Paper Code: 202509050

Attention-Guided Pooling with InceptionV3: A Novel Framework for Accurate and Interpretable Diabetic Retinopathy Detection

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Abstract

Diabetic Retinopathy (DR) is a leading cause of preventable blindness, and its increasing prevalence necessitates scalable and accurate screening solutions. Deep learning has shown immense promise for automated DR detection from retinal fundus images, yet standard models often fail to adequately localize and prioritize the subtle, variably-sized pathological features of the disease. This paper introduces a novel deep learning framework that pairs an InceptionV3 backbone with a custom Attention-Guided Global Weighted Average Pooling (GWAP) mechanism. Traditional Global Average Pooling (GAP) layers can dilute the contribution of small but critical indicators like microaneurysms. Our GWAP module learns to assign weights to different spatial regions of the feature map, forcing the model to focus on clinically relevant areas, thereby improving both diagnostic accuracy and interpretability. We conduct a rigorous evaluation on two public benchmark datasets: Kaggle APTOS 2019 (EyePACS-Q) and MESSIDOR. Through extensive experiments, including ablation studies, we demonstrate that our GWAPenhanced model significantly outperforms a standard InceptionV3 baseline and achieves competitive results against state-of-the-art methods. Furthermore, we visualize the model's attention maps, providing transparent, qualitative evidence of its ability to localize disease-relevant regions. This work represents a meaningful step towards creating more accurate, robust, and trustworthy automated systems for DR screening that can be integrated into clinical workflows. Keywords: Diabetic Retinopathy ´ Deep Learning ´ InceptionV3 ´ Attention Mechanism ´ Medical Image Analysis ´ Interpretability.

Paper code: 202509018

A Hybrid Approach for Tumor Cell Prediction in Arachis hypogaea Root Nodules Using Differentially Expressed Genes and Image Processing

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Abstract The rapid growth of genomic data and the sensitive nature of patient information demand secure, privacy-preserving, and scalable frameworks for genome sequence classification. In this work, we propose FedGenomeX (Federated Genome Exploration with Explainability), a novel deep-federated learning framework that enables distributed genomic analysis while maintaining data confidentiality. FedGenomeX integrates Transformer-based local encoders, secure aggregation with CKKS homomorphic encryption and differential privacy, FedProx based optimization for heterogeneous non-IID datasets, communication-efficient parameter pruning and knowledge distillation, and an explainability layer leveraging attention-based motif discovery and SHAP analysis. The framework ensures that raw genomic sequences remain on local devices, with only encrypted model updates shared for global model aggregation. Experiments on multi-institution genomic datasets demonstrate that FedGenomeX achieves state of the art performance with all key metrics-accuracy, precision, recall, and F1-score-reaching 0.9907, outperforming conventional centralized, deep-transfer learning, and other federated learning approaches. Furthermore, FedGenomeX balances computational efficiency and scalability across varying client configurations while providing biologically interpretable insights into sequence motifs driving classification. These results highlight FedGenomeX as a robust, secure, and interpretable solution for distributed genomic analysis, offering significant potential for real-world biomedical applications where privacy and explainability are critical.

Paper code: 202509050

Attention-Guided Pooling with InceptionV3: A Novel Framework for Accurate and Interpretable Diabetic Retinopathy Detection

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Abstract

Diabetic Retinopathy (DR) is a leading cause of preventable blindness, and its increasing prevalence necessitates scalable and accurate screening solutions. Deep learning has shown immense promise for automated DR detection from retinal fundus images, yet standard models often fail to adequately localize and prioritize the subtle, variably-sized pathological features of the disease. This paper introduces a novel deep learning framework that pairs an InceptionV3 backbone with a custom Attention-Guided Global Weighted Average Pooling (GWAP) mechanism. Traditional Global Average Pooling (GAP) layers can dilute the contribution of small but critical indicators like microaneurysms. Our GWAP module learns to assign weights to different spatial regions of the feature map, forcing the model to focus on clinically relevant areas, thereby improving both diagnostic accuracy and interpretability. We conduct a rigorous evaluation on two public benchmark datasets: Kaggle APTOS 2019 (EyePACS-Q) and MESSIDOR. Through extensive experiments, including ablation studies, we demonstrate that our GWAPenhanced model significantly outperforms a standard InceptionV3 baseline and achieves competitive results against state-of-the-art methods. Furthermore, we visualize the model's attention maps, providing transparent, qualitative evidence of its ability to localize disease-relevant regions. This work represents a meaningful step towards creating more accurate, robust, and trustworthy automated systems for DR screening hat can be integrated into clinical workflows.

Keywords: Diabetic Retinopathy ´ Deep Learning ´ InceptionV3 ´ Attention Mechanism ´ Medical Image Analysis ´ Interpretability.

DAY 1

10TH DECEMBER 2025

ORAL SESSION 2

MEDICAL BIOTECHNOLOGY

Paper Code: 202509142

Evaluation of *Kappaphycus striatus* Lectin on SARS-CoV-2 Spike Protein-Specific IgG Responses

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Abstract

The COVID-19 pandemic highlighted the urgent need for novel therapeutics that would balance vaccines and antivirals. Lectins, which are carbohydrate-binding proteins, can interfere with viral glycoproteins and modulate host immune responses. Seaweed lectins are of particular interest due to their specificity for complex glycans present on viral spikes, including SARS-CoV-2. *Kappaphycus striatus*, widely cultivated in Southeast Asia, is known for its carrageenan but also contains lectins with promising bioactivities. Little is known about the in vivo immunological role of *K. striatus* lectins. This study evaluates whether lectin from *K. striatus* affects IgG responses to the SARS-CoV-2 spike protein in mice.

Keywords: Algal lectin; IgG response; *Kappaphycus striatus*; novel therapeutics; SARS-CoV-2 spike protein

Paper Code: 202509138

Anticancer Potential of Indian Propolis Against HT29 Colon Cancer Cells

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Abstract

Indian propolis extract showed significant anticancer activity against HT29 colon cancer cells by reducing its cell viability in a dose-dependent manner, with an IC_{50} of approximately 400 µg/mL, while showing minimal cytotoxicity toward normal HEK293 cells. Morphological and nuclear assessments revealed typical apoptotic features, including chromatin condensation and cell shrinkage. Flow cytometric analysis validated a dose-dependent elevation in late apoptotic populations, with caspase-3/7 activity reaching its peak at 12 hours, signifying the early activation of the apoptotic cascade. Indian propolis significantly impeded colony formation, migration, and 3D spheroid growth of HT29 cells, indicating strong anti-proliferative and anti-metastatic properties. These results highlight the potential of Indian propolis extract as a natural safe therapeutic candidate for colon cancer management.

Keywords: Indian propolis; HT29; colorectal cancer; apoptosis; migration; spheroid inhibition

Paper code: 202509011

A pharmacophore study of campothecin derivative sobuzoxane for the treatment of angiogenesis mediated N1-N8 breast cancer as a radiosensitizer

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Abstract

Chemotherapeutic drugs are widely recognized for their targeted mechanisms that destroy rapidly proliferating breast cancer cells; however, the emergence of radiation resistance remains a major challenge in cancer therapy. To overcome this, 9-amino camptothecin has been employed during treatment to enhance the effects of radiation. In this study, pharmacophore modeling was applied to modify the structure of 9-amino camptothecin, leading to the development of its derivative, Sobuzoxane, which exhibits radio sensitizing activity through OH-lactone ester mimicry among ten identified hits. In N1–N8 breast cancer, where cancer cells spread through the lymphatic system, VEGF-B is recognized as a critical target involved in lymph angiogenesis and cellular survival. Here, ligand structures were optimized to generate more active compounds capable of targeting VEGF-B effectively. The pharmacophore models were developed by refining hydrogen bond donors and acceptors, hydrophobic interactions, and aromatic features, resulting in potential hits that satisfy key drug discovery parameters. The hits obtained from pharmacophore modeling were further evaluated through molecular docking, and ADMET studies. Docking studies revealed that **Sobuzoxane** showed stronger binding affinity with **VEGF-B** than **9-amino camptothecin**, reducing its destabilizing effect on the protein. The presence of an **antibody** enhanced hydrogen bonding within the **VEGF-B–Sobuzoxane** complex, indicating improved molecular stability and specificity. **ADMET analysis** confirmed that Sobuzoxane has good solubility and strong ligand–protein interaction potential, supporting its role as a **lead radiosensitizer** targeting VEGF-B. The results suggest that **in silico modeling** identified Sobuzoxane with **enhanced radiosensitization potential** for treating **angiogenesis-mediated N1–N8 breast cancer**.

Keywords: Angiogenesis, ADME, Camptothecin derivatives, Breast cancer, Radiosensitization, Pharmacophore study

Paper code: 202509134

Design and Evaluation of Quercetin-Integrated PVA/HEC Nanofibers for Bioactive Wound Healing Application

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ABSTRACT

Electrospun nanofibrous scaffolds are widely recognized for their structural similarity to the native extracellular matrix and their suitability for wound healing applications. In this study, quercetin-integrated poly(vinyl alcohol)/hydroxyethyl cellulose (PVA/HEC) nanofibers were successfully fabricated via electrospinning to develop a bioactive wound dressing system. The optimized PVA/HEC blend enabled uniform fiber formation and stable quercetin incorporated fibrous mat. Physicochemical characterizations using FTIR, XRD, TGA and HRSEM confirmed the homogeneous distribution of quercetin within the polymeric matrix and the preservation of nanofibrous morphology. The quercetin-loaded nanofibers demonstrated notable antioxidant and antibacterial activities, indicating their capacity to modulate oxidative stress and inhibit microbial proliferation at wound sites. In vitro drug release studies revealed a sustained and controlled release profile of quercetin over time. Biocompatibility evaluation, complemented by fluorescence-based wound scratch assay, showed enhanced fibroblast cell migration and proliferation, confirming the scaffold's ability to accelerate wound closure. These results collectively suggest that quercetin-integrated PVA/HEC nanofibers hold strong potential as a next-generation bioactive scaffold for efficient wound healing applications.

Paper code: 202509089

Effect of polyphenol extracts of *Helichrysum Maracandicum* on the passive permeability of liver mitochondrial membranes in rats with toxic hepatitis

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Abstract

This study investigates the effect of polyphenol extracts obtained from Helichrysum maracandicum on the passive ion permeability of liver mitochondrial membranes and the state of the mitochondrial permeability transition pore (MPTP) in vivo. The experimental results demonstrated that the polyphenol extracts dose-dependently increased the passive permeability of mitochondrial membranes to several cations, particularly K^+, Na^+, and H^+. The most pronounced effect was observed at a 20 mg dose, where the permeability of cations decreased in the order: $K^+ > Na^+ > H^+$. These findings suggest that H. maracandicum polyphenols directly influence the mitochondrial membrane structure and are capable of inducing the opening of the MPTP. At the same time, at lower concentrations, the extracts exhibited a membrane-stabilizing and modulatory effect, maintaining physiological ion exchange at a normal level. Therefore, the polyphenols of H. maracandicum reveal a dose-dependent dual effect, both stabilizing and inducing, and may serve as natural bioactive compounds regulating mitochondrial membrane function.

Paper code: 202509041

Identification of a novel virulence factor from *Klebsiella pneumoniae* isolates associated with intestinal perforation and neonatal sepsis

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ABSTRACT

Neonatal sepsis remains a leading cause of morbidity and mortality worldwide, particularly in low- and middle-income countries where delayed diagnosis and limited infection control measures contribute to poor outcomes. Among Gram-negative pathogens, *Klebsiella pneumoniae* has emerged as a major cause of neonatal sepsis and is frequently associated with multidrug resistance and high mortality.

This study reports two rare and clinically severe cases of ***K. pneumoniae*-associated neonatal sepsis presenting with leaky gut, intestinal perforation, and luminal fluid accumulation**. The neonates, admitted 20 days apart to the same tertiary care NICU in Jodhpur, India, developed sepsis-like symptoms with prominent gastrointestinal involvement within 60 hours of life following formula feeding. Both infants exhibited abdominal distension, bloody diarrhoea, and foul-smelling gastric aspirates. Microbiological analysis confirmed the presence of *K. pneumoniae* as the causative pathogen. What makes this study particularly noteworthy is the novel therapeutic intervention employed. A 20-minute stomach wash using sterile saline was performed to reduce the bacterial load leading to rapid clinical improvement.

To further validate this observation, we replicated the clinical condition of the neonates in a murine model of *K. pneumoniae* infection with the same isolates and repeated the stomach wash approach, which yielded similarly positive outcomes. To investigate the unusual severity of intestinal pathology, molecular characterization of the *K. pneumoniae* isolate was performed. Whole-genome analysis identified three major virulence determinants—***khe* (Klebsiella haemolysin), Type VI Secretion System (T6SS), and the *yersiniabactin* (ybt) siderophore locus**—that together likely contributed to the hypervirulent phenotype.

The ***khe*** gene encodes a pore-forming cytotoxin capable of disrupting epithelial cell membranes and compromising gut barrier integrity, thereby promoting increased permeability and bacterial translocation. This disruption not only facilitates bacterial translocation across the mucosal barrier but also contributes to vascular leakage, ultimately predisposing to intestinal edema and perforation. Purified khe protein also manifested similar gastrointestinal symptoms in animal model similar to the neonates.

The **Type VI Secretion System (T6SS)** is another major virulence determinant contributing to the pathogenic potential of this isolate. The T6SS is a complex nanomachine resembling an inverted phage tail, used to deliver toxic effector proteins directly into neighbouring prokaryotic or eukaryotic cells. In *K. pneumoniae*, T6SS has been implicated in host cell

invasion, cytotoxicity, modulation of the immune response and trigger pro-inflammatory signalling, mucosal injury and promote intestinal perforation.

The **Yersiniabactin (ybt) locus**, often part of the high-pathogenicity island (HPI), encodes a siderophore-mediated iron acquisition system. In the present context, efficient iron acquisition via ybt helped to sustain bacterial proliferation in necrotic intestinal tissue, creating osmotic gradients that drive fluid influx into the intestinal lumen and contribute to edema and distension.

Collectively, the interplay between these virulence systems—**epithelial injury by khe**, **cytotoxic effector delivery by T6SS**, and **metabolic adaptation via ybt**—likely underpins the severe intestinal pathology observed in this neonatal outbreak. This combination transforms a classical *K. pneumoniae* strain into a **hypervirulent variant** capable of inducing leaky gut, fluid accumulation, and intestinal perforation, a presentation rarely documented in neonatal sepsis.

