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SOUVENIR | NCALS-2026 | KAKATIYA UNIVERSITY

National Conference on

ADVANCES IN LIFE SCIENCES: PRESENT AND FUTURE

(NCALS-2026)

24-25TH March 2026

Organized by

Department of Zology,

University College, Kakatiya University, Warangal

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ABSTRACTS BOOK

Organized by

DEPARTMENT OF ZOOLOGY
Kakatiya University, Warangal-506009 TS, India

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Souvenir of
National Conference on ADVANCES IN LIFE SCIENCES: PRESENT & FUTURE (NCALS-2026)

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Content

PREFACE

It gives me immense pleasure to present the Souvenir and Abstract Book of the National Conference on Advances in Life Sciences: Present and Future (NCALS–2026), organized by the Department of Zoology, Kakatiya University. This conference serves as a dynamic platform for academicians, researchers, and students to share their innovative ideas and recent advancements across diverse domains of life sciences.

The overwhelming response to this conference, with a large number of quality abstract submissions from across the country, reflects the growing interest and rapid progress in interdisciplinary areas such as molecular biology, biotechnology, environmental sciences, bioinformatics, and emerging technologies including artificial intelligence in drug discovery. The abstracts compiled in this volume represent significant contributions that address contemporary scientific challenges and offer promising solutions for sustainable development and human welfare.

We sincerely acknowledge the valuable support and guidance of our Hon'ble Vice-Chancellor, distinguished guests, advisory and organizing committees, and all contributors who made this conference a success. Special appreciation is extended to the authors for their enthusiastic participation and for sharing their scholarly work.

We hope that this souvenir will serve as a useful reference and inspire further research, collaboration, and innovation in the field of life sciences.

- **Prof. Estari Mamidala**
Organising Secretary

Prof. Y. Venkaiah
Head, Department of Zoology

ABOUT THE UNIVERSITY

Kakatiya University was established on 19th August, 1976 with the upgradation of the erstwhile Post-Graduate Centre of Osmania University. The University was established primarily to fulfill the aspirations of the Telangana people for higher education.

Kakatiya University has 24 Departments with a network of 18 constituent colleges and about 529 affiliated colleges. It has Post-Graduate Colleges at Subedari (Hanamkonda), Khammam, Jangaon, Jayashankar Bhoopalpally, Mahabubabad and University Engineering College at Kothagudem. Among the affiliated colleges, the University has 395 Arts & Science; 3 Law; 8 Engineering; 53 Education; 38 Management; 8 MCA and 24 Pharmacy colleges under its jurisdiction.

The Kakatiya University was first accredited with B+ grade in the year 2003. The University was subsequently re-accredited with 'A 'grade in 2009 and 2017. It occupied 38th position in national level rankings by India Today-Nielsen Survey. Kakatiya University established Memorandum of Understanding (MoU) with several universities and research institutes for collaborative research.

Kakatiya University crossed the milestone of forty years and is poised to achieve greater academic excellence with dedication and commitment in the years to come.

ABOUT THE DEPARTMENT

The Department of Zoology was established in the year 1968 as PG Centre under Osmania University, Hyderabad. Later, it was shifted to the existing campus in 1973 as a full-fledged Department, with spacious classrooms, laboratories for students and research labs for faculty members in addition to museum, library and state-of- the-art Conference Hall, Computer Lab with internet facility, all housed in a built area of about 15,000 sft and Laboratory space of about 8,000 sft. Since then it is flourishing into a quality education centre for the students and research scholars in the subject ZOOLOGY.

The Department of Biochemistry was established in 2005 bifurcating the subject from the Chemistry department. Bio-chemistry was one of the optional papers in M.Sc. course and realizing the potential for this subject, the M.Sc. Bio-Chemistry course was started in 1999 under self-finance Scheme. It has all the necessary equipment to carry out practical class work and the faculty is putting efforts in research.

The both the Departments has well equipped laboratories, advanced research facilities. The Department does exceedingly well in the fields of higher education and research and also establishes the thrust areas like physiology, Enzymology, Seri-biotechnology, Infectious Diseases, Metabolic Disorders, Bioinformatics, Computational Biology, Environmental Biology and Entomology.

ABOUT THE SEMINAR

The National Conference on Advances in Life Sciences: Present and Future (NCALS–2026) is a multidisciplinary academic event organized to bring together researchers, academicians, and students to deliberate on recent developments and future directions in life sciences. The conference aims to foster scientific exchange, promote collaborative research, and address contemporary challenges through innovative approaches.

The scientific program is structured around a wide range of themes reflecting the diversity and integration of modern biological sciences. These include Molecular Biology, Genetics and Genomics; Cell Biology, Biochemistry and Biotechnology; Animal Biology, Physiology and Development; Biodiversity, Conservation and Wildlife Biology; Ecology, Environmental Biology and Climate Change; Microbiology, Parasitology and Immunology; and Toxicology and Environmental Health. In addition, the conference emphasizes emerging and interdisciplinary areas such as Bioinformatics and Computational Biology, Emerging Technologies and Innovations in Biology, Artificial Intelligence in Drug Discovery, and Pharmaceutical Applications in Biological Sciences.

By integrating traditional knowledge with cutting-edge technologies, the conference provides a platform for discussing innovative solutions in healthcare, environmental sustainability, and biotechnology. It encourages participants to explore novel research perspectives and contribute towards scientific advancements that benefit society at large.

This conference is expected to inspire meaningful discussions, knowledge sharing, and future collaborations in the ever-evolving field of life sciences.

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PROGRAM SCHEDULE

Day-1: March 24, 2026 (Tuesday)		
9.30–10.00 am	Registration	
10.00-10.40 am	Inauguration & Opening Remarks	
10.40-11.30 am	Keynote Lecture	**Dr. Roy Karnati** University of Hyderabad
11.30-11.35 am	Tea Break	
11.35-12.15 pm	Invited Talk-1	**Dr. Nageswara Rao Pulipati** BYCUS, Therapeutics Pvt Ltd
12.15-01.00 pm	***Oral Presentations:***	
	Theme-1: AI in Drug Discovery	Seminar Hall
	Theme-2: Animal Biology, Physiology and Development	Lecture Room-1
	Theme-3: Biodiversity, Conservation and Wildlife Biology	Lecture Room-2
1.00-2.00 pm	Lunch	
2.00-2.40 pm	Invited talk-2	**Prof. Ashok Kumar Chaubey** Chaudhary Charan Singh University
2.40-3.30 pm	Invited talk-3	**Prof. D. Kashinath** National Institute of Technology
3.30-3.40 pm	Tea Break	
3.40-4.15 pm	Invited Talk-4	**Prof. Venkateswarlu Kanamarlapudi** Swansea University UK
4.15-5.30 pm	***Oral Presentations***	
	Theme-4: Bioinformatics and Computational Biology	Seminar Hall

	Theme-5: Cell Biology, Biochemistry and Biotechnology	Lecture Room-1
	Theme-6: Ecology, Environmental Biology and Climate Change	Lecture Room-2
	Online Presentations	

Day-2: March 25, 2026 (Wednesday)		
10.00-10.40 am	Invited Talk-5	**Prof. Roja Rani** Osmania University
10.40-11.30 am	***Oral Presentations***	
	Theme-7: Emerging Technologies and Innovations in Biology	Seminar Hall
	Theme-8: Microbiology, Parasitology and Immunology	Lecture Room-1
	Theme-9: Molecular Biology, Genetics and Genomics	Lecture Room-2
11.30-11.40 am	Tea Break	
11.40-12.20 pm	Invited talk-6	**Prof. M. Madhavi** Osmania University
12.20-1.00 pm	***Oral Presentations***	
	Theme-10: Pharmaceutical Applications in Biological Sciences	Seminar Hall
	Theme-11: Toxicology and Environmental Health	Lecture Room-1
1.00-2.00 pm	Lunch	
2.00-3.30 pm	***Poster Presentations***	at Corridor of 1st Floor
3.30-4.00 pm	Valedictory Session	at Seminar Hall, Dept. of Zoology

KEY NOTE ADDRESS

DECODING ONE CARBON METABOLISM IN IDH1 MUTANT GLIOMAS: FROM METABOLIC REWIRING TO PRECISION THERAPY

Roy Karnati

Department of Animal Biology, School of Life Sciences, University of Hyderabad

ABSTRACT

Isocitrate dehydrogenase 1 (IDH1) mutations are primary drivers of low-grade gliomas, generating the oncometabolite 2-hydroxyglutarate while inducing metabolic stress and reprogramming. While generally conferring a favourable prognosis, significant clinical heterogeneity remains in IDH1 mutant astrocytoma. To address this, we first integrated transcriptomic data from the TCGA and CGGA datasets to characterize the rewiring of the One-Carbon Metabolism (OCM) network. We discovered a two-state metabolic phenotype: while most tumors downregulate proliferative pathways, a high-risk subset aberrantly reactivates proliferative OCM genes, which overrides the favourable IDH1 survival benefit and actively remodels the tumor microenvironment. This composite OCM signature serves as a potent, independent prognostic biomarker to identify an aggressive metabolic aggressor tumor. To therapeutically target the root cause of this aggressive subset, we developed an AI-driven drug repurposing pipeline to discover novel, mutant-selective IDH1 inhibitors. The random forest regression model, trained on 1631 compounds using quantitative structure-activity relationship descriptors, screened public libraries of FDA-approved drugs. Top hits were validated via molecular docking, MM/PBSA free energy calculations, and 250 ns molecular dynamics simulations. Finally, in vitro enzymatic assays confirmed top four hits that showed potential for repurposing to selectively suppress mutant activity in the micromolar range without affecting the wild-type enzyme. This study established a comprehensive precision medicine framework for IDH1-mutant glioma, integrating transcriptomic biomarker stratification for high-risk patients with the deployment of machine learning-validated, mutant-selective targeted therapeutics.

INVITED LECTURES

INVITED LECTURE-I

BIOPHARMACEUTICAL INDUSTRY IN INDIA-CHALLENGES & OPPORTUNITIES

Nageswara Rao Pulipati

Bycus Therapeutics, Hyderabad

ABSTRACT

India faces a significant gap in access to affordable biosimilars despite possessing skilled manpower, world-class biotechnology research institutions, and a robust manufacturing ecosystem. Globally, the USFDA has approved over 300 originator biologics, yet India offers only a limited portfolio of high-value biosimilars. This disparity stems primarily from two major challenges: prolonged development timelines (typically 6–8 years) and stringent regulatory requirements. Biosimilars, being complex large-molecule therapeutics unlike small-molecule generics, demand extensive physicochemical characterization, preclinical toxicology studies, comparative Phase I pharmacokinetic/pharmacodynamic (PK/PD) assessments, and Phase III efficacy/safety trials. These lengthy and resource-intensive processes deter private investment, particularly for orphan and rare-disease indications with small patient populations and limited commercial viability. Although government schemes provide grants and funding, current support remains insufficient for this deep-tech sector. In contrast, regulators in Europe (EMA) and the United States (FDA) increasingly waive comparative clinical efficacy trials under a "totality-of-evidence" approach when robust analytical similarity, in-vitro data, and sensitive PK/PD biomarkers demonstrate equivalence, supplemented by strong post-marketing pharmacovigilance. India's Draft Guidelines on Similar Biologics 2025 (released by CDSCO in May 2025) align with this global trend, explicitly permitting waivers of confirmatory Phase III trials and in-vivo animal studies when high similarity is established through advanced analytics, reducing development time and cost by 40–60% and timelines to 3–4 years. Final implementation, combined with the ₹10,000 crore Biopharma SHAKTI scheme (announced in Union Budget 2026), could attract substantial private capital, accelerate approvals, and enable affordable access for India's 1.4 billion population while supporting exports to low- and middle-income countries, generating foreign exchange.

INVITED LECTURE-II

CLIMATE CHANGE, INSECT PEST AND AGRICULTURE SUSTENANCE

Ashok Kumar Chaubey

Nematology Laboratory, Department of Zoology,
Chaudhary Charan Singh University, Meerut - 250 004

ABSTRACT

Climate change and global warming are of great concern to agriculture worldwide and are among the most discussed issues in today's society. Climate parameters such as increased temperatures, rising atmospheric CO2 levels, and changing precipitation patterns have significant impacts on agricultural production and on agricultural insect pests. Agricultural crops and their corresponding pests are directly and indirectly affected by climate change. Direct impacts are on pests' reproduction, development, survival and dispersal, whereas indirectly the climate change affects the relationships between pests, their environment and other insect species. As a result, there is a serious risk of crop economic losses, as well as a challenge to human food security. Over the past 100 years, annual rise in temperature has led to exacerbation of pest problems like Spilosoma oblique on oilseeds and vegetable crops; Helicoverpa armigera on vegetables, pulses; Plasmodiophora brassicae on crucifers; Liriomyza trifolii on vegetable crops etc. Green mirid bug, (Creontiades biseratense) has emerged as a pest of cotton in Karnataka, Tamil Nadu, Maharashtra and Andhra Pradesh. Maruca vitrata has emerged as a predominant pest in recent years in all pigeonpea and cowpea growing areas causing up to 42% damage in cowpea at Andhra Pradesh. Up to 40% of food crops are lost due to various types of pests and diseases each year, of which a large chunk (~20%) of the agro-products is damaged by the various types of the insect pests. Farmers have been battling pests and diseases since the dawn of agriculture. The desert locust is one of the most destructive pests in the world, with one small swarm covering one square kilometer eating the same amount of food per day as 35,000 people. The exceptional population growth has rising demands for crop production and accordingly, by 2050, global agricultural production will very likely need to be doubled to meet that kind of increasing demand. Large chunk of the agro-products (standing crops and store grains) are damaged by the various types of the insects. To control the insect pests, globally 4.35 million metric tons of pesticides and India is ranked 13th in terms of total pesticide use. The highest pesticide consumption in India

is Maharastra followed by Uttar Pradesh, Punjab, Telangana and Haryana. The application of pesticides is not only costly affair and increasing the production cost but also their residual effects are harmful for animals and human beings too. Some of the major pests have developed resistance against the pesticides. To minimize the use of pesticides, development of bio-pesticide is a good option. The global biopesticides market is experiencing rapid growth and is projected to reach over USD 27.06 billion by 2033. Two of the prominent genera of entomopathogenic nematodes (EPN) i.e. Steinernema and Heterorhabditis having interaction with insects and are considered globally as highly pathogenic to insects. They can be applied, at Infective Juveniles stage, in conjunction with other biological and chemical pesticides, fertilizers and soil amendments. The locally available indigenous EPN isolates are much effective and their applications are beneficial against the insect pests viz., rice leaf folder (Cnaphalocrocis medinalis); tobacco cutworm (Spodoptera litura); brinjal fruit borer (Leucinodes orbonalis); diamond back moth (Plutella xylostella); silver-leaf whitefly (Bemesia tabaci); sugar beet beetle (Psylliodes punctulata); cotton bollworm (Helicoverpa armigera); potato tuber moth (Phthorimaea operculella); spotted stalk borer (Chilo zonellus); rice yellow stem borer (Tryporyza incertulas); banana stem weevil (Odoiporus longicollis) etc.. Steinernema spp. (87 isolates) and Heterorhabditis spp. (21 isolates) have been isolated from the soils of western Uttar Pradesh and are tested against the major insect pests. The species specific formulations have been developed against Holotrichia consanguinea & H. serrata , Helicoverpa armigera and Spodoptera litura. Farmers can also initiate to develop the formulation by their own by established cottage industry and can monetary gain by reducing the application of chemical pesticides in the agriculture fields as well as by selling the EPN based bio-pesticides. The future of EPN based bio-pesticide is bright in India because of the more demand of organic products in the market.

Key Words:
Climate Change, Insect Pests, Entomopathogenic Nematodes, Biopesticide.

INVITED LECTURE-III

UNDERSTANDING MODERN DRUG DISCOVERY PROCESS AND SYNTHESIS OF NEW TACRINE/TETRAHYDRACRIDINE DERIVATIVES FOR THE DUAL ACETYL/BUTYRYL CHOLINESTERASE INHIBITION

Dhurke Kashinath

Department of Chemistry, National institute of Technology, Warangal-506004

ABSTRACT

This lecture provides a comprehensive overview of the modern drug discovery process and the fundamental principles of medicinal chemistry. It discusses the historical evolution of drug discovery from traditional plant-based remedies to contemporary rational drug design including target identification and validation, lead identification, lead optimization and steps of preclinical and clinical phases. In addition, there will be discussion on the examples for the identification of pharmacophore lead modification, use of classical and non-classical bioisosteres—to improve drug potency, selectivity, and pharmacokinetic parameters. At the end of the lecture there will be discussion on the Synthesis of new Tacrine/Tetrahydracridine derivatives for the dual acetyl/butyryl cholinesterase inhibition

References:

1. T. Shirisha, S Majhi, K. Divakar, D. Kashinath, New J. Chem., 2025, 14381-14387.
2. T. Shirisha, S Majhi, K. Divakar, D. Kashinath, New J. Chem., 2025, 49, 1072–1082.
3. T. Shirisha, S. Majhi, K. Divakar, and D. Kashinath, Organic & Biomolecular Chemistry, 2024, 22, 790-804.

INVITED LECTURE-IV

INVESTIGATION OF POTENTIAL NEW TREATMENTS FOR DIABETES, CANCER AND COVID-19

Venkateswarlu Kanamarlapudi

Professor of Molecular and Cellular Pharmacology, Institute of Life Science, School of Medicine, Swansea University, Singleton Park, Swansea SA2 8PP, United Kingdom

ABSTRACT

Type 2 Diabetes (T2D) has become one of the most serious health concerns in the world. Glucagon-like peptide receptor (GLP-1R) agonists are one of the major therapeutics for T2D. In the developed world, 1 in 2 will develop some form of cancer during their old age. Current methods for treating cancer involve radiation therapy and chemotherapy. However, resistance to these therapies is common. By targeting the cell surface receptors specifically or overexpressed in pancreatic beta-cells and cancer cells, Professor Kanamarlapudi's group's current focus is on developing peptide-based anti-diabetic and anti-cancer therapies and their relevance for developing novel antiviral treatments for COVID-19 will be discussed in the presentation.

Keywords: T2D, GLP-1R, COVID-19, Cancer, Antiviral.

INVITED LECTURE-V

CARDIOPROTECTIVE ACTION OF AMARANTHUS VIRIDIS METHANOLIC EXTRACT AND ITS ISOLATED COMPOUND KAEMPFEROL THROUGH MITIGATING LIPOTOXICITY, OXIDATIVE STRESS AND INFLAMMATION IN THE HEART

Anupalli Roja Rani

Department of Genetics, Osmania University, Hyderabad, Telangana-500007, INDIA

ABSTRACT

The current study was designed to evaluate the cardio-protective efficacy of Amaranthus viridis L. methanolic extract (AVME) and kaempferol, which was isolated from AVME in isoproterenol (ISO)-induced cardiotoxicity in rats. The rats were pre-treated with AVME (250 mg/kg body weight) and kaempferol (50 mg/kg BW) for 30 days, respectively, and then administered with ISO (20 mg/100 g body weight) on the 31st and 32nd days. We assessed the protective effects of AVME and kaempferol against ISO-induced cardiotoxicity, oxidative stress, and inflammation. The study revealed that supplementation with AVME and kaempferol significantly attenuated cardiac lipotoxicity by reducing cholesterol and triglyceride levels and simultaneously increasing the levels of high-density lipoproteins. In addition, AVME and kaempferol suppressed oxidative stress by enhancing the activities of superoxide dismutase, catalase, and glutathione peroxidase in the heart. Further, they ameliorated cardiac inflammation by mitigating the production of pro-inflammatory cytokines (tumor necrosis factor-alpha, interleukin-6, and interleukin-1β). Hence, the study results and histopathological analysis emphasized that AVME and kaempferol could be prospective prophylactic agents against ISO-induced cardiotoxicity and may be considered nutraceuticals in the prevention of cardiovascular disorders.

Keywords:
Myocardial infarction ·Pharmacognosy ·Cardiovascular disorders ·Oxidative stress ·Inflammation

INVITED LECTURE-VI

ONE HEALTH APPROACH: ANIMAL PHYSIOLOGY IN EMERGING DISEASES

M. Madhavi

Department of Zoology Osmania University, Hyderabad, Telangana India

ABSTRACT

Diseases can creating a significant impact on Healthcare systems globally, mainly in under developed Nations. There are several factors causing this infectious diseases. The factors include climatic change, environmental factors animal health as well as activity of human like globalisation, travel can lead to spread of diseases. Several vertebrae animals like Reptiles, Birds, Mammals Serves as reservoir or host for Several Viral Zoonoses. Infectious diseases associated with the interaction between humans, animals, and the environment—such as zoonotic, vector-borne, and food or water-borne diseases—remain a significant risk to public and animal health, causing substantial illness and death. It is estimated that the infectious disease of about 1400 known to affect the human. 61% of the disease are of animal origin,globally around 75% of emerging infectious diseases are Zoonotic.It means that these diseases can be transmitted between human and animals .The one health framework place an important role in the prevention and controlling of Zoonoses by integrating human, animal,environmental health through the cooperation and integration among wildlifephysician,osteopaths,veterinarians professionals, nurses, dentist, environment expects ,biochemics and others. The one health approach identifies that the human being health, environment, and animals are Linked intrisically and the efforts to the emergent diseses, issues need to the Cordinated together. The global health challenges have led to a more integrated, coordinated, practical approach designed at achieving logical and realistic solutions. In the area of outbreaks of infectious diseases, serious concerns have been present over the last two decades. New pathogens evolve and old ones reappearing, Some have potential pandemic, highlighting the continued presence of neglected zoonotic pathogens. The One Health perspective Identifies the overall well-being of human beings, environment and animals are linked intrinsically and the strategies to control the problems arising from Zoonoses need to be coordinated together. The major challenge of future is identifying the emerging zoonotic diseases, which demands higher recognition of the link between veterinary and human medicine.