Keywords: *Klebsiella pneumoniae,* Neonatal sepsis, Intestinal perforation, virulence determinants

DAY 1

10TH DECEMBER 2025

ORAL SESSION 3

PLANT BIOTECHNOLOGY

Paper code: 202509013

Theoretical study of the antioxidant mechanism of chrysin and its metabolites – a computational approach

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Abstract

Flavonoid chrysin, obtained from different plants, has different pharmacological property, due to its antioxidative effects. But low bioavailability of chrysin limits its therapeutics application. In systemic circulation, chrysin can be transported by binding with serum albumin protein. Furthermore, in hepatic circulation, two chrysin metabolites e.g. chrysin-7-O- glucuronide and chrysin-7-O-sulphate are formed by biotransformation process in liver. By using computational methods like density functional theory study, the antioxidant potential of these four compounds has been investigated. In this study, both the highest occupied molecular orbital (HOMO) and the lowest unoccupied molecular orbital (LUMO) have been identified by Gaussian software. The energies of these orbitals, as well as the energy gap between HOMO and LUMO, have been calculated. Using these calculations, it can be concluded that chrysin in its bound form with human serum albumin, is the best antioxidant among these four compounds. Since, it has the lowest energy gap between the calculated HOMO and LUMO. In this bound form, the cinnamoyl group resent in chrysin molecule participates in the charge transfer event. The antioxidant activity by donating electrons to scavenge the free radicles, has been explained for chrysin and its derivatives. This finding will help us to overcome the poor bioavailability problem of chrysin during its performance as antioxidant.

Key words: Chrysin, antioxidant activity, chrysin metabolites, DFT study, HOMO, LUMO, energy gap between HOMO-LUMO

Paper code: 20250933

Genetic variability of Bowman Birk Inhibitor relation to total trypsin inhibitor activity in soybean with or without Kunitz trypsin inhibitor

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Abstract

Soybeans are known to contain two major serine protease inhibitors: Bowman-Birk inhibitor (BBI) and Kunitz trypsin inhibitor (KTI). These are considered as anti-nutritional factors in soybean as they interfere with the digestibility of available proteins. BBI though is deeply investigated for decades due to its high therapeutic importance in the prevention of cancers. Soybean genotypes with high BBI are desired by pharmaceutical industries for the purified preparation of this nutraceutical molecule, while genotypes with low BBI and genetically eliminated KTI are desirable in soymeal manufacturing units. This study reveals the 11-fold genetic variation in BBI concentration in 95 soybean genotypes with the help of monoclonal antibodies using indirect immunoassay. With the range of 22.0 mg/g of defatted flour (PS1241)- 2.7 mg/g of defatted flour (VLS47), this study identified 3 very high and 5 very low BBI soybean genotypes. BBI contribution varied to total trypsin inhibitor activity varied from genotype to genotype and between 2 to 53.5% with average value of 11.6%. the effect of growing years on the concentration of BBI in soybean was found insignificant. BBI content in BC3F2 derived KTI-free lines was at par with the recurrent parent. Soybean genotypes with extreme BBI content and diverse genetic background identified in the study may be exploited to develop mapping population to identify genomic regions underlying the expression of BBI in soybean.

Paper Code: 202509096

A study on the role of secondary metabolites in combating lead-induced stress in *Pistia stratiotes* (Water lettuce)

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ABSTRACT

Invasive aquatic organisms represent a substantial danger to marine ecosystems, causing disruptions in ecology, and hazards to species. Our study represents the potential of *Pistia stratiotes* to absorb excess nutrients and heavy metals. This study involves the adverse effects of abiotic stress, especially lead nitrate, on aquatic environments. Lead is a toxic heavy metal that acts as an inhibitor to seed germination, hinders seedling growth, and causes oxidative stress along with cellular damage which poses a significant threat to aquatic animals. This research examined the changes in secondary metabolites like polyphenols and flavonoids as they are known because of its competence for binding heavy metals and for its antioxidant properties. Studies reveal that *Pistia stratiotes* can scavenge reactive oxygen species and chelate lead ions, thereby mitigating oxidative damage and elevating plant tolerance to lead stress. We have studied various essential factors such as phenylalanine ammonia-lyase gene activity, lipid peroxidation, proline content, and gene expression that play a crucial role in reducing metal stress. This research will help in the development of sustainable strategies for alleviating heavy metal pollution and will further help in preserving aquatic environments. This study will give us an in-depth view of the successful survival of invasive species in ecosystems, their adapting approach, and ecological impacts. Moreover, it provides their ways of management, sustainable growth, and restoration of aquatic life. This study paves the way for biodiversity conservation endeavours to bring balance to both terrestrial and aquatic ecosystems by highlighting the complex interactions between invasive species and their habitat.

Keywords: Secondary Metabolism, *Pistia stratiotes*, Lead, Phenylalanine ammonia-lyase (PAL)

Paper Code: 202509052

Secondary metabolite profiling and genetic expression of *Andrographis paniculata* (Kalmegh)

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ABSTRACT

Andrographis paniculata (Kalmegh) has been used for centuries across the Asian, American, and African continents as traditional medicine for the treatment of various diseases, including diabetes, high blood pressure, ulcers, leprosy, and malaria. All plants, including *A. paniculata*, synthesize various secondary metabolites as part of their secondary metabolism. The Phenylpropanoid pathway is one of the major pathways responsible for catalyzing the synthesis of various secondary metabolites, including polyphenols and flavonoids. In this pathway, PAL (Phenylalanine Ammonia-Lyase), the gateway enzyme, catalyzes the conversion of phenylalanine to trans-cinnamic acid, alongside CHS (Chalcone Synthase), enzyme responsible for the first committed step in flavonoid biosynthesis, and DFR (Dihydroflavonol-4-reductase), catalyzes the reduction of dihydroflavonols to leucoanthocyanidins, are among some of the most important enzymes in the synthesis of the aforementioned secondary metabolites. These secondary metabolites act as defence mechanisms against various biotic and abiotic stresses, ranging from pests and herbivores to salinity and metal-induced stress, as they possess antioxidant, antimicrobial, antiviral, and antifungal properties. These properties enable the therapeutic potential of the plant. This study employs various assays to provide a systematic profiling of the secondary metabolites, alongside exploring the gene expression patterns of key enzymes in the phenylpropanoid pathway utilizing PCR (Polymerase Chain Reaction). Additionally, the gene expressions for Metallothionein, a gene producing cysteine-rich proteins capable of metal detoxification, were also analyzed in controlled settings. The findings of this research provide valuable information regarding the secondary metabolism of *Andrographis paniculata*.

Keywords: Polyphenol, Flavonoid, Phenylpropanoid pathway, Secondary metabolites

Paper Code: 202509052

Regulation of secondary metabolite production in the two members of the Cucurbitaceae family

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ABSTRACT

The two species of the *Cucurbitaceae* family: *Momordica charantia var.* subsp. *charantia* and *Momordica charantia var. muricata* have gained increasing importance over recent years for their impeccable role in human health. Both medicinally important species synthesise natural antioxidants, like Chlorogenic acid. The Hydroxycinnamoyl-CoA:Quinate Transferase (HQT) enzyme helps in the biosynthesis of Chlorogenic acid. Other secondary metabolites are synthesised through essential pathways regulated by various enzymes encoded by respective genes. Analyzing these enzymes under stress conditions can provide insights into plant defence mechanisms. The Phenylpropanoid route is started by Phenylalanine Ammonia Lyase (PAL). Chalcone synthase (CHS) drives the formation of flavonoids. Dihydroflavonol-4-reductase (DFR) converts dihydroflavonols into leucoanthocyanidins. Superoxide Dismutase (SOD) reduces oxidative damage. The synchronous activity of these enzymes contributes to the plant's general health. A comparative analysis was done of different parts of both plants to evaluate which part can have the most beneficial effects on an individual's health upon consumption. The results obtained from the different experiments suggest the antioxidant properties of the aforementioned species, in addition to their well-known antidiabetic properties. Further, we get an insight into the plant parts that are best fit for consumption to benefit from the medicinal properties of this species.

Keywords: Anti-diabetic, antioxidants, HQT gene, *Momordica charantia*

Paper Code: 202509105

Adaptive Responses of *Lantana camara* L. to Heavy Metal Stress: Effect of Chromium Nitrate on Secondary Metabolism

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ABSTRACT

Lantana camara L. is an invasive weed that spreads rapidly owing to its quick growth and easy distribution of seeds. Due to its invasiveness, it has grown to pose a danger to biodiversity by creating dense thickets that change the ecology by outcompeting native plants for the basic resources. Other plants' germination and growth are inhibited by the allelopathic compounds emitted by this weed. Chromium, a common heavy metal contaminant, shows several morphological changes in plants. Interestingly, *Lantana camara* can develop tolerance to chromium over time, making it potentially useful for phytoremediation, the process of cleaning up contaminated soil. In this study, we performed experiments by growing it in soils containing different concentrations of Chromium Nitrate over a varying time to monitor the trend of changes in the secondary metabolite contents of the plant. This content was measured by performing the respective assays to quantify them. The study showed the undoubted potential of the plant to survive even at concentrations as high as 75 µM. Through these defence mechanisms, it has elevated the levels of available plant secondary metabolites. Understanding how this weed responds to metal stress is critical for promoting sustainable agriculture and ensuring food security.

Keywords: - Biodiversity, chromium nitrate, heavy metals, *Lantana camara*

Paper Code: 202509155

Enhancing Crop Resilience through Plant Biotechnology to Address Global Food Security Challenges

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Abstract

The integration of population growth, climate change, environmental degradation, and a decrease in the amount of land available to farm continues to create global challenges to food security. Innovative tools that aid in the development of more climate-resilient crops can be created using biotechnology. This paper focuses on the application of various branches of biotechnology, such as genetic engineering, nanotechnology, and precision biotechnology, to increase the ability of crops to withstand challenges posed by pests and climate. Innovative approaches, such as the production of transgenic crops, CRISPR genome editing, and the use of nanoscale delivery systems, facilitate advancements in the maintenance of stable yields, pest resilience, and nutrient use efficiency. Leveraging recent developments in this field of study, this paper documents the challenges posed to food security and the impact responsive biotechnology can offer in improving the adaptability and sustainability of crops. In addition to this, integrated nanotechnology sensors provide in situ real-time monitoring of crops and the optimization of pesticide, fertilizer, and herbicide application, thus reducing agriculture's impact on the environment. The unregulated application of biotechnology may compound underlying ethical, regulatory, and ecological challenges. Such applications, however, must aim to relieve and effectively respond to global hunger and adverse environmental conditions. Recommendations on the use of biotechnological tools in modern agriculture to help build a resilient and sustainable food-secure future are presented.

Keywords: Plant Biotechnology; Crop Resilience; Genetic Engineering; Nanotechnology; Food Security; Sustainable Agriculture; CRISPR-Cas.

DAY 1

10TH DECEMBER 2025

ORAL SESSION 4

ENVIRONMENTAL BIOTECHNOLOGY

Paper code: 202509118

Valorisation Of Spoiled Darjeeling (Eastern Himalaya Region) Mandarins Through Biotechnological Production of Aroma Compounds

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ABSTRACT

The objective of the present research study was to identify different aroma components obtained from Darjeeling mandarins grown in three different seasons during early, mid and late season. This study also dealt with the valorisation of spoiled mandarin (scientific name) fruits for the extraction of flavor molecules of mandarin oils. The flavor compounds present in the essential oils extracted from fresh and spoiled mandarin fruits were identified based on the mass spectrum obtained in a Gas Chromatography Mass Spectrometer. This analytical process allowed to analyze a wide range of flavor compounds (esters, aldehydes, alcohols, terpenoids). Based on the seasonal variations, there were various types of volatile compounds found in mandarin oils. The essential oil extracted from spoiled mandarin of late season showed the maximum number of aroma components in comparison to early and mid-seasons. Various new compounds were identified in spoiled mandarins, like Linalool oxide, verbenol, camphenol, β-cubebene, α-ylangene, and humulene. *Aspergillus sp. and Penicillium sp*. were isolated from the spoiled mandarins of the late season. The essential oils obtained from these two fungi-infected mandarins of late season exhibited various aroma compounds, including β-cis terpineol, α-terpineol, β-ocimene, terpinolene, trans carveol, γ-elemene, β-copaene,4 carene, α-copaene, limonene oxide, trans sesquisabinene hydrate, 8-hydroxy linalool etc.

***Keywords**:* Bio-flavor, Mandarin oil, GC-MS, Fungi, De Novo synthesis.

Paper code: 202509081

Soil Quality Assessment for Conservation Planning: Insights from PCA-Based SQI

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ABSTRACT

Soil quality assessment ensures soil management in fragile hill ecosystems of Northeast India. This study evaluated soil quality under natural fallow, cultivated, and degraded land uses at two depths (topsoil and subsoil) in Mokokchung District, Nagaland. A comprehensive set of soil physico-chemical and textural properties was analyzed and reduced to a Minimum Data Set (MDS) using Principal Component Analysis. Silt, nitrogen (N), zinc (Zn), and phosphorus (P) were retained as key indicators. Soil Quality Index (SQI) was computed using linear and nonlinear scoring functions, with both additive and weighted models. Results showed that natural fallow topsoil exhibited the highest soil quality, whereas degraded subsoil recorded the lowest. Nonlinear methods displayed greater sensitivity (CV up to 46.36%) compared to linear methods, while weighted indices provided more realistic estimates by emphasizing critical variables. These findings highlight the utility of nonlinear weighted SQI in guiding conservation practices and sustainable land-use planning in shifting cultivation landscapes.

Key words: Soil Quality Index; Minimum Data Set; Principal Component Analysis; Shifting Cultivation.

Paper code: 202509048

Corrosion Response of Twin Roll Cast AZ31 Alloy in Biologically Relevant Environments

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Abstract

This study presents an investigation on the corrosion behaviour of twin roll cast (TRC) AZ31 magnesium alloy in different biologically relevant environments. Magnesium alloys have attracted considerable attention as lightweight biomaterials for biomedical applications due to their biocompatibility and similar density as compared to human cortical bone. However, their practical use is very much limited due to rapid corrosion accompanied by hydrogen gas evolution. This work evaluates the corrosion performance of TRC AZ31 alloy in different biological environments, intended to mimic physiological and pathological variations in-vivo conditions. To quantitatively assess the corrosion kinetics, potentio-dynamic polarization, and long-term immersion tests were performed. The microstructure governs the mechanical properties as well as the degradation rate of TRC AZ31 alloy. Surface analyses revealed that intermetallic particles act as cathodic sites, driving micro-galvanic corrosion and accelerating hydrogen evolution.

Results demonstrated that aggressive environments like 0.9% NaCl solution and Ringer's solution forms an unstable protective film which leads to higher corrosion and higher hydrogen evolution, while complex biofluids like simulated body fluid (SBF) forms a stable and thick protective film, still it does not fully suppress the pitting corrosion. This work highlights the complex interplay between alloy microstructure, environmental change, and corrosion mechanisms. Understanding these factors is critical for tailoring processing methods and surface modification approaches aimed at improving corrosion resistance and hydrogen management, which are essential for expanding the use of magnesium alloys in biomedical applications.