Keywords: One Health, Infectious Diseases, Zoonotic Diseases, Emerging Diseases, Public Health, Vector borne diseases

Theme-1:

AI IN DRUG DISCOVERY

Code	Authors	Paper Title
17	Mekala Srikanth & Kuntamalla Sujatha	Pharmacophore Modeling and Molecular Docking for PI3K/AKT1 Pathway Inhibitor
37	Keerthana Chittimalla, Ashok Vanigandla	Docking Study of Pongaglabone against Nipah Virus
43	Tallamudi Swathi	AI in Drug Discovery
48	Angadi Sathish Kumar, Estari Mamidala	Machine Learning-Driven Discovery of CCR5 Inhibitors
53	Madhav Morla, Estari Mamidala	Structure-Based Discovery of CYP17A1 Inhibitors for Prostate Cancer
54	Madhav Morla et al.	Discovery of Inhibitors Targeting Nipah Virus Glycoprotein
89	Mangalagiri Bhavani	Artificial Intelligence in Protein Structure Prediction and Drug Discovery: Advances and Future Perspectives
96	Pasula Janakiramulu, Estari Mamidala	Identification of Potential EGFR Inhibitors from Gymnema sylvestre Leaf Crude Extract through GC–MS Analysis and Molecular Docking Studies
99	Dr. Pathi Chandrashekar	AI's Role in the Discovery of New Drugs, along with its Difficulties, Possibilities and Methods
102	Jyothsna Yangala, Estari Mamidala	Structure-Based Virtual Screening and Molecular Docking to Identify Potential Inhibitors of PI3Kα (H1047R Mutant)
108	Md. Sanober, Estari Mamidala	Integrated In Silico Approach for Identification of a Lead Compound Targeting HIV-1 Reverse Transcriptase
112	Dr. S. Sahiti	Role of AI in Drug Discovery from Social Work Perspective
128	Mukkera Karthik, Prof. Estari Mamidala	Pharmacophore-Based Virtual Screening of ZINC Compounds Against HIV-1 Integrase
131	Yuvaraj Sampathkumar, Kaushik Thamilchelvam, Senthil N.	Docking of Cyanobacterial Peptides Against Tapeworm Enzymes

	Rajamanickam, Vikram Godishala	
133	Himabindu Kurra, Vikram Godishala	GC-MS and Computational Screening Against Canine Distemper Virus

Presentation code: 17

LIGAND-BASED PHARMACOPHORE MODELING AND MOLECULAR DOCKING FOR THE DISCOVERY OF PI3K(P110A)/AKT1 PATHWAY INHIBITOR

Mekala Srikanth[1] and Kuntamalla Sujatha[2]

[1,2] *Department of zoology, Kakatiya university, Warangal-506009, Telangana state, India.*

ABSTRACT

The PI3K/AKT signaling cascade represents a crucial target for developing cancer therapeutics. Extensive research efforts have been focused to identifying new inhibitors targeting key kinase proteins within this pathway to advance cancer treatment. this study focuses on a computational approach to discover new inhibitors through the optimization of hits derived from previously reported PI3K and AKT inhibitors. From an initial dataset of 122,276,899 compounds sourced from the ZINC database, filtering repeatedly based on favourable pharmacokinetic properties reduced the pool to 17 ligands. A pharmacophore model was subsequently constructed using the reference drug, alpelisib, as a template. Molecular docking simulations were conducted using AutoDock Vina 4.0 against the PI3K p110α/AKT1 receptor protein (PDB ID: 4JPSA,4GV1). The filtered 10 compounds (ZINC000071768672, ZINC000071768671, ZINC000071768662, ZINC000071768663, ZINC000071768673, ZINC000071768678, ZINC000071768664, ZINC000065251501, ZINC000065251495 and ZINC000071768289) were docked into the active site of PI3K, AKT1 docking scores superior to the FDA-approved ligand (alpelisib). The top compounds exhibited extensive hydrogen bonding and hydrophobic interactions with critical amino acid residues, surpassing the interactions observed with alpelisib. In conclusion, these inhibitors may be represent potential candidates for targeting the PI3K p110α/AKT pathway and could be further investigated through in vitro studies and clinical trials as promising anticancer agents.

Key words: Cancer, AutoDock Vina, PI3K(P110α)/AKT1, ZINC Database, Pharmacophore.

Presentation code: 37

PONGAGLABRONE AS A POTENTIAL LEAD MOLECULE TARGETING THE MATRIX PROTEIN OF NIPAH VIRUS: A MOLECULAR DOCKING STUDY

Keerthana Chittimalla[1], Ashok vanigandla[2]

[1]*Department of Biochemistry, Kakatiya University, Warangal-506009 TG, India*
[2]*Department of Biochemistry, Kakatiya University, Warangal-506009 TG, India*

ABSTRACT

Nipah virus is a zootonic pathogen was firstly identified in Malaysia country in 1998 and spread all over world including West Bengal, India in 2001. The severity is causing fatal infections and mortality in humans, it is very important to discover novel inhibitor with natural sources. The current Insilco study gives antiviral flavonoid against nipah virus. The Structure of nipah virus has surface glycoproteins (G and F) for host attachment and fusion and matrix (M) protein located beneath the viral lipid envelope that plays a crucial role in virus assembly, budding, and structural organization. The study focuses on matrix protein inhibition using flavonoids. The selected flavonoid-derived phytochemical Lanceolatin, Pongaglabrone, Pongaglabol, Flavone, and Isopongaglabol were evaluated for their inhibitory potential against the target protein represented by 7SKT protein structure using molecular docking analysis. Among the tested compounds, Pongaglabrone demonstrated the highest binding affinity with a docking score of −8.07 kcal/mol, followed by Pongaglabol with −7.14 kcal/mol. Isopongaglabol and Lanceolatin exhibited moderate binding energies, whereas Flavone showed the lowest binding affinity. The inhibition occurs in the more repeated binding regions PHE283, ARG286 and ILE243.These findings indicate that flavonoid-based phytochemicals, particularly Pongaglabrone, may serve as promising lead compounds for the development of antiviral agents targeting Nipah virus proteins. Further in vitro and in vivo studies are required to validate their therapeutic potential.

Key words: Matrix protein, pongaglobrone, flavonoids,

Presentation code: 43

AI IN DRUG DISCOVERY

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Artificial Intelligence (AI) is transforming the pharmaceutical industry by accelerating and improving the drug discovery process. Traditional drug development is a lengthy and expensive procedure that can take more than 10–15 years and require billions of dollars to successfully bring a drug to market. AI technologies such as machine learning, deep learning, and data mining enable researchers to process vast amounts of biological, chemical, and clinical data efficiently. These technologies assist in identifying potential drug targets, predicting molecular interactions, and designing novel drug compounds with higher precision. AI also enables virtual screening of millions of chemical compounds to identify promising drug candidates before laboratory testing, thereby reducing time, cost, and experimental failures. Furthermore, AI supports drug repurposing by discovering new therapeutic uses for existing drugs and enhances clinical trial design by identifying suitable patient populations and predicting treatment outcomes. By integrating computational power with biomedical research, AI helps scientists understand complex disease mechanisms and develop more effective treatments. Despite its advantages, challenges such as data availability, model reliability, ethical considerations, and regulatory approval remain significant. Nevertheless, continuous advancements in AI algorithms, computational resources, and biomedical databases are expected to further strengthen its role in pharmaceutical research. Overall, AI-driven drug discovery has the potential to revolutionize healthcare by enabling faster development of safer, more effective, and personalized medicines for a wide range of diseases.

Presentation code: 48

MACHINE LEARNING-DRIVEN DISCOVERY OF HIGH-AFFINITY CCR5 INHIBITORS: AN XGBOOST VIRTUAL SCREENING OF THE FOODB DATABASE

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ABSTRACT

Human Immunodeficiency Virus (HIV) continues to pose a significant global health challenge, necessitating the discovery of novel therapeutic agents targeting key stages of viral entry. The C-C chemokine receptor type 5 (CCR5) is a critical co-receptor involved in HIV entry into host cells and therefore represents an important target for antiviral drug development. In the present study, an integrated Machine Learning (ML)-driven in silico drug discovery approach was employed to identify potential CCR5 antagonists from a dataset of 170 drug-like molecules. A robust XGBoost (Extreme Gradient Boosting) ensemble learning model was applied for predictive screening, enabling the efficient prioritization of compounds with high predicted biological activity. The shortlisted candidates were further evaluated through ADMET (Absorption, Distribution, Metabolism, Excretion, and Toxicity) prediction to assess their pharmacokinetic and safety profiles. The analysis revealed several compounds with favorable oral bioavailability and acceptable toxicity profiles. Molecular docking simulations were subsequently performed against the CCR5 receptor (PDB ID: 4MBS), revealing strong binding affinities ranging from −7.1 to −11.4 kcal/mol. Among the identified leads, FDB020301 demonstrated the highest binding affinity (−11.4 kcal/mol), exceeding that of the clinically approved CCR5 antagonist Maraviroc (−10.5 kcal/mol). Interaction analysis indicated stable binding through hydrogen bonds with TYR37 and GLN280, along with π–anion and aromatic interactions with key residues within the receptor binding pocket.

Keywords: Machine Learning; XGBoost; CCR5 receptor; Molecular docking; ADMET prediction; Anti-HIV drug discovery

Presentation code: 53

STRUCTURE-BASED DISCOVERY OF PHYTOCHEMICAL INHIBITORS TARGETING CYTOCHROME P450 CYP17A1 (CYP17A1) FOR PROSTATE CANCER THERAPY

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ABSTRACT

Prostate cancer is one of the most prevalent malignancies affecting men worldwide and is strongly associated with androgen biosynthesis. The enzyme cytochrome P450 17A1 (CYP17A1) plays a critical role in the production of androgens and represents an important therapeutic target for prostate cancer treatment. In the present study, a structure-based computational approach was employed to identify potential phytochemical inhibitors targeting CYP17A1. The three-dimensional crystal structure of CYP17A1 (PDB ID: 6WR1) was retrieved from the Protein Data Bank and used for molecular docking analysis. A library of selected phytochemicals obtained from natural sources was screened against the active site of the enzyme to evaluate their binding affinity and interaction patterns. The docking results revealed that several phytochemicals exhibited strong binding interactions with key residues within the catalytic pocket of CYP17A1. Among the screened compounds, IMPHY009079 showed the highest binding affinity with a docking score of −11.39 kcal·mol^{-1} and an estimated inhibition constant (Ki) of approximately 4.96 nM, indicating strong inhibitory potential. This compound formed hydrogen bonds with important residues such as HIS373, ILE371, and ARG96, along with extensive hydrophobic interactions involving LEU370, CYS442, VAL310, and PHE435, contributing to the stability of the ligand–protein complex. Other phytochemicals, including IMPHY008870 and IMPHY007444, also demonstrated notable binding affinities with docking scores of −10.01 kcal·mol^{-1} and −9.91 kcal·mol^{-1}, respectively, suggesting stable interactions within the active site of the enzyme. These findings highlight several promising phytochemical leads that may act as potential CYP17A1 inhibitors.

Key words: Prostate cancer, CYP17A1, phytochemicals, molecular docking, drug discovery.

Presentation code: 54

STRUCTURE-BASED DISCOVERY OF HIGH-AFFINITY INHIBITORS TARGETING THE ATTACHMENT GLYCOPROTEIN (NIV-G) OF NIPAH VIRUS

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ABSTRACT

Nipah virus (NiV) is a highly lethal emerging pathogen with no approved antiviral therapies, posing a significant global health threat. Viral entry is mediated by the attachment glycoprotein G (NiV-G) and the fusion protein (F), which initiates infection through receptor binding, making it a critical therapeutic target. Targeting NiV-G therefore represents an attractive strategy to block infection at its earliest stage. In the present study, a comprehensive in silico approach was employed to identify potential inhibitors of NiV-G, the top hit (PubChem ID: 134220125) achieved a docking score of −10.69 kcal/mol (Ki ≈ 14.6 nM), surpassing the reference Acrivastine (PubChem: 5284514; −10.0 kcal/mol; Ki ≈ 41.4 nM). Binding analyses indicate that high-affinity ligands engage a complementary mix of hydrogen bonds and extensive hydrophobic/van der Waals contacts within the receptor-binding groove. These results identify several nanomolar-range NiV-G binders as promising starting points for medicinal chemistry optimization and experimental validation. Further evaluation using molecular dynamics simulations and in vitro assays is recommended to confirm binding stability, target engagement, and antiviral efficacy.

Keywords: Nipah virus, NiV-G, fusion protein, molecular docking.