Paper code: 202509127

Ecological characteristics and hydrochemistry of the Bozsuv canal in Tashkent city

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Abstract

Clean and safe water is essential for human health and well-being. However, growing human activities are leading to severe water pollution, deteriorating its quality, particularly in big cities. The water quality directly affects aquatic systems, including rivers, lakes and canals, public health and biodiversity. This study aims to explore the ecological characteristics and hydrochemical changes in the water flow of the Bozsuv canal, which is one of the most vital sources of water to Tashkent, the capital city of Uzbekistan. The research highlights the seasonal variations in key chemical indicators such as Calcium (Ca^{2+}), Magnesium (Mg^{2+}), Nitrite (NO_2^{+}), and total hardness (TH) that impact water quality. By analyzing water samples from incoming and outgoing flows of the Bozsuv canal, the study ehibits significant increases in water hardness and pollutant concentrations from March to August, which subsequently decrease towards the end of the year. The results indicate the need for regular monitoring and effective pollution control measures essential to prevent further deterioration and to ensure the sustainability of water resources.

Paper code: 202509072

Diurnal dynamics of atmospheric microplastic content in the central regions of Uzbekistan

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ABSTRACT

Microplastics (MPs), defined as plastic particles smaller than 5 mm, have emerged as ubiquitous environmental contaminants (Zhang et al., 2020). While their occurrence in aquatic and soil systems has been extensively documented, the atmospheric transport and deposition of MPs remain an evolving research frontier(Shao et al., 2022). Recent advances highlight that atmospheric microplastics can travel long distances and deposit in remote regions, contributing to global plastic pollution cycles (Allen et al., 2019). Uzbekistan, located in Central Asia, represents an underexplored region regarding airborne microplastic pollution. This study aims to fill that gap by assessing the concentration, morphology, and temporal distribution of airborne MPs in Navoi (40°07′13″N, 65°22′40″E) and Bukhara (40°06′14″N, 64°42′17″E).

Atmospheric microplastic sampling was conducted using a Lanzoni VPPS2010 volumetric pollen trap mounted at a height of 25 meters. The device operates by drawing air through a narrow slit, where airborne particles adhere to a sticky tape mounted on a rotating drum. The drum rotates at a constant speed of 2 mm/h, allowing continuous collection over 24 hours. Samples were collected every two hours from 9:00 AM to 9:00 AM the following day, yielding 12 subsamples per site.

Collected tapes were examined under a BioBlue BB‑4253 stereomicroscope equipped with a ToupView USB 2.0 CMOS digital camera and ToupView software (v4.12.29030). Suspected microplastic particles were visually identified based on color, shape, and surface texture. To confirm their synthetic nature, the 'hot needle test' was applied following established methodologies.

Preliminary analysis revealed the presence of multiple microplastic morphotypes, including fibers and fragments. In the samples collected from traps installed in Navoi and Bukhara, 0.42 ± 0.5 and 0.35 ± 0.46 units of microplastic per cubic meter of air, respectively, were detected. Higher MP counts were observed during the morning and early afternoon, followed by a decline toward evening and night hours.

This pattern may be associated with increased human activity and wind turbulence during daytime hours. The concentration peaks correspond to the morning and afternoon periods, reflecting urban activity cycles such as transportation, construction, and surface wind resuspension. The lower night values suggest decreased emission and settling of particles. Bukhara, being more densely populated and located in a semi‑arid steppe with active traffic,

showed higher concentrations than Navoi, which is characterized by a more open landscape and moderate anthropogenic load.

These findings align with recent international studies reporting that microplastic deposition is influenced by local meteorological conditions, urbanization degree, and wind patterns.

The study confirms the presence of atmospheric microplastics in both Navoi and Bukhara regions of Uzbekistan. Temporal variations in MP concentrations over a 24-hour period highlight the importance of continuous monitoring to capture diurnal patterns. These findings contribute to the growing global dataset on airborne microplastic pollution and provide a scientific basis for future environmental management policies in Central Asia.

DAY 1

10TH DECEMBER 2025

ORAL SESSION 5

FOOD BIOTECHNOLOGY

Paper code: 202509024

Efficacy of Black Cumin in Edible Film and Edible Coating Formulation-A Review

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ABSTRACT

Recent advances in edible films and edible coatings have piqued interest for their ability to offer benefits similar to those of their plastic counterparts, which carry a negative perception due to environmental concern. Abundance of volatile oils, fibres, alkaloids, minerals and vitamins in black cumin (*Nigella sativa*) bestows potential antioxidant, antimicrobial and other health promoting activities that not only increases the nutritional profile of foods, but also enhances shelf life. The integration of black cumin (*Nigella sativa*) derivatives—including extract, essential oil, and seed cake—at concentrations ranging from 0.5% to 12% w/w into biopolymer-based edible film and edible coating matrices comprising protein, polysaccharide, chitosan, and pectin has demonstrated significant enhancement in functional attributes, notably antioxidant activity, antimicrobial potency, and optical barrier efficacy. Nonetheless, precise formulation optimization is imperative to counteract potential deleterious impacts on film structural integrity and organoleptic properties. This review delineates the advancement of *Nigella sativa*-based edible films and edible coatings exhibiting bioactive functionalities conducive to human health and food safety, thereby offering a sustainable alternative to conventional harmful plastic-derived packaging systems.

Keywords: Black cumin; edible film; edible coating; antioxidant

Paper code: 202509074

Formulation and Physicochemical Characterization of Fish Skin (*Labeo rohita*) Oil Incorporated Mayonnaise

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Abstarct

The present work is involved in preparing mayonnaise from fish skin oil (FSO) extracted from the skin of *Labeo rohita*. Mayonnaise was prepared with lemon juice, egg yolk, FSO, salt, sugar. The prepared mayonnaise subjected to physicochemical characterization via acid value, peroxide value and free fatty acid content. Its proximate composition was determined and results revealed that it has crude protein content 1.27 ± 0.02 %, total lipid 75.62 ±0.01%, total carbohydrate 9.12 ± 0.03% , moisture content of 13.69 ± 0.03 , ash content 0.30 ± 0.01% and pH of 4.15 ± 0.01. It was also subjected to FT-IR analysis and compared with that of a market product. Sensory evaluation for taste, odour, flavour, colour, appearance was also satisfactory. Prepared mayonnaise was also checked for storage stability for 30 days at room temperature of 30ºC and results revealed that the mayonnaise deteriorated after 12th day of room temperature storage.

Keywords: Fish Skin, Oil, Mayonnaise, Omega 3 Fatty Acids.

Paper code: 202509022

Investigating Thermal Process-Induced Functional Changes in Little Millet: A RSM-based Comparative Insight

Chitrini Das[1], Arunava Sinha[1], Navin Kumar[1], Sudhriti Maity[1], Prapti Dey[1], Debpriya Saha[1], Monika Paul[1], Saikat Mazumder[1*]

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ABSTRACT

Little millet is a nutritious whole-grain and gluten-free cereal. It is also rich in diverse macro and micronutrients such as carbs, protein, fiber, and lipids, and phytochemicals, which promote heart health, facilitate digestion, etc. When millets are processed, they undergo a variety of changes with respect to their functional and biological properties, which can be advantageous regarding convenience in consumption. To address this, this study investigated how microwave and induction heating alter key functionalities of little millet flour. The grains were washed and processed in a microwave and induction (grain-to-water ratio is 1:7) under specified time-temperature conditions, followed by drying (50°C) and milling. The use of microwave (110–170°C; 2–8 min) and induction (120–160°C; 2–8 min) allowed tunable changes of little millet flour functionality: WSI was stable with minor changes at higher temperatures (0.10-0.17), which allowed the maintenance of constant solubility under different conditions. WAC rose gradually with time and temperature (0.04-6.77 g/g microwave; 0.17-7.68 g/g induction), so hydration could be controlled. OAC was examined with mustard and sunflower oil, and it significantly improved, especially in the case of mustard oil for induction conditions (up to 7.82 g/g) and intense uptake over sunflower oil and microwave conditions (up to 2.83 g/g), showing extensive lipid-binding modulation.

Keywords: Little millet, Thermal Processing, Water solubility index (WSI), Water absorption capacity (WAC), Oil absorption capacity (OAC)

Paper code: 202509140

Genetic variability of Bowman Birk Inhibitor relation to total trypsin inhibitor activity in soybean with or without Kunitz trypsin inhibitor

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Abstract

Soybeans are known to contain two major serine protease inhibitors: Bowman-Birk inhibitor (BBI) and Kunitz trypsin inhibitor (KTI). These are considered as anti-nutritional factors in soybean as they interfere with the digestibility of available proteins. BBI though is deeply investigated for decades due to its high therapeutic importance in the prevention of cancers. Soybean genotypes with high BBI are desired by pharmaceutical industries for the purified preparation of this nutraceutical molecule, while genotypes with low BBI and genetically eliminated KTI are desirable in soymeal manufacturing units. This study reveals the 11-fold genetic variation in BBI concentration in 95 soybean genotypes with the help of monoclonal antibodies using indirect immunoassay. With the range of 22.0 mg/g of defatted flour (PS1241)- 2.7 mg/g of defatted flour (VLS47), this study identified 3 very high and 5 very low BBI soybean genotypes. BBI contribution varied to total trypsin inhibitor activity varied from genotype to genotype and between 2 to 53.5% with average value of 11.6%. the effect of growing years on the concentration of BBI in soybean was found insignificant. BBI content in BC3F2 derived KTI-free lines was at par with the recurrent parent. Soybean genotypes with extreme BBI content and diverse genetic background identified in the study may be exploited to develop mapping population to identify genomic regions underlying the expression of BBI in soybean.

ABOUT SPEAKER

Dr. Gaurab Gangopadhyay

Professor, Biological Sciences Bose Institute, Kolkata, India

Dr. Gaurab Gangopadhyay is a Professor in the Department of Biological Sciences (formerly Plant Biology) at Bose Institute, Kolkata — a leading researcher in plant molecular biology, genomics, and proteomics. His research group works on improving plants' resistance to biotic and abiotic stress, with recent achievements including the creation of transgenic pineapple over-expressing the gene AcSERK3 to confer fungal-disease tolerance.

An integrative omics approach for improvement of sesame, an emerging oilseed crop

Abstract

Sesame is an emerging oilseed crop for research. We have been working on it for the last seventeen years. We have developed several improved genotypes of sesame, which have been deposited in the national repository. Today, I'll share with you our efforts in sesame improvement through conventional breeding coupled with state-of-the-art omics research. Among the various omics technologies, Genome sequencing and Genome-Wide Association Studies (GWAS) identify genes (QTLs) linked to desirable traits, such as oil content, yield components, and stress tolerance (including drought and salinity). Transcriptomics has revolutionized crop improvement by analyzing all RNA transcripts to reveal gene expression and identify Differentially Expressed Genes (DEGs), ultimately leading to the development of gene-specific markers. Metabolomics is a promising approach for deciphering various metabolic networks linked to biotic and abiotic stress tolerance in plants. It fosters metabolomics-assisted breeding. Ultimately, Metagenomics revolutionizes crop improvement by analyzing the total DNA from soil/plant microbes, revealing hidden genetic potential for improved nutrient use, stress tolerance, and disease resistance, which leads to eco-friendly biofertilizers/biopesticides, smarter breeding, and sustainable farming practices. I'll try to give a holistic and integrative view of these omics techniques in our sesame improvement programme.

ABOUT SPEAKER

Dr. Sulagna Basu

Scientist G

ICMR - National Institute for Research in Bacterial Infections, India

Dr. Sulagna Basu is a senior scientist (Scientist-G) at ICMR - National Institute for Research in Bacterial Infections (formerly NICED), Kolkata. Her work zeroes in on antimicrobial-resistance among Gram-negative bacilli in neonatal infections — including carbapenem and colistin resistance in pathogens like *Escherichia coli*, *Klebsiella pneumoniae* and *Acinetobacter baumannii* — and on colonization patterns of neonatal gut microbiota. Over the years she has co-authored dozens of peer-reviewed papers (on molecular epidemiology, resistance gene transmission, efflux-pump mediated drug resistance) and led major projects investigating extended-spectrum β-lactamase (ESBL), plasmid-mediated AmpC, carbapenemase genes (e.g. bla_NDM), and resistance dynamics in neonatal sepsis across multiple regions of India (and in global collaborations). In 2025 she co-authored a commentary in a high-impact journal calling attention to the urgent need to mitigate antimicrobial resistance to protect newborn lives.

ABOUT SPEAKER

Dr. Swastika Paul

Co-founder & Chief Scientific Officer at ExSURE, India

Dr. Swastika Paul is Co-founder and Chief Scientific Officer of ExSURE Private Limited — a biotech startup based in Bhubaneswar, India. Under her scientific leadership, ExSURE develops a patented exosome-based drug-delivery platform designed to target cancer cells — including cancer stem cells — with chemotherapy payloads, aiming to minimize collateral damage to healthy tissues and significantly reduce toxicity and relapse risk. Founded in 2021 by Dr. Paul and her co-founder Abhishek Dutta, ExSURE has already completed preclinical studies, launched R&D exosome-isolation reagents, and secured a seed fund from Unicorn India Ventures in 2025 to accelerate non-clinical studies and scale operations. The startup aims to translate academic insights on exosomes into a clinically viable, less-toxic cancer therapy — bridging molecular-level innovation with real-world patient impact.

International Conference on Biotechnology & Biological Sciences

10th to 12th December 2025

Day 2: 11th December 2025

Oral Presentations

DAY 2

11TH DECEMBER 2025

ORAL SESSION 6

MEDICAL BIOTECHNOLOGY

Paper code: 202509037

Phytoconstituents and HSP-70, the cancer biomarker: A molecular docking approach

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ABSTRACT

In Lung Cancer, induction of HSP70 expression may be considered as biomarker for acquiring resistance to radiotherapy. The biomarker-Heat shock protein 70 (HSP70, MW ~70 kDa) is highly conserved protein, over expressed in cancer tumours and present in cell membranes, release into the extracellular space. Hence, efforts are to be made to inactivate this protein. The contemporary research is very hopeful about the time bound detection of the secreted protein using biosensors in placebo and delivering drug molecules instantaneously, of course using microfluidics-based mechanism to deliver drug impregnated enveloped protein nanocages (NPC)s for assenting role. In this context, the small lead molecules like herbal constituents may be considered as safe, cost-effective target-oriented drugs meant for nanoparticle impregnation. This fragment of research work was defined for proposition of relevant drug candidates of plant origin for the affirmative interaction with HSP 70 protein, of course using Nano particles as vehicles, transported by microfluidics. The PDB files of HSP 70 protein, beta Caryophyllene, Citronellal, D Patchoulene, Geraniol, Limonene and Piperine were refined, using appropriate bioinformatics tool, impelled to enter inside the NPCS. Further were subjected to molecular docking study and the degree of interaction was assessed by conventional Hydrogen bond formation. It was evident that, Piperine and Geraniol with formation of H-bonds. However, there was no H- bond formation with other phytoconstituents. It is concluded that there was intermolecular affirmative interaction of Piperine and Geraniol with HSP70, paving a way to implementation of safe drugs for cancer therapy using contemporary techniques.

Keywords: *Phytoconstituents, HSP 70, cancer Biomarker, Nanocarrier, Molecular docking*

Paper code: 202509009

Biofilms and Antimicrobial Resistance: A Hidden Driver in the One Health AMR Crisis

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Abstract

Antimicrobial resistance (AMR) is a grand challenge threatening global health, food systems, and ecosystems. Biofilms—structured microbial communities encased in an extracellular matrix—are a pervasive but underappreciated driver of AMR across the One Health continuum (humans, animals, and the environment). Biofilm physiology elevates antimicrobial tolerance through diffusion barriers, altered microenvironments, stress responses, and persister formation, while promoting the horizontal gene transfer (HGT) of resistance determinants. In clinical care, biofilms complicate device-associated infections, chronic wounds, and respiratory disease. In agri-food systems, they colonize farm environments, food processing equipment, and aquaculture infrastructure. In natural and built environments, biofilms act as reservoirs and reactors for resistance genes and antibiotic residues. This review synthesizes current understanding of biofilm-driven AMR across One Health, highlights advances in detection and control, and outlines policy, surveillance, and research priorities to address this hidden driver.

Keywords: Antimicrobial Resistance; Biofilms; One Health; Extracellular Polymeric Substances; Persisters; Horizontal Gene Transfer; Diagnostics; Therapeutics; Wastewater; Surveillance

Paper Code: 202509076

Whole-Genome Insights into High-Risk *Escherichia coli* Lineages Carrying OXA-48-like Carbapenemases: First Genomic Evidence of OXA-484 in India

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ABSTRACT

Carbapenemase-producing *Escherichia coli* have emerged as a major clinical threat; yet, genomic data on OXA-48-like–producing isolates from India remain extremely limited. This study integrates whole-genome analysis of carbapenem-resistant *E. coli* high-risk clones carrying OXA-48-like carbapenemases, including the first molecular identification of OXA-484-producing *E. coli* in India.

A total of 164 *E. coli* were collected between 2017 and 2023 at the National Repository of Antimicrobial Resistant Bacteria (NRAMRB), ICMR-NIRBI, Kolkata, from the Postgraduate Institute of Medical Education and Research, Chandigarh, a nodal centre of AMRSN. Isolates were predominantly recovered from urine and peripheral blood, followed by pus/exudate, stool, and other clinical specimens. Antibiotic Susceptibility Testing showed high resistance rates to ciprofloxacin, cefuroxime, ceftriaxone, trimethoprim/sulfamethoxazole, and cefepime. Carbapenem resistance (meropenem, ertapenem, imipenem) ranged from 24–26%, with ertapenem showing the highest non-susceptibility. Resistance to colistin was rare. Approximately fifty-three percent of isolates were multidrug-resistant. Carbapenemase production was detected among 27% of *E. coli* by the modified carbapenem inactivation method. Conventional PCR identified *bla*$_{\text{OXA-48-like}}$ genes in *E. coli* and *bla*$_{\text{NDM}}$ in 41. Additional ARGs included *bla*$_{\text{CTX-M}}$, *bla*$_{\text{TEM}}$, *bla*$_{\text{CIT}}$, *bla*$_{\text{DHA}}$, *armA*, *rmtB*, *aac(6')-Ib-cr*, *qnrB*, *qnrS*, and multiple efflux-pump genes.

Ten OXA-48-like–producing isolates underwent whole-genome sequencing on the Ion Torrent S5 platform. WGS revealed different variants of *bla*$_{\text{OXA-48-like}}$ genes. Three *E. coli* carrying only *bla*$_{\text{OXA-181}}$, all belonging to high-risk clone ST410 (CC23, phylogroup C, serotype O8:H9) while seven isolates produced dual carbapenemases (OXA-48-like + NDM-5). Of these seven, four belonged to high-risk clone ST405 (CC405, phylogroup D, serotype O102:H6), harbouring either *bla*$_{\text{OXA-181}}$ or *bla*$_{\text{OXA-232}}$ with *bla*$_{\text{NDM-5}}$. The remaining three belonged to

ST448, ST2099, and ST8346; among these, ST2099 and ST8346 harboured $bla_{\text{OXA-484}}$ with or without $bla_{\text{NDM-5}}$, marking the first detection of OXA-484-producing *E. coli* in India. The remaining isolate carried $bla_{\text{OXA-181}}$ + $bla_{\text{NDM-5}}$.

Plasmid analysis revealed a diverse plasmid replicons including ColKP3, IncFIA, IncFIB, IncX3, IncFII, IncY and Col variants. F-type pMLST profiles were heterogeneous (e.g., F1:A1:B49, F59:A4:B1, F48:A1:B49). All $bla_{\text{OXA-48-like}}$ genes were located on ColKP3 plasmids (4.7–61.1 kb) with a conserved architecture of IS*3000*–ΔIS*Ecp1* upstream and Δ*lysR*–Δ*ere*–Δ*repA* downstream, followed by an IS*Kpn19*–*tnpR*–*qnrS1* module resembling Tn6292. $bla_{\text{NDM-5}}$ was carried on IncFII plasmids or integrated into chromosome, flanked by IS*Aba125* and downstream *bleMBL*–*trpF*–*dsbD*. Conjugation assays showed that $bla_{\text{OXA-48-like}}$ genes were non-transmissible, consistent with localization on non-conjugative ColKP3 plasmids. Electroporation yielded transformants carrying either $bla_{\text{OXA-48-like}}$ or $bla_{\text{NDM-5}}$, but never both, confirming their location on separate plasmids.

To contextualize these isolates globally, a core genome SNP phylogeny was constructed using study isolates and global *E. coli* genomes carrying $bla_{\text{OXA-48-like}}$ from different countries and clinical sources. The isolates showed relatedness to global *E. coli* (104–2668 SNP distances) reported from India, South Korea, Denmark, Spain, United States etc.

This study provides the first genomic evidence of OXA-484-producing *E. coli* in India and highlights the dissemination of high-risk clones carrying OXA-48-like carbapenemases, often co-harbouring NDM-5 and diverse plasmid backgrounds. These findings underscore the urgent need for strengthened genomic surveillance of emerging carbapenemase variants in *E. coli* high-risk clones in India.

Keywords: *E. coli,* High-risk clones, carbapenem resistance, OXA-48-like, NDM, WGS, India

Paper code: 202509129

Exploring Hematological Biomarkers through Data Mining for Multi-Disease Prediction

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ABSTRACT

Blood is a complex mixture of Plasma, Red Blood Cell (RBC), White Blood Cell (WBC) and Platelets. The different blood component indices have different intra- and inter-relations, which renders them non-specific indicators for early illness prediction. The study's goal is to forecast complicated diseases by modeling the diverse properties of blood components. The Complete Blood Test (CBC) data from 364 patients is gathered and analyzed in this study. The dataset underwent feature engineering and data pre-processing in order to identify outliers. Lastly, in order to create a statistical model utilizing machine learning for the early detection of cancer and autoimmune diseases, this work aims to correlate the diverse correlations between platelets and WBC and RBC indices. In order to improve the model's accuracy and significance level, multicollinearity is also detected and eliminated from the effect variables. Using Total Leukocyte Count (TLC) as a single biomarker, the study discovered that around 3.7% of male patients (average age: 65) and 3.5% of female patients (average age: 41.5 years) had significant abnormalities and cancerous potential that required immediate medical intervention. Red Cell Distribution Width (RDW) and hemoglobin (HGB) are adversely correlated with TLC when it comes to illness screening, however packed cell volume (PCV) and platelet PLT are positively correlated. The authors expect that more thorough study will be conducted in the future to fully explore the potential of liquid biomarkers for illness prediction, clinical validation, and adoption.

Paper Code: 202509153

The Silent Epidemic: Chronic Arsenic Exposure and Carcinogenesis in the Gangetic Delta

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Abstract

Chronic arsenic contamination of groundwater in the Gangetic Delta—spanning West Bengal, India, and Bangladesh—remains one of South Asia's most persistent environmental health crises. This case-study–driven research synthesizes clinical, and molecular evidence to examine the relationship between arsenic exposure and carcinogenic outcomes in highly affected communities in West Bengal. Geological investigations indicate that arsenic present in Holocene sediments is mobilized into shallow aquifers through natural geochemical processes characteristic of the Bengal Delta Plain, a finding consistently documented across multiple field studies. Case analyses from contaminated districts of West Bengal reveal long-term consumption of arsenic-laden groundwater as a major driver of dermatological, systemic, and oncological disorders, with particularly high incidence rates of skin and oral cancers.

Classified as a Group 1 human carcinogen, inorganic arsenic exerts its pathogenicity through multi-pathway mechanisms. Case-specific molecular profiling demonstrates that chronic exposure induces oxidative stress, generation of reactive oxygen species, genomic instability, and suppression of DNA repair pathways. Furthermore, field-based dermatological and clinical assessments report elevated rates of hyperkeratosis, basal cell carcinoma, squamous cell carcinoma, and oral precancerous lesions across the region.

This study highlights substantial heterogeneity in exposure levels, biomarker reliability, and dose-response relationships, underscoring critical gaps in early detection and risk assessment. The findings emphasize the urgency of strengthening epidemiological surveillance, validating molecular biomarkers for exposure and early carcinogenesis, and expanding community-level risk analysis frameworks. These integrated approaches are essential for reducing long-term carcinogenic outcomes and informing effective mitigation strategies for arsenic-affected populations in the Gangetic Delta of West Bengal.

Key words: Arsenic exposure, carcinogenesis, Gangetic Delta, ground water

Paper Code: 202509158

Advances in Stem Cell and Regenerative Medicine for Overcoming Barriers in Tissue Repair and Organ Regeneration

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Abstract

Research in stem cell therapy has become one of the fastest-growing branches of regenerative medicine, overcoming barriers in the fields of tissue repair and organ regeneration. Mesenchymal stem cells, embryonic stem cells, and induced pluripotent stem cells can differentiate into different types of cells, facilitating repair of damaged tissue and degeneration. Until recently, the advancement of stem cell therapy in the clinic has been slow because of cell viability, cell differentiation, and immunorejection. The first step to solving these problems in the clinic has been the integration of tissue engineering, in which stem cells and cell scaffolding biomaterials are integrated to augment the stem cell therapy. Improving biomaterials and adding growth stimulators and genetic modifications are ways to augment stem cell therapy. Recent studies have shown that integration of advanced biomaterials and stem cells in conjunction with gene therapy and 3D bioprinting can stimulate tissue regeneration and improve phase 2 tissue repair. The use of stem cell-specific growth factors and targeted therapy with stem cell regenerating therapy augmented with nanoparticles opens new avenues to augment regeneration therapy. Following a review of development updates on stem cell-based therapies, I detail their use in bone and cartilage regeneration, cardiovascular repair, neurodegenerative disorders, and organ transplantation. The integration of stem cells and tissue engineering brings the first real promise of overcoming the challenges of devastating disease and injury. It is the new frontier in regenerative medicine.

Keywords: Stem cells, tissue regeneration, regenerative medicine, stem cell therapy, biomaterials, organ regeneration, mesenchymal stem cells.

Paper Code: 202509160

A REVIEW OF PHARMACOGENETIC STUDIES CONCERNING GENETICS AND TREATMENT RESPONSE IN PARKINSON'S DISEASE

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Abstract

Parkinson’s disease (PD) is a neurodegenerative disorder that progressively deteriorates the nervous system. Its causes are multifaceted, involving environmental influences, genetic predispositions, and epigenetic modifications. The main and inciting symptoms of PD are a combination of motor (bradykinesia, rest tremor and rigidity) and non-motor (hallucinations, compulsive behaviours and sleep disorders) symptoms. Current therapies primarily involve a combination of drugs aimed at managing the symptoms of the disease by replacing the depleted dopamine without underlining the cause of the disease. Although beneficial, these therapies display a concerning amount of heterogeneity in drug response. Pharmacogenetics, a part of pharmacogenomics, helps to highlight the genetic factors that contribute to such heterogeneity in drug response. In the treatment of patients with PD, pharmacogenetic studies are particularly important given the variability of results, primarily concerning levodopa and dopaminergic therapies. This review covers the genetic mutation related to PD genes such as LRRK2, SNCA, and PARK2, which will be taken into account concerning their effects on disease progression and drug response. Genetic polymorphisms can significantly modulate the efficacy and adverse effects of drugs in patients with PD, influencing drug metabolism, transport, and receptor binding, among others, and involve genes such as CYP2D6 and COMT. This would be achieved through the application of pharmacogenetic insights that allow for tailored therapy approaches, optimize dosages, reduce adverse effects, and ensure better patient outcomes. Personalized medicine in PD could potentially enable improvement in treatment strategies based on an individual genetic profile and thereby enhance management for this complex disease.

Keywords: Pharmacogenetics, Parkinson's Disease, Genetic Variability, Drug Response, Neurodegenerative Disorders, Personalized Medicine.

DAY 2

11TH DECEMBER 2025

ORAL SESSION 7

MICROBIAL BIOTECHNOLOGY

Paper code: 202509056

Isolation, characterization and application of chlorpyrifos resistant bacteria from tropical agricultural soil

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Abstract

Pesticides have played a pivotal role in shaping India's agricultural landscape. In India, 51.4% insecticides are being used among the pesticides, especially organophosphate such as chlorpyrifos (CPF), parathion, monocrotophos etc., due to its broad range of insect targets. The environmental persistence of CPF raises serious ecological and health concerns due to its bioaccumulation potential and toxicity to non-target organisms. This study focuses on the isolation, identification, screening and characterization of CPF-degrading bacterial strains from agricultural soils with prolonged pesticide exposure. Soil samples were collected from the contaminated sites and CPF residue and its metabolites were analyzed using GC-MS. 19 CPF resistant bacteria were isolated from the contaminated soil using mineral salt media, capable of utilizing CPF as a sole carbon source at 50 mg L^{-1} concentration. All the isolates were screened out for tolerance potential against CPF ranging 0-2000 mg L^{-1}. From the results it has been observed that out of nineteen, only five bacterial isolates i.e. IS-2, IS-5, IS-9, IS-12, IS-19 have a tolerance level up to 2000 mgL^{-1}. On the basis of 16S rRNA gene sequencing, these isolates were identified as *Staphylococcus hominis* BHUA2402, *Myroides profundi* BHUA2405, *Burkholderia cepacia* BHUA2409, *Pseudomonas plecoglossicida* BHUA2412, *Burkholderia* sp BHUA2419. respectively. These bacterial strains showed catalase activity, IAA production, multi-pesticide tolerance, HCN production. A consortium of above bacteria has shown significant increase in growth attributes of *Spinacia oleracea* L. (palak) plants exposed to pesticide contaminated soil. These findings offer promising implications for bioremediation strategies in pesticide-contaminated areas emphasizing ecological restoration and sustainable agricultural practices.