Presentation code: 89

ARTIFICIAL INTELLIGENCE IN PROTEIN STRUCTURE PREDICTION AND DRUG DISCOVERY: ADVANCES AND FUTURE PERSPECTIVES

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ABSTRACT

Artificial Intelligence (AI) has transformed many scientific fields, particularly life sciences and biomedical research. One of the most promising applications of AI is in protein structure prediction and modern drug discovery. Proteins play a crucial role in biological systems because their structure determines their function. Understanding the three-dimensional structure of proteins is essential for identifying biological mechanisms, disease pathways, and therapeutic targets. Traditional experimental methods such as X-ray crystallography, cryoelectron microscopy, and nuclear magnetic resonance spectroscopy have been widely used for determining protein structures. However, these methods are often expensive, time consuming, and technically challenging. Artificial intelligence provides powerful computational tools that help researchers predict protein structures quickly and accurately by analyzing large biological datasets. In recent years, machine learning and deep learning algorithms have demonstrated remarkable success in predicting protein folding patterns and molecular interactions. These computational approaches reduce research time and accelerate the development of new medicines. AI technologies also assist scientists in identifying drug targets, predicting drug protein interactions, optimizing drug molecules, and performing virtual screening of chemical compounds. This paper discusses the importance of artificial intelligence in protein structure prediction and highlights its applications in modern drug discovery. It also reviews the advantages, limitations, and future prospects of AI driven approaches in biomedical and pharmaceutical research.

Keywords: Artificial Intelligence, Protein Structure Prediction, Drug Discovery, Machine Learning, Bioinformatics.

Presentation code: 96

IDENTIFICATION OF POTENTIAL EPIDERMAL GROWTH FACTOR RECEPTOR (EGFR) INHIBITORS FROM GYMNEMA SYLVESTRE LEAF CRUDE EXTRACT THROUGH GC–MS ANALYSIS AND MOLECULAR DOCKING STUDIES

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ABSTRACT

The medicinal plant Gymnema sylvestre is widely recognised in traditional medicine for its diverse pharmacological properties, including antidiabetic, anti-inflammatory, and anticancer activities. The present study aimed to identify potential inhibitors of the Epidermal Growth Factor Receptor (EGFR) from the crude leaf extract of Gymnema sylvestre using phytochemical profiling and molecular docking approaches. Fresh leaves were collected, washed, air-dried at room temperature, and made into a fine powder. The powdered material was subjected to methanolic extraction using a Soxhlet apparatus equipped with a reflux condenser, and the resulting extract was filtered and analysed through GC–MS to determine its phytochemical composition. GC–MS analysis identified 63 phytochemical compounds in the extract. Structurally active compounds were selected for molecular docking against EGFR, showing binding energies ranging from −3.3 to −6.9 kcal/mol. Among them, 1,3,5-Triazine-2,4-diamine, N,N'-bis(1-methylethyl)-6-(methylsulfonyl) exhibited a notable docking score of −6.1 kcal/mol, forming a hydrogen bond with Met793 and hydrophobic interactions with Met790, Leu844, Ala743, Val726, and Gly796. The interaction profile was compared with the standard inhibitor Afatinib (−8.8 kcal/mol), which interacted with key residues including Phe723, Asp855, Met790, Val726, and Leu844. These findings suggest that the identified compound may serve as a potential EGFR inhibitor, warranting further in vitro and in vivo validation.

Keywords: Gymnema sylvestre, EGFR, GC–MS Analysis, Molecular Docking, Anticancer

Presentation code: 99

AI'S ROLE IN THE DISCOVERY OF NEW DRUGS, ALONG WITH ITS DIFFICULTIES, POSSIBILITIES AND METHODS.

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ABSTRACT

With increased speed, precision, and efficiency, artificial intelligence (AI) has the potential to completely transform the drug discovery process. However, the availability of high-quality data, the resolution of ethical issues, and the understanding of the limitations of AI-based methods are all necessary for the successful implementation of AI. The advantages, difficulties, and disadvantages of AI in this area are examined in this article, along with potential methods and tactics for getting over the current barriers. The application of explainable AI, data augmentation, and AI integration with potential advantages of pharmaceutical research.

Keywords: Artificial intelligence, medicine development, difficulties, and AI limitations.

Presentation code: 102

STRUCTURE-BASED VIRTUAL SCREENING AND MOLECULAR DOCKING TO IDENTIFY POTENTIAL INHIBITORS OF PI3KA (H1047R MUTANT)

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ABSTRACT

The phosphatidylinositol-3-kinase alpha (PI3Kα) enzyme plays a crucial role in cell growth, survival, and cancer progression. Mutations in PI3Kα, particularly the H1047R mutation, are frequently associated with tumor development, making it an important therapeutic target. In the present study, an in silico structure-based drug discovery approach was employed to identify potential inhibitors of PI3Kα. The crystal structure of PI3Kα (H1047R mutant) complexed with wortmannin (PDB ID: 3HHM) obtained from the Protein Data Bank was used as the target protein. A total of 216 bioactive compounds were retrieved from the PubChem database and subjected to virtual screening. Drug-likeness evaluation based on Lipinski's rule of five and ADMET prediction using the Deep-PK resulted in the selection of five promising compounds. These filtered compounds were further subjected to molecular docking using AutoDock Vina to evaluate binding affinity and interaction profiles with the target enzyme. The docking results revealed that the selected ligands exhibited binding energies ranging from −6.9 to −9.0 kcal/mol. Among them, compound CID162641672 showed the highest binding affinity (−9.0 kcal/mol) with two hydrogen bond interactions involving GLY451 and HIS450. Several hydrophobic interactions with key active site residues further stabilized the ligand–protein complexes. These findings suggest that the identified compounds may serve as potential lead molecules for the development of PI3Kα inhibitors, although further experimental validation is required.

Key words:
PI3Kα inhibitor, molecular docking, virtual screening, ADMET prediction, AutoDock Vina, structure-based drug design.

Presentation code: 108

INTEGRATED IN SILICO APPROACH FOR IDENTIFICATION OF A LEAD COMPOUND TARGETING HIV-1 REVERSE TRANSCRIPTASE

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ABSTRACT

Human Immunodeficiency Virus type-1 (HIV-1) reverse transcriptase (RT) remains a critical therapeutic target for antiretroviral drug development. In this study, a ligand-based pharmacophore modeling approach was employed using Nevirapine as the reference compound to identify potential RT inhibitors. The pharmacophore model was constructed and used for virtual screening via Pharmit, followed by similarity-based retrieval of compounds from the ZINC Database, yielding 57 candidate molecules. Drug-likeness evaluation using Lipinski's rule of five resulted in 47 compounds passing the criteria. Further ADMET profiling using ADMETlab 3.0 significantly narrowed the pool, with only one compound satisfying stringent pharmacokinetic and toxicity parameters. Molecular docking analysis was then performed against HIV-1 RT to validate binding affinity. The reference drug Nevirapine exhibited a binding energy of −6.0 kcal/mol, whereas the identified lead compound demonstrated a comparatively improved binding energy of −6.6 kcal/mol. These findings suggest that the screened lead compound possesses favorable binding potential and acceptable pharmacokinetic properties, warranting further investigation. This study highlights the effectiveness of an integrated pharmacophore-based virtual screening and ADMET-guided filtering approach in identifying potential HIV-1 RT inhibitors.

Key words: Pharmacophore screening; nevirapine; molecular docking; ADMET prediction; reverse transcriptase inhibitors; virtual screening

Presentation code: 112

BRIDGING HEALTH INEQUITIES: THE ROLE OF AI IN DRUG DISCOVERY FROM SOCIAL WORK PERSPECTIVE

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This abstract explores the transformative potential of Artificial Intelligence (AI) in drug discovery and its implications for addressing persistent health inequities. AI technologies have significantly accelerated the identification of novel drug candidates, reduced research costs, and improved efficiency in pharmaceutical development. However, these advancements often remain concentrated in high-resource settings, limiting their accessibility and benefits for marginalized and underserved populations. This paper examines how AI driven drug discovery can be aligned with principles of social justice to ensure equitable healthcare outcomes. From a social work perspective, the study highlights the critical role of practitioners in advocating for inclusive policies, ethical AI practices, and equitable distribution of medical innovations. Social workers can act as intermediaries between communities, healthcare providers, and policymakers, ensuring that the needs and voices of vulnerable groups are integrated into technological advancements. Furthermore, concerns related to data bias, affordability, and access are discussed, emphasizing the need for socially responsible AI frameworks. The paper concludes by suggesting collaborative strategies between social work professionals, researchers, and policymakers to bridge the gap between innovation and accessibility. Integrating social work values into AI-driven drug discovery can contribute to more inclusive, ethical, and sustainable healthcare systems, ultimately reducing disparities and promoting health equity on a global scale.

Key Words: Artificial Intelligence, Drug Discovery, Health Inequities, Social Work, Ethical Health Care access

Presentation code: 128

PHARMACOPHORE-BASED VIRTUAL SCREENING AND MOLECULAR DOCKING OF ZINC DATABASE COMPOUNDS AGAINST HIV-1 INTEGRASE

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ABSTRACT

HIV-1 integrase is a critical enzyme involved in the integration of viral DNA into the host genome and represents an important therapeutic target in antiretroviral drug discovery. In this study, a pharmacophore-based virtual screening approach was carried out using Pharmit, with Dolutegravir as the reference drug. The pharmacophore model included aromatic groups, hydrogen bond donors, hydrogen bond acceptors (4), hydrophobic groups (2), and a negative ionizable feature. A total of 13,127,550 compounds from the ZINC database were screened, and the resulting hits were filtered using Lipinski's Rule of Five, yielding 12 drug-like candidate molecules. Molecular docking was subsequently performed against HIV-1 integrase (PDB ID: 3S3M) using AutoDock Vina. Among the screened compounds, ZINC000299738148 and ZINC000299738315 emerged as the top lead candidates, with binding energies of −9.7 kcal/mol and −9.4 kcal/mol, respectively. Notably, ZINC000299738148 exhibited a stronger binding affinity than the reference drug Dolutegravir (−9.5 kcal/mol), while ZINC000299738315 showed comparable binding performance. Both lead compounds demonstrated stable interactions with key active site residues, including ARG350, GLN215, HIS213, and SER216, similar to Dolutegravir, indicating a conserved binding mode. These findings suggest that the identified compounds may serve as promising inhibitors of HIV-1 integrase and warrant further investigation.

Keywords: HIV, Integrase, pharmacophore, molecular docking, vina

Presentation code: 131

MOLECULAR DOCKING AND PHARMACOKINETIC EVALUATION OF CYANOBACTERIAL NON-PROTEIN PEPTIDES AS INHIBITORS OF KEY TAPEWORM ENZYMES

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ABSTRACT

Cyanobacteria are phototrophic prokaryotes that play vital roles in global carbon and nitrogen cycling, with many species capable of biological nitrogen fixation. These organisms produce diverse secondary metabolites, including non-protein peptide compounds such as Cryptophycin B, Calothrixin A, Calothrixin B, and Tolyphycin, which exhibit various bioactive properties. Tapeworms (class Cestoda) are parasitic flatworms that serve as bioindicators for environmental pollutants and depend on enzymes including Triosephosphate Isomerase and Superoxide Dismutase for their growth and survival. This study investigates the potential biochemical interactions between cyanobacterial metabolites and tapeworm enzymes through molecular docking analyses. Water samples collected from salt pans in Marakkanam, India, yielded 11 microalgae isolates. In silico screening was performed using databases and software tools including the Protein Data Bank (PDB), PubChem, BioViaDraw, Q-SiteFinder, and ADME prediction tools. Molecular docking simulations were conducted using AutoDock to evaluate binding affinities between four cyanobacterial non-protein peptide compounds and the two target tapeworm enzymes. Protein-ligand interactions were visualized and analyzed using Visual Molecular Dynamics (VMD). Among the compounds tested, Cryptophycin B demonstrated the highest binding affinity toward both Triosephosphate Isomerase and Superoxide Dismutase. These findings suggest that Cryptophycin B may possess significant potential to

interact with key tapeworm enzymes, indicating a possible biochemical basis for ecological relationships between cyanobacteria and cestodes in natural environments. Further investigations are warranted to elucidate the functional significance of these interactions.