Keywords: Chlorpyrifos Metabolites, Bacterial strains, Bioremediation, Tropical agriculture

Paper code: 202509149

Biotechnological Work Exploring the Antibacterial Activity of Plant Extracts Against Human Pathogenic Foodborne Bacteria

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Abstract

Traditional medicine encompasses a wide range of knowledge, skills, and practices based on the theories, beliefs, and experiences of diverse cultures. Traditional medicinal plants have been an essential part of the health care systems of many societies around the world, with a history spanning more than 4,000 years. The cuurent study was carried out to investigate extracts of *Artemisia vulgaris*, *Nigella sativa, Origanum majorana, Moringa oleifera, Tetragonolobus purpureus, Camellia sinensis, Dolomiaea costus, Urtica dioica, and Ephedra viridis* for their potential activity against human bacterial pathogens using agar diffusion method (ADM). Also, both Minimal Inhibitory Concentration (MIC) and Broth Microdilution (BMD) assays were used to determine the MIC50 of the samples. Phytochemical analysis of the test samples was also performed to determine their natural antibacterial content. The activity of plant extracts was evaluated against four bacterial pathogens namely *Staphylococcus aureus*, *Bacillus subtilis*, *Proteus vulgaris*, and *Escherichia coli*.

The largest zones of bacterial inhibition of ADM were obtained from *U. dioica* seeds, over both *B. subtilis* and *S. aureus*, whose width reached 23.83 mm and 17.83 mm, respectively. In addition, *N. sativa* was second in its ability to inhibit the same bacterial species compared to the other species, while *M. oleifera* caused obvious growth inhibition of *B. subtilis*. *C. sinensis* showed moderate activity against *E. coli* and *S. aureus* and *P. vulgaris*.

Furthermore, the results of BMD test showed that *U. dioica* and *M. oleifera* and *N. sativa* and *C. sinensis* were effective against the tested bacteria, as the MIC50 values calculated on the basis of standard curves ranged from 14.15-271.44 mg/ml against the tested bacterial species.

Chemical analysis showed that the tested plants contained a large and variable amount of antibacterial agents.; *U. dioica* contains large amounts of glycosides, while *M. oleifera* contains a high percentage of saponins. Regarding *C. sinensis*, it had a high content of phenols, tannins and flavonoids. This difference in the antibacterial content of these plants is what explains their strong and different ability to inhibit bacterial growth.

Key words: Foodborne bacteria, herbal medicine, pathogenic bacteria, plant saps, Palestine

Paper code: 202509006

Identification of pancreatic lipase inhibiting endophytic secondary metabolites of *Aspergillus fischeri VO1R*

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Abstract

Obesity is considered to be a global problem that can contribute to the development of various diseases such as dyslipidemia, metabolic syndrome, hypertension, and an increased risk of cardiovascular mortality. WHO has identified obesity as one of the leading health problems of the 21st century; with more than 1 billion adult world population overweight, at least 300 million of them are obese. A wide range of therapeutic strategies have been proposed to prevent and treat obesity, including pharmacotherapy, diet therapy, surgery, and behavioral therapy. One of the practical therapeutic approaches to the prevention of obesity is to slow down the absorption of fatty acids by inhibiting pancreatic lipase, the primary digestive enzyme that catalyzes the hydrolysis of ester bonds of tri- and diglycerides to monoglycerides and free fatty acids. The escalating prevalence of obesity necessitates the exploration of novel therapeutic avenues. This study presents a unique approach by presenting data on the extraction and identification of inhibitory secondary metabolites from the total ethyl acetate extract of the endophyte *Aspergillus fischeriVO1R* from the root of the plant *Viola odorata*. These metabolites demonstrate a potent ability to suppress the activity of pancreatic lipase by 91.5%. Notably, the highest inhibitory activity, amounting to 84.9%, is concentrated in butanol fractions. Further separation of the butanol fraction of *A.fischeri VO1R* by thin-layer chromatography reveals the most active fraction B-2 with Rf 0.75, exhibiting an inhibitory activity of 57.2%. HPLC-MS methods confirm that the inhibitory fraction of B-2 consists of polyphenols identified as cinnamic acid, lariciresinol-sesquilignan, and hydroxyphloretin 2'-O-xylosyl-glucoside.

Paper Code: 202509151

Exploring the Antibiofilm Potential of Green Synthesized Zinc Oxide Quantum Dots (ZnO QD) From *Chenopodium album* against *Pseudomonas aeruginosa* and *Staphylococcus aureus Biofilm*

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ABSTRACT

Developing novel and eco-friendly antimicrobial drugs is imperative due to the increasing problem of biofilm-associated illnesses in healthcare environments. This study investigated the antibiofilm properties of green-synthesized zinc oxide quantum dots (ZnO QDs) made from the plant *Chenopodium album* against recalcitrant biofilms formed by *Pseudomonas aeruginosa* and *Staphylococcus aureus* biofilms. The synthesized ZnO QD's crystalline structure and nanoscale size, which are essential to their antibacterial activity, were characterized by UV-Vis and FTIR spectroscopy. This was further supported with X ray diffraction studies and Scanning electron microscopic images with a size of approximately 22 nm. The results showed that the ZnO QDs successfully prevented both bacterial species from forming biofilms. The antimicrobial efficacy was first established, showing that the ZnO QDs exhibited potent activity against both bacteria, with a Minimum Inhibitory Concentration (MIC) of 26µg/mL for *P. aeruginosa* and 15µg/mL for *S. aureus*. Critically, the QDs demonstrated significant antibiofilm activity. At the tested concentrations, the ZnO QDs achieved a maximum inhibition of 87.21±0.72% in *P. aeruginosa* biofilm formation and a 92.36±0.12% % reduction in *S. aureus* biofilm mass.

Additional ZnO QDs have demonstrated possible anticancer effects as studied against A375 and V79 cells. Furthermore, these QDs minimal hemolytic activity highlights their potential for biological uses, and they are non-toxic to fish and mung beans confirming their safety.

These findings confirm that the green-synthesized ZnO QDs from *C. album* are highly effective against two key clinical pathogens and offer a sustainable, non-toxic alternative for combating biofilm-related infections. The results strongly support the potential of these biogenic nanoparticles for future development as topical antimicrobials or as coatings for medical devices.

Keywords: ZnO Quantum Dots, Antibiofilm Activity

Paper Code: 202509156

Revolutionizing Drug Design with Bioinformatics and AI to Combat Multi-Drug-Resistant Pathogens

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Abstract

The emergence of drug-resistant pathogens, particularly multidrug-resistant (MDR) bacteria, continues to evolve rapidly and remains a global health threat. Because of their lengthy timeframes and exorbitant development costs, traditional methods of drug discovery have not worked. The application of bioinformatics and artificial intelligence (AI) to drug design could change that. AIs, especially machine learning (ML) and deep learning (DL) techniques, can sift through enormous databases to uncover new drug targets, predict and assess molecular interactions, and refine leads. Leveraging bioinformatics with AIs offers an opportunity to fast-track MDR pathogen drug candidate discovery. Recently, AI's capacity to improve various drug discovery processes, notably target discovery, molecular docking, and drug efficacy and toxicity testing, has been documented. This paper describes advancements in computational tools for drug design in bioinformatics to illustrate AI's value. In addition, the paper assesses the time and cost of drug development and the challenges of data, algorithm training, and ethics in clinical trials. The integration of artificial intelligence with bioinformatics will most likely expedite the discovery of novel therapeutic agents. This combination will provide a strong response to the worldwide challenges posed by MDR pathogens. Keywords: Multi-drug-resistant pathogens, Artificial intelligence in drug discovery, Bioinformatics, Machine learning in drug design, Drug-resistant bacteria, Deep learning algorithms, Drug target identification

Paper Code: 202509157

Tackling Antimicrobial Resistance through Biofilm Disruption and Advanced Biotechnological Approaches

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Abstract

AMR, or Antimicrobial Resistance, has become a worrying global health concern, making infections harder to treat and increasing global morbidity and mortality. Bacteria become chronic and hard to treat infections due to biofilm formation, one of the top mechanisms used to resist antibiotics. This paper reviews attempts to newly incorporate biotechnologies in the attempts to break biofilm formations and attempt to combat Antimicrobial Resistance. Bioactive compounds synthesizing actinobacteria from the marine environment and bioactive compounds synthesizing Streptomyces species that inhibit biofilm formation can be a target for new antimicrobial agents. Current research highlights the effective targeting of biofilm-associated pathogens using nanoparticle technology, bacteriophage therapy, and CRISPR genetic editing. The combination of these advanced technologies with precision medicine and rapid diagnostics in underserved countries holds promise for treatment customization. The paper addresses overcoming AMR in a multi-tiered strategy with the use of immunotherapy, bacteriophages, and surface modification. Novel antibiofilm agents and other new innovations in therapy are vital for tackling the urgent problem of biofilms and pathogens that are resistant to drugs. Finally, the paper underscores the significance of translational research and international collaboration to transfer such innovations from the laboratory to the battlefield, in an effort to alleviate the global threat posed by AMR. Keywords: Antimicrobial resistance (AMR), Biofilm inhibition, Marine actinobacteria, Bacteriophage therapy, CRISPR-Cas gene editing, Nanotechnology, Immunotherapy

DAY 2

11TH DECEMBER 2025

ORAL SESSION 8

ENVIRONMENTAL BIOTECHNOLOGY II

Paper Code: 202509140

GIS-based evaluation of groundwater table, groundwater mineralization, and soil salinity in Khovos District, Syrdarya province, Uzbekistan

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Abstract

Unsustainable agricultural practices drive spatial patterns of shallow groundwater table, mineralization and soil salinization, thereby creating constrains for sustainable farming in arid and semiarid regions. In this study, the shallow groundwater table, groundwater mineralization, and soil salinization in irrigated lands of Khovos district, Syrdarya province, Uzbekistan were analysed based on a five-year field data, and mapped using Inverse Distance Weighting (IDW) interpolation method in GIS software. The study results reveal that the groundwater table has slightly declined in the last two years, with depths recorded at 2–3 m (33,699 ha) and 3–5 m (22,260 ha). However, it has also become evident that the mineralization of groundwater has increased corresponding to the declining groundwater table, with 98% irrigated land within the district being highly mineralized (3 g/l) and very highly mineralized (4–5 g/l). In terms of soil salinity, slightly saline lands were dominant over the study period, which accounted for 73.1% of the area, while moderately salinized soils occupied only a small part (26.9%). The results indicate that the reclamation status of irrigated lands in Khovos District is unsatisfactory, which could be worsened in the near upcoming years. The outcomes obtained from this study will allow the governing bodies and responsible organizations to understand the spatiotemporal patterns of the shallow groundwater table and mineralization, and soil salinity in Khovos district and provide vital information for effective land management and salt-leaching practices in Uzbekistan.

Paper Code: 202509057

Design and Evaluation of Quercetin-Integrated PVA/HEC Nanofibers for Bioactive Wound Healing Application

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ABSTRACT

Electrospun nanofibrous scaffolds are widely recognized for their structural similarity to the native extracellular matrix and their suitability for wound healing applications. In this study, quercetin-integrated poly(vinyl alcohol)/hydroxyethyl cellulose (PVA/HEC) nanofibers were successfully fabricated via electrospinning to develop a bioactive wound dressing system. The optimized PVA/HEC blend enabled uniform fiber formation and stable quercetin incorporated fibrous mat. Physicochemical characterizations using FTIR, XRD, TGA and HRSEM confirmed the homogeneous distribution of quercetin within the polymeric matrix and the preservation of nanofibrous morphology. The quercetin-loaded nanofibers demonstrated notable antioxidant and antibacterial activities, indicating their capacity to modulate oxidative stress and inhibit microbial proliferation at wound sites. In vitro drug release studies revealed a sustained and controlled release profile of quercetin over time. Biocompatibility evaluation, complemented by fluorescence-based wound scratch assay, showed enhanced fibroblast cell migration and proliferation, confirming the scaffold's ability to accelerate wound closure. These results collectively suggest that quercetin-integrated PVA/HEC nanofibers hold strong potential as a next-generation bioactive scaffold for efficient wound healing applications.

Paper Code: 202509152

Preliminary investigation on the occurrence and associated risks of Microplastics, Polyaromatic Hydrocarbons in the Ansupa Wetland: A Ramsar site in Odisha, India

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Abstract

Microplastics (MPs) and polycyclic aromatic hydrocarbons (PAHs) pollution together pose significantly higher ecological and health risks in freshwater ecosystems than either pollutant alone. However, studies on distribution and associated risks of MPs and PAHs pollution in relation to hydrological parameters are limited. The present study investigates the occurrence, spatial distribution, interrelationship of MPs, PAHs, and hydrological parameters, and their ecological risks in Ansupa Lake. Surface water samples were collected from 8 different locations and analysed using standardized physico-chemical, spectroscopic, microscopic, and chromatographic methods. The average abundance of MPs and PAHs were found to be 15.5±17.3 mg/L and 0.13±0.16 mg/L respectively. MPs were extracted, and characterize using microscope and Fourier-Transformed Infrared Spectroscopy (FTIR) whereas PAHs were characterized in High Performance Liquid Chromatography (HPLC). The results revealed 10 different polymers such as Polyurethane (PU), Polyethylene terephthalate (PET), Polyvinyl chloride (PVC), Polystyrene (PS), Polypropylene (PP), Acrylonitrile butadiene styrene (ABS), High density polyethylene (HDPE), Low density polyethylene (LDPE), Polyethylene (PE), and Polyamide (PA) with highest occurrence of PET, PE, HDPE, and LDPE (100%) followed by PVC, PS, and ABS (87.5%). Twelve different types of PAHs were found among which benzo [b] fluoranthene (87.5%) showed highest % occurrence. Low molecular weight (LMW) PAHs consisting of 3-ring PAHs was observed in high concentration than high molecular weight (HMW) PAHs. Source diagnostic ratio showed both petrogenic and pyrolytic origin of PAHs with pre-dominance of petrogenic PAHs. The principal component analysis (PCA) was carried out and results shown strong correlation between MPs with transparency, dissolved oxygen (DO), alkalinity, conductivity, and total dissolved solid (TDS), and PAHs with air temperature, whereas no significant relation was observed in between MPs and PAHs. The pollution load index (PLI), and polymer hazard index (PHI) of MPs ranged between 1-4.35 and 25- 437587.5 respectively, depicting low level of PLI with presence of high-extremely hazardous polymer types. Whereas, the ecological risk assessment (ERA) of PAHs was found to be at high risks.