Keywords: Cyanobacteria, Tape worm, non-peptide protein compounds, Molecular Simulations, Triosephosphate isomerase, Superoxide dismutase

Presentation code: 133

GC-MS ANALYSIS AND COMPUTATIONAL SCREENING OF CYMBOPOGON CITRATUS PHYTOCHEMICALS AGAINST THE TETRAMERIC ATTACHMENT GLYCOPROTEIN OF CANINE DISTEMPER VIRUS

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ABSTRACT

Cymbopogon citratus (lemongrass) is widely utilized in traditional medicine, with its therapeutic properties attributed to a diverse array of secondary metabolites. This study aimed to characterize the phytochemical constituents of the methanolic extract of *C. citratus* and evaluate their potential as antiviral agents against canine distemper virus (CDV) through computational methods. Phytochemical profiling was performed using Gas Chromatography-Mass Spectrometry (GC-MS). Subsequent in silico analyses were conducted to predict the pharmacological and toxicological properties of the identified compounds. Molecular simulations were employed to investigate the interaction dynamics between these phytochemicals and the tetrameric attachment glycoprotein of CDV, a critical therapeutic target for viral entry inhibition. GC-MS analysis revealed a complex phytochemical composition comprising terpenes (Eucalyptol, β-Ocimene, 3-Carene, Thymol), nitrogen-containing compounds (2-Toluic hydrazide, benzo[h]quinoline derivatives), and other bioactive molecules including cyclobarbital and organosilicon compounds. The presence of these pharmacologically significant compounds corroborates the traditional medicinal applications of the plant. Molecular simulations demonstrated that the conformational flexibility of the CDV attachment glycoprotein plays a pivotal role in receptor-ligand interactions. Several phytochemicals exhibited favorable binding characteristics, suggesting potential inhibitory activity against viral attachment mechanisms. Cymbopogon citratus represents a promising source of bioactive compounds with potential therapeutic applications. The computational findings indicate that select lemongrass-derived phytochemicals warrant further investigation as candidate inhibitors of CDV attachment glycoprotein. These results provide a foundation for subsequent in vitro and in vivo studies to validate the antiviral efficacy of these compounds against canine distemper virus.

Keywords: *Cymbopogon citratus*, GC-MS, phytochemicals, molecular simulations, canine distemper virus, antiviral agents

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STUDIES ON THE COMPARATIVE MORPHOLOGY OF SCENT APPARATUS IN HALYS DENTATUS AND CORIDIUS JANUS

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ABSTRACT

The scent apparatus of stink bugs (Hemiptera: Pentatomidae) plays a vital role in chemical defence and interspecific communication, yet species-level comparative studies remain limited. The present investigation focuses on the comparative morphology of the metathoracic scent apparatus in two pentatomidae species, Halys dentatus and Coridius janus. Detailed examinations were conducted using standard dissection procedures and light microscopy to document variations in the ostiole, peritreme, associated glandular structures, and evaporative areas. Distinct interspecific differences were observed in the shape, orientation, and structural elaboration of these components. Halys dentatus exhibited a more prominently developed peritreme and complex evaporative surface sculpturing, while Coridius janus showed comparatively simpler gland openings and reduced peritremal extensions. These morphological distinctions highlight the potential taxonomic value of the scent apparatus and provide insights into species-specific ecological adaptations and chemical defence strategies. The study contributes to improving diagnostic characters for pentatomidae systematics and enhances understanding of functional morphology within the group.

Keywords: Halys dentatus, Coridius janus, Pentatomidae, scent apparatus, metathoracic scent gland, ostiole,

Presentation code: 14

INDIAN MACKEREL AS THE CHEAPEST SOURCE OF NUTRIENT

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ABSTRACT

Majority of societies possess fish as favorite food stuffs. Fish is the one of the important food component that contains all nutritional components and it is the source of energy for human beings. It is also rich source of vitamins and minerals for young and old age people. Fish meat contains high amount of polyunsaturated fatty acids which play an important role in reducing cholesterol preventing number of coronary heart diseases and risk of dementia which includes alzheimer's diseases. Fish consumption also improves immunity against number of human pathogens as it posses' antimicrobial peptides. The Indian Mackerel (*Rastrelliger kanagurta*) is a major marine resource in Indian marine waters and constitutes among the top three national fish commodities. Indian mackerel, *R. kanagurta* belongs to family Scombridae and it is commonly found in coastal areas of Indian Ocean. It is abundant in Red Sea and Arabian Gulf. It is important pelagic fisheries resource along with sardines constituting 7.2% of total marine fish landings. The size of the Indian Mackerel varies with 20 – 22 cm in most of the fish catches. The bulk of the production is obtained from Kerala to Goa i.e. west coast. Indian Mackerel is one of the commonly available and economic fish which is sold in fish markets around Indian and world. This fish is characterized by possessing dark bands which is due to myoglobins and high lipids. Indian Mackerel is an excellent, affordable source of high-quality protein with all essential amino acids providing approximately 22-25 gm protein for every 100gm of serving. This fish is highly nutritious packed with omega 3 fatty acids, selenium, vitamins B12 & D. It contains low mercury and nutrient dense staple food. The high protein content of the fish helps to support muscle maintenance, while omega – 3 fatty acid and help in maintain heart health and brain function. As this fish is soft, flaky, moist and packed with all nutrients for overall well being, it is one of healthiest fish that can be part of regular meals and cheapest source of protein.

Presentation code: 18

REVIEW ON FRESHWATER CAGE CULTURE IN INDIA

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ABSTRACT

Cage culture is a significant aquaculture method for fish farming in natural water bodies, such as reservoirs, lakes, and rivers. In India, this technique has gained prominence due to the rising demand for fish and the availability of extensive inland water resources. This review gathers and examines data from published research papers, reports, and scientific databases concerning freshwater cage culture in India. Various species, including Indian major carps (Catla catla, Labeo rohita, Cirrhinus mrigala), pangasius (Pangasianodon hypophthalmus), tilapia (Oreochromis niloticus), and catfishes, are effectively raised in floating cages. India has over three million hectares of reservoir resources that are ideal for cage aquaculture. The benefits of cage culture include efficient water resource use, enhanced fish growth, and increased income opportunities for fish farmers. However, challenges such as disease outbreaks, feed expenses, environmental effects, and management limitations remain considerable.

Keywords: Cage culture, Freshwater aquaculture, Fish production in cage, India, Environmental impact

Presentation code: 30

ROLE OF ANTIBIOTICS WITH REFERENCE TO BIOMASS AND SILK GLAND DEVELOPMENT IN MULBERRY SILKWORM, *BOMBYX MORI*

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ABSTRACT

Sericulture, one of the most sustainable agro based industry, largely depends on the health and productivity of the silkworm Bombyx mori. The use of antibiotics in sericulture has gained attention for their potential role in enhancing digestion, larval growth, and silk yield. Moreover, the silkworm serves as an excellent experimental model, offering a simple cost effective and ethical means for evaluating the efficacy of antibiotics. Silkworms have emerged as reliable model organism for quantitatively evaluating the therapeutic effects and efficacy of different antibiotics. The compatibility of antibiotics with silkworms is reinforced by their established application in drug screening and pathogenicity studies attributed to their short life cycle and ethical suitability as experimental models. Hence, the present review emphasizes the role of antibiotics as economical agent in disease management , improving of production efficiency which is reflected in the commercial traits of mulberry silkworms.

Key words: Antibiotics, silkworm, therapeutic effects, commercial traits, cocoon quality.

Presentation code: 32

PROTEIN PATTERNS OF PAROTOID GLAND EXTRACT AND ITS SECRETION OF BUFO MELANOSTICTUS (SCHNEIDER) THROUGH UREA-SDS-PAGE

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ABSTRACT

The present investigation has been undertaken to study the Electrophoretic banding patterns of proteins were analyzed qualitatively in the parotoid gland extract and its secretion of common Indian toad Bufo melanostictus through 12% Urea-SDS-PAGE. The patterns of protein bands indicated a distinct pattern of six protein bands with some other additional bands with weak staining were observed in the parotoid gland extract and four protein bands in parotoid gland secretion and one additional band with weak staining. The protein patterns were identified by using running marker relative molecular standards of approximately 14-200 KDa. Rm values of proteins bands were calculated accordingly. The electrophoretogram revealed that both the protein patterns of Parotoid gland extract and its secretion showed homology in protein bands with minor variations.

Key words: Parotoid gland, Bufo melanostictus, Rm value, Urea-SDS-PAGE.

Presentation code: 58

EXAMINING THE EXTENT OF KNOWLEDGE AMONG FISH FARMERS ON COMPOSITE FISH CULTURE PRACTICES IN BAPATLA, ANDHRA PRADESH, INDIA

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ABSTRACT

This research evaluates the understanding of 60 fish farmers in Bapatla District, Andhra Pradesh, regarding composite fish culture practices employing an ex post facto design for the years 2024–25. Findings from a 41-item knowledge assessment revealed that 68.33% of participants possessed medium knowledge, 18.33% had high knowledge, and 13.34% demonstrated low knowledge. The farmers showed proficiency in nutrient management and species selection, achieving scores between 90% and 96.67%, yet exhibited significant deficiencies in their comprehension of pesticide application (30%) and stocking rates (15%). Regression analysis ($R^2 = 0.6898$) indicated that education, social participation, and engagement with extension services were significant predictors of knowledge ($p < 0.05$). It is essential to implement targeted extension programs to bridge these knowledge gaps and promote the sustainable adoption of composite fish culture practices.

Key words: Composite Fish Culture, Fish Farmers, Knowledge Assessment.

Presentation code: 81

SLEEP DISORDER - IMPACT ON METABOLIC HEALTH

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ABSTRACT

There is growing evidence supporting a strong association between sleep disorders and metabolic health outcomes. Early detection and focused intervention for sleep disturbances can significantly improve metabolic profiles and prevent the onset or progression of complications. Timely management not only enhances sleep quality but also assists in better control of metabolic conditions such as diabetes and obesity, emphasizing the importance of integrating sleep health into routine metabolic disorder management. The association of sleep disorders and metabolic health was found to be bidirectional and further future studies are needed which explains the contributing factors for the link and to integrate molecular level analysis. The bidirectional relationship aids to utilize the precision medicine based on personalized therapy in a more effective way.

Keywords: Sleep disorder, Metabolic health, Bidirectional, Precision medicine

Presentation code: 94

EFFECTS OF VARIOUS NUTRIENT SUPPLEMENTED ARJUNA LEAVES ON LARVAL GROWTH AND POST COCOON PARAMETERS OF SILKWORM

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ABSTRACT

The present study depicts the effect of various nutrient supplemented feed on the biological and commercial traits of tasar silkworm (Antheraea mylitta). The growth and development, silk productivity of the tasar silkworm are significantly influenced by the quality of the leaves of the host plant (Terminalia arjuna) fed during 5th instar larva till spinning. The silkworm larvae at 5th instar stage were taken and fed with fresh and healthy arjuna leaves coated with Glycine, tyrosine, casein, sucrose and vitamin C in different combinations. Results of the current study revealed that the average weight of silkworm larvae and the post cocoon parameters were significantly improved in the worms fed with nutrient supplemented leaves as compared to the control. The larvae fed with nutrient supplemented leaves showed the maximum cocoon weight, cocoon length, cocoon width, cocoon shell ratio as compared to the control group. It is evident from the results that the nutrient supplemented leaves have a positive effect on the commercial and biological traits of Antheraea mylitta.