Keywords: MPs, PAHs, FTIR, HPLC, PLI, PHI, PCA, ERA

Paper Code: 202509114

Detoxification of soil cadmium- analysing the potential of LDH as an adsorbent

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Abstract

One of the key environmental issues is heavy metal contamination where by cadmium (Cd) is one of the toxic and long-lasting pollutants of industrial effluents and soil. Cadmium was chosen to research on because it is highly mobile, bio-accumulative and has a very serious effect on human health and the ecosystem even at low levels. Layered Double Hydroxide (LDH) synthesized by co-precipitation method acts as an adsorbent for metal ions. In the present research the possibility of LDH and LDH/Biochar (LDH/BC) composite have been used in cadmium detoxification. The changes in the soil physical and chemical characteristics were analysed with Cd dosed soil, LDH and LDH-biochar remediated soils and changes in the proliferation of soil microbes was also analysed. It has been found that LDH-biochar based materials is a promising adsorbent even better than LDH itself and can be used in the removal of heavy metals and soil purificationin a sustainable manner.

Keywords- Ion adsorption, soil decontamination, heavy-metal toxicity, microbial consortium, soil parameters

Paper Code: 202509007

Biochar-Treated Rice Effluent: A Sustainable Strategy for Enhanced Reusability as Potable Water

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Abstract

Rice mill wastewater contains a high concentration of organic and other pollutants put threat to agriculture if released without treatment. This research investigates the utilization of rice husk biochar as a sustainable material for treating and enhancing the quality and potential reuse of rice mill effluent. This work assesses crucial factors, including the decrease in lignin and phenolic compounds, alterations in physicochemical properties, and the effects of treatment on microbial communities. The application of biochar facilitated the adsorption-based pollutant removal, resulting in an overall enhancement of water quality. The results indicate that biochar-assisted treatment can serve as an effective and environment friendly method for managing rice mill wastewater, allowing for its safe reuse as potable water and contribution towards sustainability.

Keywords: Biochar, Rice mill wastewater, Lignin removal, Phenol reduction, Microbial community, Sustainability, Reusability.

Paper Code: 202509132

Conversion of grey water to potable water using LDH-Biochar composite

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Abstract

The global freshwater crisis is exacerbated by the over-exploitation and pollution of limited resources. A significant portion of domestic wastewater is greywater, which is generated from activities like bathing and laundry and constitutes up to 70% of household water consumption. Unlike black water, greywater has a lower organic and nutrient load, making it a prime candidate for recycling. This study investigates a novel method for converting grey water into potable water using a LDH-Biochar composite. The composite aims to leverage the synergistic adsorption properties of Layered Double Hydroxides (LDH) and the high surface area and filtration capabilities of Biochar to effectively remove contaminants. The research evaluates the efficiency of this composite in purifying greywater to meet drinking water standards, presenting a sustainable and innovative solution to alleviate water scarcity by enabling safe water reuse.

Paper code: 202509159

Nanobiotechnology for Sustainable Environmental Bioremediation and Industrial Waste Cleanup Solutions

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Abstract

Escalating urban development and industrial growth have tremendously increased the environmental impacts and the uncontrolled introduction of dangerous pollutants into the air, soil, and water bodies. Pollution, especially with respect to organic dyes, heavy metals, and various carcinogenic industrial extracts, is harmful to ecosystems and human health. The old school, and often useless, approaches of chemical and physical processes, and other classic waste treatments, remain energy-deficient and unable to exhaust toxic waste. The combination of bioremediation and nanotechnology promises to efficiently replace traditional pollutant mitigation techniques due to the high surface area, reactivity, and selective degradation characteristics of nanoparticles. This study analyzes the various nanomaterials used in the bioremediation of industrial effluents, including carbon nanotubes, metal oxide nanoparticles, and quantum dots. We assess the use of various nanomaterials and their effectiveness in the removal of heavy metals and organic pollutants, and the impact and toxicity limitations encountered. The conclusion of the study is to shift focus to the considerably rapid and efficient wastewater treatment processes provided by nanobioremediation. Enhanced effectiveness, in the order of multiple magnitudes, emphasizes the importance of this approach. The review underscores the importance of refining bioremediation processes with added designed nanoparticles to form a bridge with the treatment of industrial wastewater.

Keywords: Nanobioremediation, Industrial wastewater treatment, Nanomaterials, Environmental cleanup, Heavy metals, Organic pollutants, Sustainable technologies

DAY 2

11TH DECEMBER 2025

ORAL SESSION 9

CONCEPTS OF LAW AND MANAGEMENT IN BIOTECHNOLOGY

Paper Code: 202509001

Assisted Reproductive Technology and Hindu Succession: Reconciling Biotechnology with Lineage Law

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Abstract

This paper delves into the intricacies of modern biological advancements in the field of artificial womb technology (ART) and the Hindu Succession laws in India. ART pose serious biological and legal challenges to the current Hindu law of succession. Due to the absence of explicit statutory provisions, key issues such as legitimacy, inheritance rights, and the legal recognition of heirs conceived through ART remain unresolved.

Biologically, ART methods—including in vitro fertilization and surrogacy—enable conception beyond traditional reproductive boundaries. These developments raise critical questions about parentage, lineage, and the determination of rightful heirs, particularly in cases involving third-party donors or posthumous reproduction.

Legally, the Hindu Succession Act of 1956 does not sufficiently address the status or inheritance rights of children born through ART. Hindu succession law traditionally prioritizes legitimacy and proven lineage for inheritance and coparcenary rights. However, these requirements do not adequately reflect the complexities created by reproductive biotechnology in light of recent developments like ART. Although courts have begun to recognize preserved genetic material as inheritable and have considered posthumous reproduction in specific cases, significant ambiguity persists regarding whether children conceived after a biological parent's death qualify as legal heirs and how cloned individuals might be treated under inheritance law.

Such a situation calls for a regulated means of Assisted Reproductive Techniques (ARTs), and a blanket ban should be deemed unfeasible considering the immense benefits of ART. Therefore, this paper deals with the impact of reproductive human clones on Family and Succession laws and discusses the measures to resolve the various intricacies involved thereof.

Paper Code: 202509025

Possibilities of assessing cluster potential in regions & Increasing the ecological efficiency of training in higher education

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Abstract

This article examines the necessity of cluster formation, the implementation of cluster policies, the opportunities and key advantages they offer, and the importance of assessing cluster potential. It outlines directions and essential aspects of evaluating cluster potential in different regions. Moreover, it substantiates that, taking into account the specific conditions of various regions in our country, clustering can be carried out based on defined ranges of assessment levels. Based on the conclusions drawn, proposals and recommendations for effectively evaluating regional cluster potential have been developed.

Key words. Region, cluster, potential, cluster potential, range, assessment.

Paper Code: 202509146

Assessing and detecting spatiotemporal land use/cover changes in Uzbekistan using sentinel-2 imageries

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Abstract.

Understanding Land use and Land cover (LULC) change is important in environmental modification and natural resource management. This study analyzed the dynamic changes of LULC in the Syrdarya province of Uzbekistan from 2017 to 2024 by applying AI-based classification Sentinel-2 data. The results of the study indicate that certain LULC categories have experienced shifts in extent. While the built-up areas expanded from 40,082 ha to 47,670 ha and the water bodies increased from 13,785 ga to 16,912 ha between 2017 and 2024, other LULC types such as bare land exhibited a substantial decrease from 1,136 ha to 305 ha with the cropland and rangeland experiencing moderate decline to fluctuations. Also, a correlation analysis was performed to better understand the interrelationship between these LULC categories. The flooded vegetation and water bodies ($R = 0.62$), built-up areas and water bodies ($R = 0.69$), bare land and cropland ($R = 0.56$) showed a strong positive relationship. However, the strong negative correlations between cropland and water bodies ($R = -0.60$), built-up areas and cropland ($R = -0.58$), bare land and water bodies ($R = -0.84$), bare land and built-up areas ($R = -0.85$), and rangeland and cropland ($R = -0.88$) were detected. As one of the primary driving factors of the LULC types, the province's population has been considered. The most positive correlation ($R=-0.96$) was found between population and built-up areas.

DAY 2

11TH DECEMBER 2025

POSTER SESSION 1: MEDICAL BIOTECHNOLOGY

Poster code: Biospec/PO-01

Antimicrobial Resistance in Food Systems in the Post-COVID-19 Era: Emerging Challenges and Mitigation Strategies

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ABSTRACT

Antimicrobial resistance (AMR) is increasingly recognized as one of the most pressing global public health challenges with significant implications for food safety and security. The COVID-19 pandemic has not only strained healthcare systems worldwide but has also contributed indirectly to the acceleration of AMR due to the extensive and indiscriminate use of repurposed drugs. During the pandemic, a variety of antimicrobials, including ivermectin (IVM), hydroxychloroquine (HCQ), doxycycline (DO), ceftriaxone (CTR), azithromycin (AZM), and cefixime (CFM), have been widely administered for prophylaxis and treatment despite limited evidence of efficacy. The downstream effects of such usage on the food chain remain poorly understood, especially in developing countries, where veterinary and agricultural antibiotic stewardship is often limited. In this study, we investigated the occurrence and implications of AMR linked to these COVID-19–associated drugs in selected food matrices, including fish, chicken, and milk. The microbial isolates obtained from these samples were screened for resistance, and their minimum inhibitory concentrations (MICs) and inhibition percentages were determined. The results revealed a concerning level of resistance to multiple classes of the tested drugs, suggesting that the residues and environmental dissemination of these antimicrobials may have imposed selective pressure on foodborne microbial communities. The persistence of resistant bacteria in food systems increases the risk of the transmission of resistance genes to human pathogens, thereby aggravating the public health burden. These findings underscore the urgent need for integrated surveillance frameworks to monitor antimicrobial residues and resistance patterns in food systems in the post-COVID-19 era. Stronger regulatory oversight on veterinary and agricultural antimicrobial usage, coupled with awareness initiatives and the adoption of one health-based strategy, is critical to mitigate the spread of AMR. This study highlights emerging challenges and provides a framework for developing mitigation strategies that ensure food safety and public health protection in the wake of the pandemic.

Poster code: Biospec/PO-05

Co-Production of KPC-2 with NDM-1,5 or OXA-232 in *Klebsiella pneumoniae* ST1741 and ST2534: Emerging Threat in a Neonatal Care Setting

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Background- *Klebsiella pneumoniae* carbapenemase (KPC), a class A serine β-lactamase, hydrolyzes a broad range of β-lactams, including carbapenems. KPC-producing *K. pneumoniae* is endemic in many regions with frequent reports of hospital outbreaks. The plasmid- and transposon-mediated spread of *bla*KPC-2 has accelerated its global dissemination. Co-occurrence with other carbapenemase genes, such as *bla*NDM and *bla*OXA-48-like has led to emergence of dual carbapenemase producers, significantly restricting treatment options-especially in high-risk populations like neonates. This study investigates the prevalence, co-occurrence, and transmissibility of carbapenemase genes in KPC-producing *K. pneumoniae* isolated from neonatal bloodstream infections over a six-year period.

Methods- Blood isolates from septicemic neonates (2019–2024) were identified and tested for antimicrobial susceptibility using the VITEK 2 Compact system. PCR was used to detect carbapenemase genes (*bla*NDM, *bla*KPC, *bla*OXA-48-like) along with additional resistance and virulence-associated genes. KPC-producing strains underwent molecular typing and whole-genome sequencing. Conjugation assays were performed to assess gene transmissibility.

Results- Over the course of the study, six *K. pneumoniae* isolates carrying the *bla*KPC-2 gene was recovered from neonatal bloodstream infections. These isolates demonstrated extensive resistance to multiple antimicrobial agents, with retained susceptibility only to gentamicin, tigecycline, colistin, and occasionally ciprofloxacin. Ertapenem MICs ranged from 32 mg/L to >128 mg/L, indicating significant resistance to carbapenems. In addition to *bla*KPC-2, two other carbapenemases: *bla*NDM-1,5 and *bla*OXA-232 accompanied by a broad array of resistance genes targeting β-lactams, aminoglycosides, fluoroquinolones, and other antimicrobial classes, along with several virulence-associated genetic markers. Four strains carried dual carbapenemase genes: *bla*KPC-2+*bla*NDM-1 (n=1), *bla*KPC-2+*bla*NDM-5 (n=2), *bla*KPC-2+*bla*OXA-232 (n=1). Pulsed-field gel electrophoresis demonstrated genotypic variability, with isolates belonging to both well-established high-risk clones (sequence type-ST15, ST48, ST147) and undocumented STs i.e., ST1741 and ST2534. *bla*KPC-2 alone or in combination with *bla*OXA-232 was non-transferable, but exhibited successful horizontal

transfer in the presence of *bla*NDM. Strains revealed presence of diverse replicons (IncFIB, IncFII, IncR, ColKP3, IncM2, Col440I, and repB). Notably, *bla*KPC-2 was located on a ~75kb IncFII, *bla*NDM-5 on a 137kb IncFIB, and *bla*OXA-232 on a 6.14kb ColKP3 plasmid. Analysis of the genetic surroundings revealed conserved mobile elements commonly associated with global dissemination: *bla*KPC-2 within IS*Kpn7*-IS*Kpn6* on Tn*4401*b, *bla*NDM-1,5 between ΔIS*Aba125*-bleMBL on ΔTn*125* and *bla*OXA-232 between ΔIS*Ecp1*-Δ*lysR* on ΔTn*2016*.

Conclusion- This study is the first to report *bla*KPC-2 in ST1741 and ST2534. The presence of *K. pneumoniae* co-harboring *bla*KPC-2 with *bla*NDM-1,5 or *bla*OXA-232 in high-risk clones from neonatal bloodstream infections represents a serious public health threat. Such strains show extensive resistance to critical antibiotics, severely limiting treatment options in neonates. Although *bla*KPC-2 has been sporadically reported in the Indian subcontinent, its co-transfer with *bla*NDM in an NDM-endemic region is particularly concerning. These findings highlight the risk of rapid dissemination and underscore the need for ongoing molecular surveillance, antimicrobial stewardship, and stringent infection control in neonatal units.

Keywords: Dual carbapenemase (*bla*KPC-2 with *bla*NDM-1,5 or *bla*OXA-232) producing *K. penumoniae*, *bla*KPC-2 in ST1741 and ST2534, Neonatal sepsis.

Poster code: Biospec/PO-03

Characterization of gut resistome in healthy mother-infant dyads, focusing on betalactam resistance in Enterobacterales

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Background

The development of the gut microbiome is the foremost event that occurs post-birth and is primarily influenced by the delivery mode. The endogenous gut microbiota is dynamic and diverse, including small quantities of enteropathogens from Enterobacteriaceae and Enterococcaceae families. These pathogens harbour antibiotic resistance determinants that confer evolutionary advantages facilitated by horizontal gene transfer within the gut's dense microbial ecosystem, making it a major reservoir for resistance determinants. This study evaluated the presence of resistance determinants in stool specimens from healthy mother-infant pairs to assess antimicrobial resistance carriage.

Methods

Bacterial strains were isolated from stool specimens of healthy mother-infant pairs following standard stool culture procedure. Meconium was collected from neonates, and follow-up stool specimens were collected at 7-15 days and six months after birth. Bacterial identification was conducted using conventional biochemical tests and VITEK® 2 Compact system. For all strains, antibiotic susceptibility testing (AST) and detection of resistance determinants, including carbapenemases, were carried out. Strains that possessed carbapenemases were confirmed by Sanger sequencing and further subjected to whole-genome sequencing. Genetic relatedness among the bacterial strains was assessed by pulsed-field gel electrophoresis (PFGE).

Results

A total of 58 bacterial strains were isolated from the stool specimen, comprising 25 strains from 14 mothers and 33 strains from 15 infants. Among infants, 5 were delivered vaginally and 10 via caesarean section. All meconium samples were culture-negative. Most bacterial strains were isolated during 7–15 days of age (n=26, from 15 infants), with further strains collected at the 6-month follow-up (n=7, from 5 infants). Strains were identified as *Escherichia coli* (n=35), *Klebsiella pneumoniae* (n=21), and *Enterobacter cloacae complex* (n=2). Among maternal specimens, *E. coli* (33%) was predominant, while both *E. coli* and *K. pneumoniae* were equally prevalent (27%) in infants. AST of all 58 strains revealed that 15.5% were multidrug-resistant (MDR). Approximately 50% of the strains exhibited resistance to fluoroquinolones and second- and third-generation cephalosporins, while carbapenem resistance was detected in 7% of the strains. Among species-specific MDR rates, *E. coli* and *K. pneumoniae* exhibited MDR phenotypes in 20% and 19% of strains, respectively. Resistance determinants included *bla*CTX-M (48%), *bla*TEM (40%), *bla*OXA-1 (22%), and *bla*SHV (19%). Fluoroquinolone resistance determinants, such as *qnrS* (27%), *oqxAB* (27%), *qnrB* (15%) and *aac(6')-Ib-cr* (12%) were also detected. Four *K. pneumoniae* strains harboured *bla*NDM. Sanger sequencing identified three (n=3/4) as *bla*NDM-5 and one as *bla*NDM-1, distinguished by point mutations (G262T, A460C). Wholegenome sequencing revealed that NDM-positive *K. pneumoniae* strains belonged to ST14 (n=3; *bla*NDM-5) and ST29 (n=1; *bla*NDM-1). PFGE analysis revealed clonal diversity among isolates, with four clonal clusters (A to D). Cluster D, comprising three NDM-5-producing *K. pneumoniae* strains, exhibited >95% genetic similarity.

Conclusions

This study highlights the early gut colonization of antimicrobial-resistant bacteria in healthy infants, with *E. coli* and *K. pneumoniae* being the predominant gut colonizers. The presence of MDR strains and clinically relevant resistance determinants, including *bla*CTX-M, and *bla*NDM-1-NDM-5, even in healthy individuals, indicates the silent spread of antimicrobial resistance within the community.

Keywords**:** resistome; antibiotic resistance genes; gut microbiome; mother-infant pairs.

Poster code: Biospec/PO-06

Disarming Iron Piracy: Carbon-Doped Nickel Nanoparticles Inhibit Siderophore-Mediated Virulence in Foodborne *Pseudomonas* from Tilapia Gut

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ABSTRACT

The acquisition of iron via siderophores is a key virulence mechanism in many bacterial pathogens, often linked to biofilm formation and oxidative stress regulation. This study investigates the gut microflora of *Oreochromis niloticus* (tilapia), a widely consumed food fish, to isolate siderophore-producing strains and explore non-antibiotic strategies for their control. Commensal pathogens with strong siderophore and biofilm-forming capabilities may contribute to toxin accumulation in fish muscle and pose a risk of oral transmission to humans. Using the CAS assay, *Pseudomonas* emerged as the dominant siderophore producer, surpassing *Escherichia*, *Klebsiella*, and *Staphylococcus* spp. Crude extracts from these bacteria induced oxidative stress in fish liver and muscle, as shown by H_2O_2 scavenging assays at 230 nm. Green tea extract, natural biopolymers, nickel nanoparticles (NiNPs), and carbon-doped NiNPs (NiC) were tested as anti-virulence agents. NiC demonstrated superior performance across assays: it showed potent cytotoxicity in the MTT assay (absorbance 0.0108 vs. 0.9256 for control), significant antibiofilm activity (0.3094 vs. 0.8012), and robust biofilm eradication (0.3261 vs. 0.808). DNA degradation was confirmed via comet assay, and SDS-PAGE revealed downregulation of ornithine hydroxylase, essential for pyoverdine (Siderophore) synthesis. Fluorescence quenching indicated ~30% reduction in pyoverdine signal, while molecular docking confirmed strong NiC-ornithine hydroxylase interaction (−12.0 kcal/mol). One-way ANOVA showed statistical significance ($F = 5.22$, $p = 0.00124$). These findings establish NiC as an effective, eco-friendly anti-siderophore and anti-quorum sensing agent. Its ability to disrupt virulence and iron piracy pathways in *Pseudomonas* offers promising protection in aquaculture and potential barriers to human transmission.

KEYWORDS : Nickel Nanoparticle; Carbon-doped Ni Nanoparticle; Anti-siderophore assay; Ornithine hydroxylase.

Poster code: Biospec/PO-07

EXPLORING THE ROLE OF SEED PROTEIN HYDROLYSATES IN HUMAN HEALTH: APPLICATIONS IN DISEASE PREVENTION AND MANAGEMENT- REVIEW

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ABSTRACT

The seeds of many plants, which naturally have a high protein and necessary amino acid content, are used to make seed protein hydrolysate (SPH). Some of the most popular seeds for making SPH include quinoa, moringa, sesame, and soybeans. Each of them has unique functional qualities and nutritional profiles. Their solubility, digestibility, emulsification, and utility are all enhanced by SPH, which makes it simple to integrate them into a variety of food industries, such as the bread, beverage, and meat sectors. Since SPH is typically made from culinary waste, industrial, or agricultural leftovers like oilcake, defatted seed meals, or even entire seeds, the market potential is boosted.

These raw materials, which are frequently thrown out or utilized mostly as inferior feed products, are increasingly drawing interest from academics and enterprises due to their nutritional profile that benefits consumers. They also encourage innovation in sustainable food, which makes it a popular study topic. By converting seed waste into a well-known hydrolysate, they increase the food's protein content while simultaneously reducing waste production and enhancing the circular bio economy. Additionally, SPH contains a number of bioactive peptides that are essential for preventing illness, including anti-inflammatory, antidiabetic, and anticancer properties. One of the most important elements of SPHs is the bioactive peptides, which are normally actively working in the human body, boosting their activities and helping the prevention of chronic diseases.

The goal of this review is to focus on the uses of protein hydrolysate in both illness prevention and treatment. Along with discussing the nutritional and functional benefits of SPH and how they are now a part of contemporary food systems, it places a strong focus on scientific developments and a sustainability-driven strategy.

Poster code: Biospec/PO-09

Conventional vs. Platelet Rich Plasma -Assisted Recovery in Canine IVDD

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ABSTRACT

Intervertebral disc disease (IVDD) is a primary cause of acute thoracolumbar spinal cord dysfunction in dogs, particularly in chondrodystrophic breeds. This report documents the diagnostic evaluation, therapeutic management, and neuromotor evolution of a canine patient presenting with thoracolumbar IVDD (T11–T12) associated with congenital vertebral aplasia and chronic meningeal fibrosis, abnormalities that can exacerbate spinal cord compression and restrict epidural reserve. Computed tomography identified a mineralized disc extrusion producing moderate dorsal spinal cord compression, while neurological examination revealed severe non-ambulatory paraparesis with preserved deep pain perception. Initial conservative treatment with non-steroidal anti-inflammatory, corticosteroid, and neuromodulatory agents resulted in only partial functional improvement, increasing the Olby score from 3/14 to 6/14 without re-establishment of postural reactions or coordinated gait.

Given the limited response to medical therapy, a regenerative protocol based on paravertebral platelet-rich plasma (PRP) infiltrations was initiated. PRP was prepared using a double-centrifugation method from citrated whole blood and activated with calcium chloride before administration. Four infiltrations were performed at 14-day intervals under aseptic conditions and mild sedation, with neurological status monitored using the Olby Scale.

A marked acceleration of functional recovery was observed following PRP therapy. Within five days of the first infiltration, the patient achieved coordinated weight-bearing (Olby 10/14), with subsequent sessions producing progressive improvement to 11/14, then 12/14, culminating in near-complete recovery (13/14) after the fourth infiltration. Functional gains obtained during PRP therapy surpassed both spontaneous recovery observed during the medication-free period and the limited improvement recorded under pharmacological treatment alone. Restoration of proprioception, normalization of postural reactions, and stabilization of dynamic balance suggest that PRP may support neural repair through modulation of neuroinflammation and enhancement of axonal conduction via platelet-derived growth factors.

The findings indicate that paravertebral PRP may serve as a minimally invasive and biologically active adjunctive therapy for canine thoracolumbar IVDD with incomplete lesions, particularly in patients showing suboptimal response to conventional treatment. Controlled clinical trials are warranted to validate these observations and optimize therapeutic protocols.

Keywords: Intervertebral disc disease; platelet-rich plasma; regenerative therapy

DAY 2

11TH DECEMBER 2025

POSTER SESSION 2: MEDICAL BIOTECHNOLOGY

Poster code: Biospec/PO-15

Identification of Platelet-Derived Extracellular Vesicle Proteins as Peripheral Biomarkers for Neurodegenerative Diseases

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ABSTRACT

Neurodegenerative diseases (NDDs) are chronic, progressive conditions marked by the gradual loss of nerve cells, leading to cognitive, motor, and behavioural deficits. While early diagnosis is crucial for enhancing treatment outcomes, existing biomarkers frequently depend on brain tissue or cerebrospinal fluid, which are challenging and invasive to get hold of. This limitation has driven interest in peripheral biomarkers, particularly those obtained from blood. Platelets exhibit numerous structural and metabolic similarities to neurones, rendering them potentially useful candidates; yet, their short lifespan and instability reduce their diagnostic use. Platelet-derived extracellular vesicles (PEVs), which include microparticles and exosomes, provide a more stable and storable alternatives that share proteomic origin with platelets. Although there is substantial evidence connecting platelets to neurodegeneration, the function of PEVs is yet inadequately investigated. This study examines whether proteins transported by PEVs indicate disease-related alterations linked to neurodegenerative disorders. Utilising a curated collection of 327 proteins discovered via mass spectrometry from activated platelet-derived extracellular vesicles *(Aatonen et al., 2014)*, we conducted a comprehensive study of existing literature to ascertain disease-specific associations, considering only 6 NDDs (Alzheimer's disease, Parkinson's disease, Multiple Sclerosis, Amyotrophic Lateral Sclerosis (ALS), Huntington's disease, and Creutzfeldt–Jakob disease). A comprehensive literature review identified 148 disease-linked proteins across six NDDs. Of these, around 30% of the proteins showed elevated RNA expression (>100 nTPM) in the cerebral cortex and were selected for further analysis. Within this cortex-expressed subset, ~45% of the proteins participated in nervous system development (STRING analysis). Within this subset, a substantial proportion (~76%) of proteins were associated with Alzheimer's disease; among these, approximately 63% exhibited a disease association confidence score (CFG score) greater than one. Furthermore, ~25% of the subset showed significant alteration in the temporal cortex in disease, and ~22% were detected in calcium ionophore-activated microparticles. These findings suggest that if disease-associated alterations in the identified proteins are validated in platelets, comparable changes are likely to be reflected in their extracellular vesicles. This strengthens the potential of PEVs as reliable, accessible, and clinically relevant biomarkers for the early detection of neurodegenerative disorders. Additional experimental validation in patient-derived specimens will be crucial to ascertain their diagnostic significance.

Keywords: Neurodegenerative diseases (NDDs); Platelets; Platelet-derived extracellular vesicles (PEVs); Biomarkers

Poster Code: Biospec/PO-17

GENE EXPRESSION ANALYSIS OF EFFLUX AND INFLUX (OCT1) TRANSPORTERS IN DIFFERENT CML PHASES

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ABSTRACT

The Philadelphia (Ph) chromosome is produced by the reciprocal translocation of chromosomes 9 and 22, which is a hallmark of chronic myeloid leukaemia (CML), a clonal myeloproliferative illness. Organic cation transporter 1 (OCT-1) and organic cation/carnitine transporter 2 (OCTN2) are two membrane transporters that are necessary for the entry of imatinib into cells. Consequently, as their low expression lowers the intracellular imatinib concentration, membrane transporters have also been identified as significant factors to poor treatment response. Consequently, OCT-1, the primary influx transporter implicated in imatinib absorption in CML cells, has been identified as a critical predictor of intracellular imatinib levels attained in cells that contribute to imatinib resistance in CML patients. Investigating the gene expression of key transporters, such as P-glycoprotein (Pg-P), Multidrug Resistance Protein 1 (MRP1), Lung Resistance Protein (LRP), and Breast Cancer Resistance Protein (BCRP), during various stages of chronic myeloid leukaemia (CML) and following treatment was the aim of this study. There were five healthy controls and 120 patients with chronic myeloid leukaemia (CML). Depending on their diagnosis, the patients were grouped. Thirty patients had breast cancer, thirty had accelerated phase, thirty had blastic crisis, thirty had aphasia, thirty had chronic pain, and thirty had chronic CML. Imatinib (N=58), hydrea (N=32), or a combination of the two (N=30) were administered to the patients. Using matched blood and bone marrow samples, gene expression analysis was carried out to assess MDR marker expression throughout a range of disease stages and therapeutic approaches. The results provide insight on the mechanisms behind transporter-mediated drug resistance and might help improve CML patients' treatment regimens.

Keywords: CML, influx, drug entry, BCR-ABL1

Poster code: Biospec/PO-23

Molecular pathogenesis of Hypervirulent *Klebsiella pneumoniae* (hvKp) induced liver abscess: roles of autophagic and apoptotic pathways

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Abstract

Klebsiella pneumoniae (Kp) is a significant pathogen causing sepsis, urinary tract infections, pneumonia, and other critical infections in adults and neonates. According to WHO critical priority pathogen list, 2024; Carbapenem resistant Klebsiella pneumoniae ranks top as one of the notorious pathogens causing deadly life-threatening infections in both clinical and community setting. The Acquisition and evolution of its genetic factors led to form two pathotypes: classical *K. pneumoniae* (cKp) and hypervirulent *K. pneumoniae* (hvKp). Over the past two decades, hvKp has been associated with a distinct invasive syndrome characterized by liver abscesses, now emerging as a global health concern. Among several *K. pneumoniae* serotypes, K1 and K2 are reported to be associated with this hvKp mediated invasive liver disease. For improving clinical intervention, it is essential to understand the molecular pathogenesis of each stage of the liver damage and abscess progression.

Considering the above facts, this study conducted a comparative analysis for the pathogenesis of cKp and hvKp induced liver infection to elucidate the precise molecular mechanisms underlying hvKp-mediated liver abscess formation using both *in vitro* and *in vivo* murine models.