Keywords: *A. mylitta*, Glycine, Silkworm, Supplemented leaves, tasar.

Presentation code: 105

COMPARATIVE STUDY OF TISSUE-SPECIFIC ESTERASE ISOENZYME PATTERNS IN TWO FRESHWATER TELEOSTS: *CATLA CATLA* AND *TILAPIA MOSSAMBICA* OF DIFFERENT ORDERS

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ABSTRACT

Esterases are a diverse group of hydrolytic enzymes involved in vital physiological processes such as detoxification, neurotransmission, and the metabolism of endogenous and xenobiotic compounds, and they are widely recognized as sensitive biochemical markers in ecotoxicological and comparative studies. The present investigation aimed to analyze the tissue-specific distribution and electrophoretic mobility (Rm values) of esterase isoenzymes in two freshwater teleost fishes belonging to different taxonomic orders, *Catla catla* (Cypriniformes) and *Tilapia mossambica* (Perciformes). Zymogram analysis using native polyacrylamide gel electrophoresis was carried out on six tissues—gill, liver, intestine, muscle, brain, and eye—and the detected isoenzymes were classified into Carboxylesterases (CE), Esterase-resistant to inhibtors (ER), Cholinesterases (ChE), and Choline-esterase like enzmes (CHsp), types based on their sensitivity to specific inhibitors such as paraoxon and eserine. The results revealed clear interspecific and tissue-specific differences in esterase profiles, with *C. catla* exhibiting a more complex pattern comprising six isoenzyme zones (Rm values: 0.96, 0.86, 0.76, 0.56, 0.45, and 0.33), whereas *T. mossambica* showed a simpler pattern with three zones (Rm values: 0.96, 0.75, and 0.66). In *C. catla*, the Rm 0.56 zone was consistently observed across all tissues but displayed functional variation, acting as CE in the liver and ER in the gill, indicating tissue-dependent biochemical roles; similarly, in *T. mossambica*, the Rm 0.75 zone was ubiquitous, functioning as CE in metabolically active tissues such as liver and brain and as CHsp in muscle and intestine. Organ-specific expression was also evident, with unique high-mobility zones (Rm 0.96 and 0.86) in the intestine of *C. catla*, while in *T. mossambica*, the Rm 0.96 band appeared as a common marker in gill, liver, and intestine. Notably, isoenzymes sharing similar electrophoretic mobility often differed in their inhibitor sensitivity across tissues, suggesting the presence of distinct tissue-specific isoforms. Overall, the findings demonstrate that esterase

isoenzyme patterns are both species-specific and tissue-dependent, reflecting underlying physiological adaptations, and underscore their potential application as reliable biomarkers for monitoring environmental pollution and assessing the impact of organophosphate and carbamate pesticides in aquatic ecosystems.

Keywords: *Catla catla, Tilapia mossambica,* Esterase Isoenzymes, Zymogram, Rm Value, Biomarkers, Tissue Specificity.

Theme-3:

BIODIVERSITY, CONSERVATION AND WILDLIFE BIOLOGY

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Presentation code: 2

BIODIVERSITY CONSERVATION AND EMERGING CHALLENGES AFFECTING THE RESILIENCE OF THE TASAR SILKWORM IN SERICULTURE

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ABSTRACT

Tasar sericulture, based on the forest – dwelling silkworm Antheraea mylitta, represents an ecologically sensitive and livelihood –oriented production system that is highly dependent on forest biodiversity. The resilience and productivity of tasar silkworm culture are closely linked to the diversity of host plants, silkworm genetic resources, and functional ecological interactions within natural and semi natural ecosystems. In recent years, increasing climate variability – manifested through irregular rainfall patterns, rising temperatures, and extreme weather events has emerged as a major challenge, adversely affecting host plant phenology, larval development, cocoon yield, and silk quality. Alongside climatic stress, anthropogenic pressure such as deforestation, habitat fragmentation, host plant depletion, and the increasing incidence of pests and diseases have further threatened the sustainability of tasar silkworm populations. Erosion of biodiversity reduces genetic adaptability and disrupts ecological balance, thereby increasing the vulnerability of silkworms to environmental stresses and disease outbreaks. Conservation of key tasar host plants, including species of Terminalia and Shorea, is therefore critical for ensuring nutritional security, stabilizing rearing environments, and sustaining forest – based sericulture system. Biodiversity – based practices in tasar sericulture, such as mixed host plantations, conservation of silkworm ecotypes, eco – friendly pest management, and the promotion of natural enemies and soil microbial communities, play a vital role in enhancing ecosystem resilience. These practices improve larval health, strengthen disease resistance, support nutrient cycling, and contribute to stable cocoon productivity under variable climatic conditions. A sustainable pathway for tasar silkworm culture requires the integration of biodiversity conservation with climate – adaptive sericulture practices and community – based forest management. Such an integrated approach not only strengthens ecological integrity and system resilience but also enhances the socio-economic viability of forest – dependent communities. Overall, biodiversity conservation emerges

as a strategic and sustainable framework for ensuring the long – term resilience, productivity, and environmental sustainability of tasar sericulture in a changing climate.

Keywords: Tasar sericulture, Antheraea mylitta, biodiversity conservation, climate variability, host plant diversity, ecosystem resilience, sustainable sericulture, forest – based livelihoods.

Presentation code: 13

COMPARATIVE ASSESSMENT OF EARTHWORM DIVERSITY AND COMMUNITY STRUCTURE UNDER CHEMICAL AND ORGANIC FARMING SYSTEMS

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ABSTRACT

Earthworms are recognized as soil ecosystem engineers whose diversity and functional activity are highly sensitive to present conventional agricultural management practices. Intensive chemical farming, characterized by repeated applications of synthetic fertilizers and pesticides, has been reported to reduce earthworm abundance, biomass, and species richness, thereby impairing soil aggregation and nutrient cycling (Pelosi et al., 2014; Miglani et al., 2020). In contrast, organic systems that incorporate compost, crop residues, and reduced pesticide use tend to enhance earthworm populations and associated ecosystem services (Fonte et al., 2023). The present study comparatively evaluates earthworm diversity, density, biomass, and functional groups in chemically managed and organically cultivated fields across replicated sites. Field sampling was conducted using hand-sorting and mustard expellant extraction methods (1 m² quadrats), followed by taxonomic identification and classification into epigeic, endogeic, and anecic groups. Soil physico-chemical parameters including pH, electrical conductivity, organic carbon, available NPK, and moisture were analyzed to determine their relationships with earthworm communities. Additionally, laboratory bioassays assessed sub-lethal effects of commonly used agrochemicals on survival and cocoon production. Results indicated significantly higher species richness, Shannon diversity index, and biomass in organic fields compared to chemically treated soils. Chemical farming sites exhibited reduced abundance and dominance of stress-tolerant taxa, correlated with lower organic carbon and higher pesticide exposure. These findings underscore the ecological costs of intensive agrochemical inputs and highlight organic management as a sustainable alternative for conserving soil biodiversity. Long-term monitoring integrating biological and chemical indicators is recommended to support resilient agro-ecosystems for sustainable agriculture and food security.

Keywords: Chemical farming, earthworm diversity, soil parameters, sustainable agriculture.

Presentation code: 16

SACRED AND SUSTAINABLE: ROLE OF MADHUCA LONGIFOLIA VAR. LATIFOLIA (MAHUA, IPPA) AS A MULTIPURPOSE FOREST ELEMENT IN TELANGANA, INDIA

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ABSTRACT

Madhuca longifolia var. latifolia (Roxb.) *A. Chev.* [=*Madhuca indica*, Sapotaceae: Mahua, ippa] is an socio-economically and ecologically significant multipurpose forest tree species that widely distributed in the dry deciduous forests of Telangana, India. It plays a pivotal role in sustaining rural and tribal livelihoods, particularly among forest-dependent communities. The ethnic people do not cut mahua tree, as this regarded as a sacred tree and the belief promotes in-situ conservation and ensuring sustainable use. The tree provides a wide range of non-timber forest products (NTFPs), including flowers (corolla), fruits, seeds and leaves. The flowers, rich in fermentable sugars, are traditionally used for food, beverage preparation (local liquor, ippa sara), nutraceuticals, and while the seeds yield oil which is being used in cooking, worship, medicine, candle making, soap making, and biofuel industries. Various plant parts possess significant medicinal properties such as anti-inflammatory, antimicrobial, antioxidant, and therapeutic activities. The wood of mahua serves as fuel, for agricultural implements and seed cake as fodder. It contributes to ecological stability by improving soil fertility, supporting biodiversity, shelter to many wildlife and serving as a drought- and fire-resistant component in forest ecosystem. In Telangana, mahua holds cultural, livelihood significance and forming an integral part of traditional knowledge. Unfortunately, research and educational institutions have not been able to address the actual potential of this tree in NTFP sector at ground level till now. Despite its immense potential, the species remains underutilized in organized sectors, necessitating scientific interventions for value addition, conservation, and sustainable management. It is highly important tree species to generate commerce, socio-economic upliftment of tribal people that is regarded as sustainable multipurpose tree species (MPTS) with economic, ecological and cultural importance in Telangana State.

Presentation code: 33

QUALITATIVE AND QUANTITATIVE TYPOGRAPHY OF SOIL MICRO ARTHROPODS

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ABSTRACT

Thus an attempt was made to observe and investigate different ecosystems, analysis of the structure and community of several groups of soil micro arthropods in relation to the seasonal variation in the abiotic environment in three fields and the role of these soil micro arthropods in the litter decomposition nutrient cycling. Interaction of biological, chemical and physical characteristics with each other and a wide range of biotic communities mainly depend on the below and above vegetation type of the true soil layers. The macro and micro arthropods communities act as biological characteristics. In this present study investigations were conducted on the effects of Herbicides, Fungicides and Insecticides, all groups of pesticides on qualitative and quantitative typography of soil micro arthropods associated with Cotton and Capsicum fields. This process was aiming of field level study on the special role of these soil microarthropod diversity, population fluctuation and population density during the two cultivation seasons particularly loss of several microarthropod populations in relation with pesticides application.

Key words: soil micro arthropods, biotic, population

Presentation code: 41

CONSERVATION AND SUSTAINABLE MANAGEMENT OF BIODIVERSITY ASPECTS - A CASE STUDY OF FOREST ECOSYSTEM

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ABSTRACT

Forest ecosystems function as complex biological networks where visible biodiversity is strongly supported by an invisible yet highly diverse microbial community. This case study explores the conservation and sustainable management of biodiversity in forest ecosystems with a special focus on microbial diversity. Microorganisms such as soil bacteria, fungi, and actinomycetes play a fundamental role in ecosystem functioning by regulating nutrient cycling, organic matter decomposition, soil formation, and plant–microbe interactions. Forest soils and leaf litter provide ideal conditions for diverse microbial populations that contribute to ecosystem resilience and productivity. However, increasing anthropogenic pressures such as deforestation, land-use change, pollution, and climate variability threaten the stability of both macro- and micro-biodiversity. Understanding microbial diversity is therefore essential for developing effective biodiversity conservation strategies. Sustainable forest management practices, including habitat protection, controlled resource use, and ecological monitoring, can help maintain microbial balance and support long-term ecosystem sustainability. This case study highlights the ecological significance of forest microorganisms and emphasizes their role in maintaining biodiversity and environmental health.

Keywords: Biodiversity Conservation, Microbial Diversity, Forest Ecosystems, Soil Microorganisms, Biogeochemical Cycles, Carbon Sources, Temperature, Environmental Sustainability.