In vitro invasion assays using Huh7 human hepatocellular carcinoma cells revealed that hvKp isolates exhibited significantly greater invasiveness compared to cKp. This heightened invasion capacity resulted in substantial endothelial disruption and loss of cellular membrane integrity. Moreover, hvKp infection triggered a marked increase in intracellular reactive oxygen species (ROS), which in turn activated autophagy and apoptotic signalling pathways, contributing to cellular damage. To characterize *in vitro* autophagic response, key biomarkers were evaluated. The results showed hvKp infection caused increased expression of LC3B, indicating enhanced autophagosome formation. Additionally, elevated levels of LAMP1, a lysosomal membrane protein, suggested increased lysosomal involvement and autophagosome-lysosome fusion. The decreased level of p62 (SQSTM1), a selective autophagy adaptor protein, indicates that autophagic flux was functioning efficiently during hvKp infection.

To further investigate disease progression *in vivo*, BALB/c mice were infected with cKp and hvKp isolates. Survival kinetics demonstrated a higher mortality in hvKp-infected mice, accompanied by pronounced hepatic damage. Consistent with this phenotype, serum biochemical markers, serum glutamic oxaloacetic transaminase (SGOT/AST) and serum glutamic pyruvic transaminase (SGPT/ALT), showed significant elevation following hvKp infection. Histopathological examination of liver tissues confirmed damage in hepatic architecture, extensive tissue injury, infiltration of inflammatory immune cells and necrosis in

the hvKp infected group. Western blot and ELISA analyses further demonstrated that hvKp infection induced strong upregulation of pro-inflammatory cytokines, including IL-6, IL-8, TNF-α, and IL-1β, compared with both uninfected controls and cKp-infected mice.

In summary, hypervirulent *Klebsiella pneumoniae* induces profound hepatic injury through ROS-mediated activation of apoptotic and autophagy-related pathways. Dysregulation of autophagic markers such as LC3B, LAMP1, and p62 contributes to cellular damage and promotes abscess formation, highlighting the limitations of standard antibiotics and the urgency for targeted therapies.

Keywords: Klebsiella pneumoniae, Liver abscess, hvKp, apoptosis, autophagy

DAY 2

11TH DECEMBER 2025

POSTER SESSION 3: ENVIRONMENTAL AND PLANT BIOTECHNOLOGY

Poster code: Biospec/PO-02

Ultrasound-Assisted Processing of Black Garlic: Effects on Functional and Bioactive Properties

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ABSTRACT

Black Garlic (BG) is a product which is aged from whole garlic under a specific temperature and humidity by the Maillard reaction and possesses a unique, sweet, and less-spicy taste and a less intense odour compared with Raw Garlic (RG). The traditional aging process of BG necessitates a considerable investment of time (30-45 days), culminating in elevated market costs, while the scientific standardization of this process remains inadequately explored. Compositional changes are occurred during the aging process i.e. decrease in the amount of thiosulfinate and increase in the amount of Total Soluble Solids (TSS), reducing sugar, fructose, Hydroxymethyl furfural (HMF), S-allyl cysteine (SAC), polyphenols and volatile compounds. In this study, emerging technology such as ultrasound has been employed as a pre-treatment to shorten the aging time of peeled garlic. Ultrasonication is characterized by the generation of sound waves that exceed the audible spectrum for humans, wherein microbubbles are formed, expand, and ultimately collapse as a result of acoustic cavitation. Control Black Garlic (CBG), following the peeling process, was placed in an airtight container and subjected to aging at 70°C within a hot air oven. Conversely, for ultrasound-treated Black Garlic (UBG), the peeled garlic was pre-treated using ultrasound at temperatures of 35°C and 40°C for intervals of 10 minutes, 15 minutes, and 20 minutes (Frequency 24kHz, Power 55W), and subsequently maintained for aging under analogous conditions. Physicochemical changes and antioxidant activity of the samples were assessed at specific intervals. Results indicated that the aging duration for UBG was completed in 6 days, in contrast to the 11 days required for CBG, as evidenced by the observable colour transformation of the garlic. The contents of Reducing Sugar and HMF exhibited an increase from 0.055g/100g ±0.2 (RG) to 13.01g/100g ±0.5 (UBG) and from negligible (RG) to 0.554g/kg ±0.04 (UBG), respectively, demonstrating the occurrence of the Maillard reaction throughout the aging process. The physicochemical and antioxidant evaluations further revealed that

BG possesses a higher antioxidant capacity compared to RG. Consequently, the findings of this study advocate for the employment of ultrasound as a pre-treatment method that can effectively reduce the processing duration of BG while concurrently enhancing its antioxidant activity.

Keywords: Black Garlic; Maillard reaction; Ultrasonication; Antioxidant capacity

Poster code: Biospec/PO-16

Decrypting the molecular mechanism of antioxidant enzymes' regulation in reference to reactive oxygen species and reactive nitrogen species in higher plants

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Abstract

The production of reactive oxygen and nitrogen species (ROS and RNS respectively) inside the cell is the inevitable consequence of the aerobic metabolism. ROS and RNS have diverse source of production and mode of signaling. While both ROS and RNS can be accounted either separately or in concert to control both the physiological and pathological aspects of plants, however the harmful effects of them cannot be overlooked. Both ROS and RNS under certain unfavourable environmental conditions, can get toxic and lead to the oxidative and nitrosative stresses in plants that can incur damaging effects on several biomolecules which can ultimately lead to cell death. To counteract these destructive effects, plants have developed the antioxidant machineries: non-enzymatic as well as enzymatic. The enzymatic antioxidant scavengers have different levels of regulation to increase their sensitivity to any redox imbalance and harmful deviation in the immediate milieu hence ensuring their effective functioning. The present study has been focused on the molecular details of the network involving ROS and RNS signaling and how the antioxidants, especially their enzymatic arm, acts in concert to maintain the non-toxic level of ROS and RNS under stress condition, while allowing the essentially 'good part' of their signaling to continue, for the plants to survive.

Keywords: Reactive oxygen species, Reactive nitrogen species, Antioxidant enzymes, Stress

Poster Code: Biospec/PA-04

Cross-Talk Between phytohormones and acetylcholine: A transcriptomic approach to plant hormonal signaling in Solanum lycopersicun

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ABSTRACT

Acetylcholine (ACh), a classical neurotransmitter in animals, has recently emerged as a potentia signaling molecule in plants, with roles beyond its known metabolic and transport functions, In this studv. wc investigated thc transcriptomic cffects of ACh application on 30-days-old tomato sccdlings to explore its role in regulating plant development at transcriptomic level. Transcriptome analysis indicated that ACh treatment promoted the differential expression of 1690 genes in S. lycopersicum seedlings (1215 upregulated and 475 downregulated genes), GO enrichment and KEGG pathway analyses rcvealed that cxogenous ACh application was associated with a substantial incrcasc in the genes related to sevcral mctabolic processes, biosynthctic proccss, immunc responsc, and multiplc developmental processes including the photomorphogeneis, plant architecture, root development, and defense responses. Our RNA-seq analysis revealed significant changes in the expression of genes associated with multiple phytohormonc signaling pathways. ACh application lcd to the upregulation of auxin-responsive genes, including Auxin Response Factors (ARFs), SAURs, and MIZU-KUSSEI 1, indicating enhanced auxin signaling and its downstream effects on root morphogenesis. 'The protein- protein interaction network further highlighted ARFs and SAURs as central hubs, supporting ACh's role in rcorganizing root systcm architecture under normal conditions. Subscqucnt cxpcriments showcd hat acctylcholinc favors root formation whilc limiting shoot and callus dcvclopment, in linc with tho ranscriptomic findings. Collectively, these findings position ACh as a plant regulatory molecule tha orchestrates hormonal crosstalk especially through _auxin-centric pathways, while integrating cytokinin, GA, ABA, and JA signaling. By promoting root development, modulating hormone balance and priming stress responses, ACh functions as a developmental coordinator with potential applications n improving rooting efficiency and stress resilience in crops. Its role as a natural regulator of physiological and biochemical processes makes it an intriguing target for further research in plan biology. Future studics should aim to idcntify ACh rcceptors, downstream cffectors, and plant-specific cholincrgic componcnts to fully decode its signaling mcchanisms

Keywords: Acctylcholine (ACh), Solanum lycopersicum, Transcriptome, Auxin signaling

DAY 2

11TH DECEMBER 2025

POSTER SESSION 4: ENVIRONMENTAL AND PLANT BIOTECHNOLOGY

Poster Code: Biospec/PO-19

Bioluminescence in the light of climate change

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Abstract

Amid the escalating threats of climate change, bioluminescent organisms—including dinoflagellates, ctenophores, and certain fish—face severe stress as rising sea surface temperatures and ocean acidification disrupt the fundamental luciferin-luciferase reaction, diminishing their light production, elevating metabolic costs, and triggering poleward migrations that disrupt native food webs and alter carbon-cycling patterns. Compounded by deoxygenation, pollution, and shifting rainfall, these changes not only risk the loss of a natural wonder but also threaten the ecological functions bioluminescence supports, such as communication, predation, and camouflage; yet, these sensitive organisms also serve as vital bioindicators for ocean health, highlighting hypoxic zones and acidification while inspiring sustainable biomimetic technologies and underscoring the urgent need for emission reductions and marine conservation to avert an irreversible blunder.

Keywords : Bioluminiscence, Climate Change, Ecology, Luciferin – Luciferase reaction, Carbon cycling, Pollution

Poster Code: Biospec/PO-22

Potential of Hydroethanolic Extracts of *Asparagus racemosus* Willd as an Effective Source of Medicinally Important Metabolites

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ABSTRACT

Asparagus racemosus Willd. (common name: Shatavari) is a frequently used and well-known plant that has been used for a long time in traditional Indian systems of Medicine, such as Ayurveda. The roots of this plant are rich in secondary metabolites such as saponins, flavonoids, phenolics and alkaloids, which are bioactive. Hydroethanolic extractions are considered quite efficient as ethanol mixed with water is capable of dissolving both polar and nonpolar compounds. This allows comprehensive recovery of the constituents. In our poster, we have summarised the potential of hydroethanolic extracts of *A. racemous* as a natural source of therapeutic or medicinal compounds. Survey and analysis through various studies and research media showed that key metabolites such as steroidal saponins and flavonoids, which are known for their strong antioxidant and anti-inflammatory properties, are present in *A. racemous.* These metabolites influence a range of therapeutic activities, including immunomodulation, stress reduction and gastrointestinal protection. The results suggest that hydroethanolic extracts of *A. racemosus* can serve as a promising natural source of medicinal compounds. Therefore, *A. racemosus* has strong potential for further biotechnological applications in drug formulation and nutraceutical development. This review provides an understanding and foundation for the standardized use and industrial development of this traditional medicinal herb.

Keywords: *Asparagus racemosus*, Hydroethanolic Extract, Steroidal Saponins, Antioxidant.

Poster Code: Biospec/PO-21

Bacopa monnieri (L.) Wettst.: A Potential Source of Compounds with Wound Healing Properties

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ABSTRACT

Wound healing is a biological process that involves inflammation, tissue growth, and restructuring. Researchers have long explored natural products as treatments to speed up this process and improve its quality. *Bacopa monnieri* (L.) Wettst. is an Ayurvedic medicine which is known for its neuroprotective and antioxidant benefits. Recent studies suggest that it may also help with tissue repair. Compounds found in Bacopa, like bacosides, flavonoids, and saponins, are noted for their anti-inflammatory, antimicrobial, and antioxidant effects, which are all helpful in wound healing. Early studies show that extracts from *Bacopa monnieri* can promote cell growth, collagen production and new blood vessel formation, leading to quicker recovery and better tissue restoration. This poster outlines the pharmacological potential of *Bacopa monnieri* as a bioactive source for wound healing, highlighting its mechanisms of action, therapeutic significance, and future possibilities for developing plant-based treatments for wound care.

Keywords: Neuroprotective; Bacosides; Flavonoids; Saponins

Poster Code: Biospec/PA-24

BIOFILMS: THE HIDDEN CAUSE OF ANTIMICROBIAL RESISTANCE

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ABSTRACT

Biofilms are highly organized microbial communities enveloped by an extracellular polymeric substance matrix. The ability of microorganisms to survive in hostile environments and their great contribution to antimicrobial resistance make biofilms a hidden but important driver of chronic and recurrent infections. Wounds, mucosal surfaces, medical devices, and various industrial systems host biofilms. The biofilm-embedded microorganisms may manifest 100–1000-fold higher resistance to antibiotics compared with their planktonic counterparts. This review describes the different stages of biofilm formation, its structural complexity, and the various synergy-exerting mechanisms of antimicrobial tolerance. The most important contributors are restricted diffusion of antibiotics through the EPS matrix, altered microenvironment conditions, dormant persister cells, increased expression of efflux pumps, induction of stress responses, and enhanced horizontal gene transfer. These adaptations together drastically reduce therapeutic efficacy and enhance the spread of resistance determinants. Clinically, infections associated with biofilms occur in cystic fibrosis, chronic wounds, urinary tract infections, endocarditis, and implant-related infections. Newer approaches such as quorum-sensing inhibitors, enzymatic dispersion agents, physical disruption methods, and combination therapy provide hope for combating AMR associated with biofilms. In combating the global crisis of AMR, there is a need for deeper understanding of biofilm biology and the need for the development of improved antimicrobial therapies.

Keywords: Biofilms**,** Extracellular polymeric substance (EPS)**,** Antimicrobial resistance (AMR)**,** Persister cells**,** Combination therapy

Poster Code: Biospec/PA-25

The Dual Threat: Enzymes as Antimicrobial and Antibiofilm Agents

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Abstract

Enzyme-based antimicrobials have emerged as promising bio-therapeutics capable of targeting both planktonic and biofilm-embedded pathogens. Key enzymes, including lysozymes, DNases, endolysins, lipase and proteases, exert targeted bactericidal activity by hydrolyzing essential cellular components such as peptidoglycan, extracellular DNA, and structural proteins. Their capacity to degrade the extracellular polymeric substance (EPS) matrix disrupts biofilm integrity, inhibits bacterial adhesion, and enhances antibiotic diffusion, thereby overcoming major limitations associated with conventional antimicrobial therapies. These biocatalysts are inherently biodegradable, exhibit high substrate specificity, and demonstrate reduced cytotoxicity toward host tissues, supporting their application in clinical domains such as wound management, cystic fibrosis therapy, oral healthcare, and prevention of medical device-associated infections, as well as in industrial sectors including food safety and antifouling technologies. Nonetheless, translational challenges persist, including enzyme instability in physiological environments, narrow activity spectra, structural heterogeneity of biofilms, and risks of immunogenic responses. Ongoing innovations in protein engineering, formulation technologies, and targeted delivery strategies are rapidly improving enzyme robustness and therapeutic efficacy. Collectively, enzyme-based interventions represent a sustainable and potent approach to combat persistent biofilm-associated infections and mitigate the growing threat of antimicrobial resistance.

Keywords: Enzyme therapeutics, Antimicrobial resistance, Biofilm disruption, EPS degradation, Enzyme stability

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