Presentation code: 44

IMPACT OF SOUTH-EASTERN FLORA ON BIODIVERSITY OF TELANGANA

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ABSTRACT

Flora plays a fundamental role in maintaining ecological balance and supporting biodiversity in terrestrial ecosystems. The south-eastern region of Telangana is rich in plant diversity due to varied climatic conditions, soil types, and forest ecosystems. Districts such as Hanmakonda, Warangal, Mulugu, Jayashankar Bhupalpally, Karimnagar, and Khammam contain diverse vegetation ranging from dry deciduous forests to agricultural and semi-urban landscapes. This study focuses on the impact of south-eastern flora on biodiversity in selected regions of Telangana, particularly Hanmakonda and Warangal districts. The objective is to analyze plant diversity and evaluate its ecological importance in sustaining regional biodiversity. Information was collected through field observations, literature surveys, and regional botanical records. The vegetation includes forest trees, medicinal plants, and commonly cultivated agricultural crops that contribute to ecological stability and provide habitats for various organisms. Important medicinal plants identified include *Azadirachta indica* (Neem), *Ocimum tenuiflorum (Tulsi), Aloe vera, Withania somnifera (Ashwagandha), Tinospora cordifolia (Guduchi), Phyllanthus emblica (Amla), and Curcuma longa (Turmeric).* These are widely used in traditional medicine and local healthcare practices. Additionally, widely grown agricultural plants such as Mangifera indica (Mango), Tamarindus indica (Tamarind), Cocos nucifera (Coconut), Ficus religiosa (Peepal), Ficus benghalensis (Banyan), Moringa oleifera (Drumstick tree), Oryza sativa (Rice), Zea mays (Maize), and Gossypium species (Cotton) support biodiversity by providing food, shelter, and ecological services for many organisms.

Keywords: Cotton flora, Medicinal plants, Soil microorganisms, AHM.

Presentation code: 51

MINING THE DEEP COULD MUTE THE SONGS OF SPERM WHALES

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ABSTRACT

Deep-sea mining in the Clarion-Clipperton Zone (CCZ) of the eastern Pacific Ocean targets polymetallic nodules rich in nickel, cobalt, copper, and manganese, essential for green technologies, but poses severe risks to sperm whale (Physeter macrocephalus) populations through noise pollution and habitat disruption. This study investigates how intensive mining operations involving heavy machinery, sediment plumes, and continuous anthropogenic noise could mask sperm whales' complex coda clicks, codas, and songs critical for social communication, foraging, navigation, and reproduction in their deep-diving habitats exceeding 1,000 meters. A comprehensive literature review and analysis of recent expeditions, including a 13-day Greenpeace Arctic Sunrise survey in the CCZ, documented 74 acoustic detections and sightings of sperm whales, Risso's dolphins, common dolphins, and unidentified delphinids, confirming their presence in mining-proposed areas. Quantitative assessments reveal that mining-generated noise, propagating hundreds of kilometers via ocean sound channels, overlaps with whales' sensitive frequency bands (often 5-30 kHz), potentially causing behavioral disruptions, displacement from foraging grounds, and long-term population declines. Sediment plumes may further exacerbate impacts by altering deep-sea food webs, indirectly affecting prey availability like squid and fish. Visualizations from mining survey graphs illustrate affected zones overlapping whale migration corridors. This research highlights extensive, potentially irreversible ecological damage, urging stringent environmental impact assessments, international moratoriums, and sustainable alternatives to nodule extraction to safeguard these vulnerable mega fauna and abyssal biodiversity.

Key words: Deep-sea mining, sperm whale songs, Clarion-Clipperton Zone, noise pollution, poly metallic nodules, cetacean communication, sediment plumes, marine biodiversity, anthropogenic impacts, CCZ ecosystem.

Presentation code: 63

ECOLOGICAL AND BEHAVIOURAL STUDY OF CHIROPTERA (MEGA AND MICRO BATS)

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ABSTRACT

Any member of the only class of mammals with the ability to fly is a bat (order Chiroptera).The order is typically separated into two distinct suborders: the Microchiroptera (little bats found all over the world) and the Megachiroptera (the giant Old World fruit bats). The majority of bats are insectivorous, and humans rely on them mostly for seed dispersal, pollination, and insect predation. Others consume fruit and help spread seeds, but in some situations, bananas and figs need to be harvested early or covered with nets to keep fruit eating bats away. The guano (droppings) of insectivorous bats is still used for agricultural fertilizer in many countries. Large bat colonies frequently live in monuments and public structures in tropical areasandtrees drawing attention due to their collective odor, guano, and noise. Although many bats have very specific roost requirements in terms of light, temperature, and humidity, their distribution is restricted. Bats pick a range of daytime roosts. Although this changes according on sex, season, and reproductive activity, each species prefers a specific type of roost. Many families of bats use their hind feet, wrists, and thumbs to walk or crawl on both horizontal and vertical surfaces. Many may easily move forward or backward, making it easy to enter and exit cracks. Microchiroptera bats use echolocation, or "sonar," to locate themselves acoustically. They listen to the echoes coming back from nearby objects while emitting brief highfrequency sound pulses that are often well above human hearing. Bats use echolocation to recognize and follow insects while they are in flight. Bats have been the focus of negative tales in Western society, yet in other parts of the Orient, these animals are associated with pleasure, long life, and good fortune.

Presentation code: 71

DIVERSITY OF ARTHROPODS IN NARSAMPET MANDAL OF WARANGAL DISTRICT, TELANGANA

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ABSTRACT

Soil arthropods play an important role in maintaining and sustaining soil health and ecosystem productivity. Acari, collembolan, symphylan, millipedes, termites and ants are the main organisms involved in decomposition, comminution, activation of microbial activities, bioturbation, humification and regulation of nutrient losses. Arthropods also provide provisional, supporting and regulating services. the Arthropod fauna was collected by pit fall trapping for estimating the abundance and diversity of the fauna obtained during the period 2024-25. The observed orders are Aranea (33%), Diptera (12%), Orthoptera (14%), Collembola (21%), Hymenoptera (Red ants) (9%), Hymenoptera (Black ants) (8%), Isoptera (1%), Hymenoptera (wasp) (1%), Coleoptera (0.5%) and Hemiptera (0.5%).The dominance order is Aranea and followed by Collembola, Orthoptera, Diptera, Hymenoptera (Red ants), Hymenoptera (Black ants), Isoptera, Hymenoptera, Coleoptera and Hemipteran throughout the study period. The highest number of Arthropods were recorded in Maize field and followed by Cotton and Mirchi fields respectively. Agricultural intensification reduces taxonomic richness and diversity across taxonomic groupings, having the greatest negative impact on soil biota. When compared to the natural landscape, agricultural management operations such as tillage, fertilizer, pesticide and reduced crop diversity have a negative effect on biotic composition and abundance. In the present results the reduced number of arthropods in the Mirchi field is because of greatest application of pesticides.

Key words: pitfall, arthropod, diversity and collembola

Presentation code: 78

MINING THE DEEP COULD MUTE THE SONGS OF SPERM WHALES

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ABSTRACT

Deep-sea mining in the Clarion-Clipperton Zone (CCZ) of the eastern Pacific Ocean targets polymetallic nodules rich in nickel, cobalt, copper, and manganese, essential for green technologies, but poses severe risks to sperm whale (Physeter macrocephalus) populations through noise pollution and habitat disruption. This study investigates how intensive mining operations involving heavy machinery, sediment plumes, and continuous anthropogenic noise could mask sperm whales' complex coda clicks, codas, and songs critical for social communication, foraging, navigation, and reproduction in their deep-diving habitats exceeding 1,000 meters. A comprehensive literature review and analysis of recent expeditions, including a 13-day Greenpeace Arctic Sunrise survey in the CCZ, documented 74 acoustic detections and sightings of sperm whales, Risso's dolphins, common dolphins, and unidentified delphinids, confirming their presence in mining-proposed areas. Quantitative assessments reveal that mining-generated noise, propagating hundreds of kilometers via ocean sound channels, overlaps with whales' sensitive frequency bands (often 5-30 kHz), potentially causing behavioral disruptions, displacement from foraging grounds, and long-term population declines. Sediment plumes may further exacerbate impacts by altering deep-sea food webs, indirectly affecting prey availability like squid and fish. Visualizations from mining survey graphs illustrate affected zones overlapping whale migration corridors. This research highlights extensive, potentially irreversible ecological damage, urging stringent environmental impact assessments, international moratoriums, and sustainable alternatives to nodule extraction to safeguard these vulnerable mega fauna and abyssal biodiversity.

Key words: Deep-sea mining, sperm whale songs, Clarion-Clipperton Zone, noise pollution, poly metallic nodules, cetacean communication, sediment plumes, marine biodiversity, anthropogenic impacts, CCZ ecosystem.

Presentation code: 90

ALL INDIA TIGER ESTIMATION 2026 (AITE-2026): AN OVERVIEW OF INDIA'S LARGEST WILDLIFE MONITORING PROGRAMME

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ABSTRACT

The tiger is a powerful icon of conservation in forested ecosystems. The Government of India has leveraged the iconic status of the tiger to promote conservation of biodiversity, ecosystem functions, goods and services by launching Project Tiger in 1972, subsequently gazetting tiger reserves through legislation and allocating appropriate resources for their conservation. The nationwide monitoring initiative known as the All India Tiger Estimation (AITE) is conducted every four years to assess tiger population size, distribution, habitat condition and prey availability across the country. The All India Tiger Estimation 2026 represents the sixth cycle of large-scale wildlife survey and is expected to integrate advanced technologies with traditional field-based ecological methods. AITE-2026 combines sign surveys, line-transect sampling, camera trapping, genetic analysis and geospatial modelling to generate accurate estimation of tiger population and evaluate ecosystem health. The survey covers more than 400,000 km² of forest landscapes across India and involves tens of thousands of forest staff and wildlife researchers. This article provides an overview of the objectives, methodology, phases, technological innovations and conservation significance of AITE-2026.

Key words: Tiger Conservation, Project Tiger, Tiger Reserves, Camera Trapping, Sign Surveys

Presentation code: 104

TRADITIONAL MEDICINAL USES OF MEDICINAL PLANTS IN KAKATIYA UNIVERSITY, WARANGAL, TELANGANA STATE

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ABSTRACT

Medicinal plants have long been an integral part of traditional healthcare systems, particularly in India where indigenous knowledge is preserved through generations. The main objective of this study was to identify medicinal plant species, document their traditional uses, and analyze their distribution based on plant families, parts used, and medicinal applications. A systematic field survey was conducted across different locations of the campus, where plant specimens were collected, photographed, and identified using standard botanical references. Ethnobotanical information was gathered from literature sources and local traditional knowledge, and data were organized into tabular and analytical formats. A total of 37 medicinal plant species belonging to various families were recorded with Fabaceae (16.21%) being the dominant family. Plant part analysis indicated that leaves were the most frequently used part (31.80%). The medicinal use analysis showed that the highest proportion of plants (27.02%) were used for the skin, hair and dental problems. The study concludes that traditional medicinal plants play a crucial role in primary healthcare and biodiversity conservation. Documentation and analysis of such knowledge can support future pharmacological research and sustainable utilization of plant resources.

Key words:
Medicinal plants, Ethnobotany, Traditional knowledge, Kakatiya University, Plant diversity, Herbal medicine, Biodiversity conservation.

Presentation code: 107

STUDY ON AQUATIC BIRDS OF VRINDAVAN, MATHURA, UTTAR PRADESH, INDIA

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ABSTRACT

Aquatic birds are those birds, which live in and around water medium or on shores. They feed on mud, sand for aquatic insects, arthropods. Mathura city is well surrounded by riverine systems (Yamuna River) and has multiple wetlands with a long stretch of shoreline around Yamuna River. Waders are found in these aquatic bodies and shores. The species of different families were found in the study period. The Yamuna River, particularly in the Vrindavan-Mathura region, serves as a critical habitat supporting diverse avian communities. In this study, it is found that across the riverine areas of Mathura, with the family Anatidae emerging as the most dominant. The findings underscore the ecological significance of avian diversity, highlighting their role in essential ecosystem services such as pollination, seed dispersal, and nutrient recycling. Birds act as bioindicators, making their presence and diversity vital for ecological assessment and monitoring river health. The study emphasizes the urgent need for conservation strategies to safeguard these species and their habitats against anthropogenic pressures, ensuring the sustainability of the Yamuna River ecosystem.

Key words: Pollutants, Contaminated water, Aquatic avian fauna, Vrindavan-Mathura city, waders and shorebirds

Presentation code: 129

ANTHROPOGENIC PRESSURES ON WILDLIFE HABITATS: AN ECOLOGICAL ASSESSMENT OF ENVIRONMENTAL STRESSORS AND BIODIVERSITY LOSS

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ABSTRACT

Anthropogenic activities have fundamentally altered the Earth's biosphere, leading to unprecedented levels of environmental stress on wildlife habitats. This ecological assessment explores the multifaceted nature of anthropogenic pressures—including habitat fragmentation, land-use change, pollution, and climate change—and their cumulative impact on global biodiversity. As human populations expand and industrial demands increase, natural landscapes are increasingly transformed into fragmented patches, isolating species and disrupting critical ecological processes such as gene flow, migration, and nutrient cycling. The study categorizes environmental stressors into direct and indirect drivers of biodiversity loss. Direct stressors, such as deforestation for agriculture and infrastructure development, result in immediate habitat destruction. Indirect stressors, including the introduction of invasive species and chemical runoff, degrade the quality of remaining habitats, rendering them unsuitable for specialist species. By employing various ecological indicators and spatial analysis, this assessment highlights the narrowing threshold of resilience within diverse ecosystems. The findings indicate a strong correlation between the intensity of human interference and the rate of local extinctions, with apex predators and specialized endemic species being the most vulnerable to these shifts. Furthermore, the research emphasizes the role of environmental toxicology and pollution as silent drivers of population decline. Persistent organic pollutants and heavy metals bioaccumulate through trophic levels, compromising the reproductive success and physiological health of wildlife. This ecological degradation not only threatens individual species but also destabilizes ecosystem services that are vital for human survival, such as water purification and carbon sequestration. In conclusion, the assessment calls for an integrated conservation framework that moves beyond isolated protected areas. It advocates for the restoration of ecological corridors, the implementation of sustainable land-management practices, and the enforcement of stringent environmental regulations to

mitigate human-induced stressors. Addressing these anthropogenic pressures is essential for halting the current trajectory of biodiversity loss and ensuring the long-term functional integrity of the world's natural habitats.

Key Words:
Anthropogenic Impact, Habitat Fragmentation, Biodiversity Loss, Ecological, Resilience, Environmental Stressors, Conservation Biology.

Theme-4:

BIOINFORMATICS AND COMPUTATIONAL BIOLOGY

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Presentation code: 1

BIOINFORMATICS AND COMPUTATIONAL BIOLOGY: INTEGRATIVE TOOLS AND APPROACHES FOR DECODING BIOLOGICAL COMPLEXITY

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ABSTRACT

The rapid development of high-throughput experimental technologies has led to an unprecedented accumulation of biological data across genomics, transcriptomics, proteomics, and metabolomics. Managing and interpreting these complex datasets has become a critical challenge in contemporary biological research. Bioinformatics and computational biology have emerged as integrative disciplines that combine biological knowledge with computational, mathematical, and statistical methodologies to transform large-scale data into meaningful biological insights. These fields extend beyond data processing and play a central role in modelling biological systems, identifying functional patterns, and predicting molecular behaviour. This concept paper presents an integrative framework illustrating the relationship between biological data sources, computational tools, and application domains. Key approaches such as sequence analysis, structural bioinformatics, machine learning–based analytics, and systems biology modeling are highlighted as interconnected components of a unified analytical pipeline. These methods collectively support functional annotation, network-level interpretation, and predictive modeling of biological processes. The proposed framework emphasizes applications in genomics, precision medicine, drug discovery, biotechnology, and evolutionary biology, demonstrating how computational approaches accelerate discovery and support translational research. The paper also addresses current challenges associated with data heterogeneity, scalability, and interpretability of computational models, particularly those based on artificial intelligence. Future perspectives highlight the importance of multi-omics integration, explainable artificial intelligence, and standardized computational infrastructures to enhance biological understanding. Overall, this concept-driven overview underscores the essential role of bioinformatics and computational biology in decoding biological complexity and advancing data-driven research in life sciences, biotechnology, and medicine worldwide.

Keywords: Bioinformatics; Computational biology; Integrative framework; Multi-omics; Systems biology; Precision medicine

Presentation code: 11

ANTI-HIV POTENTIAL OF NOVEL COMPOUNDS AS HIV-1 REVERSE TRANSCRIPTASE INHIBITORS: A COMPUTATIONAL APPROACH

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ABSTRACT

Human Immunodeficiency Virus (HIV) is the etiological agent of Acquired Immunodeficiency Syndrome (AIDS) that has created a major health care problem not only in India but also globally. HIV/AIDS continues to be one of the major challenges before the scientific community. Currently, the treatment is focused on highly active antiretroviral therapy (HAART), and its complications are multifarious, prolonged, and expensive. To solve the issues related to the difficulties in bringing better anti-HIV agents to the market, several drug development strategies have been undertaken for decades. The main objective of this study is to perform in silico screening of phytochemicals and validate the anti-HIV candidates in vitro. To identify the HIV reverse transcriptase inhibitors by in silico method and to evaluate the anti-HIV activity of selected phytochemicals by in vitro. Through the literature survey and the construction of a phytochemical library, promising hits of the HIV-1 targets identified. Selected phytochemicals screened to check their anti-HIV efficacy by using molecular docking .The determination of the anti-HIV activity of the in silico hits will be carried out by an MTT assay in PBMC cells. The docking showed that ursolic acid and betulinic acid exhibited strong binding affinity with key residues Trp 229, Lys 103, Tyr 188, Glu 138, Tyr 181, and Val 179; binding energies were comparable to the standard drug efavirenz. The result of this study is the need for clinical trends in the treatment of HIV infection and to develop economically viable drugs for human use and develop new therapeutic approaches.

Key words:
HIV- 1RT, betulinic acid, energy, efavirenz, therapeutic, PBMC cells, MTT assay

Presentation code: 38

COMPUTATIONAL DOCKING ANALYSIS FOR IDENTIFYING NATURAL INHIBITORS OF TEM-1 B-LACTAMASE

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ABSTRACT

TEM-1 β-lactamase is a class A enzyme widely distributed among pathogenic bacteria and plays a major role in the hydrolysis of β-lactam antibiotics, contributing to antibiotic resistance. In bacteria like Escherichia coli, Klebsiella pneumoniae, and Haemophilus influenzae, the TEM gene produces this enzyme, making drugs such as ampicillin ineffective. The present study investigated the inhibitory potential of a flavonoid-derived phytocompound against this enzyme using computational molecular docking analysis. The interaction between TEM-1 β-lactamase and Eupatin -flavonoid derived compound was evaluated and compared with the reference inhibitor Clavulanic acid. The reference inhibitor showed binding energies ranging from −4.7 to −6.5 kcal/mol, while the phytocompound demonstrated a stronger binding affinity with a docking score of approximately −7.35 kcal/mol. The ligand was found to occupy the catalytic pocket of the enzyme and formed stable interactions with key active-site residues, indicating its potential to inhibit TEM-1 β-lactamase activity. Overall, the results suggest that this phytocompound may serve as a promising lead candidate for the development of new β-lactamase inhibitors. However, additional studies such as molecular dynamics simulations, pharmacokinetic analysis, and experimental validation are required to further confirm its stability and therapeutic potential in combating β-lactamase-mediated antibiotic resistance.

Keywords:
Antibiotic resistance, TEM-1 β-lactamase, Molecular docking, In silico.

Presentation code: 61

IN-SILICO INVESTIGATION OF LIGAND BINDING INTERACTIONS WITH PDK1 PROTEIN USING MOLECULAR DOCKING

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ABSTRACT

Molecular docking is a computational approach widely used in drug discovery to predict the interaction between small molecules and target proteins. In the present study, molecular docking analysis was performed to investigate the binding affinity and interaction patterns of selected ligands with the protein structure 1W1G, a key component associated with the PDK1 signaling pathway. The three-dimensional structure of the target protein was obtained from the Protein Data Bank, and docking simulations were carried out using Autodock tools. Prior to docking, the protein structure was prepared by removing water molecules and adding necessary hydrogen atoms, while ligands were optimized to ensure proper geometry. Both blind docking and active site-based docking approaches were explored to identify potential binding pockets and interaction residues. The docking results revealed favorable binding interactions between the ligand molecules and specific amino acid residues within the binding region, including hydrogen bond interactions with residues such as Val542. The binding energy scores suggested stable ligand-protein complexes, indicating potential inhibitory activity against the target protein. These findings demonstrate the usefulness of molecular docking as a preliminary tool for understanding molecular interactions and guiding further experimental studies in drug discovery and molecular biology.

Presentation code: 68

MACHINE LEARNING APPLICATIONS IN GENOMIC DATA ANALYSIS

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ABSTRACT

The development of high throughput sequencing technologies has resulted in rapid growth in genomic data. Analyzing and interpreting this large volume of data has become a major barrier for researchers. Machine learning, a branch of artificial intelligence has evolved as an effective computational approach for handling complex biological datasets and extracting meaningful patterns from genomic information. Machine learning tools such as decision trees, random forests, support vector machines and neural networks are extensively used in genomic research. These tools help in tasks such as genome annotation, gene prediction, classification of gene expression patterns and identification of regulatory sequences. By learning from large datasets, machine learning models can identify relationships within genomic data that may not be effectively detected through traditional analytical methods. Machine learning plays an important role in identifying genetic variations associated with diseases. It is widely used in areas such as biomarker discovery, personalized medicine and prediction of disease susceptibility. Advanced approaches such as deep learning further enhance the analysis of complex genomic structures and interactions, contributing to a better understanding of biological systems. Overall, machine learning provides important tools for managing and interpreting genomic data. Its integration with bioinformatics and computational biology has significantly improved the efficiency and accuracy of genomic research. The continued development of machine learning methods is expected to accelerate discoveries in genomics and support the advancement of precision medicine and biological research.

Keywords: Machine Learning, Genomics, Bioinformatics, Gene Prediction, Genomic Data Analysis, Artificial Intelligence.

Presentation code: 73

STRUCTURE-BASED IN-SILICO DISCOVERY OF INHIBITORS AGAINST RV1422 (CUVA) OF MYCOBACTERIUM TUBERCULOSIS

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ABSTRACT

Tuberculosis disease caused by Mycobacterium tuberculosis yearly causes millions of deaths. The front-line anti-TB drugs, isoniazid, rifampin, streptomycin, ethambutol and pyrazinamide are becoming less effective due to emergence of multi-drug resistance pathogens which demands for urgent finding of new drugs. In this situation, Rv1422 is emerging as a new drugs target in Mycobacterium tuberculosis, because of its critical roles in carbon sources utilization for optimal growth, cell wall development regulation & virulence. Rv1422 is shown to utilize UDP-N-acetylglucosamine during cell wall development in Mycobacterium tuberculosis. Inhibition of this function of Rv1422 may leads to impair the growth or death of bacteria. Here, computational approach has been adopted to find Rv1422 inhibitors. From ChEMBL35 database, 2.74 million compounds were retrieved and using filters such as: Lipinski's rule of five, REOS, PAINS, followed by Butina clustering to remove redundancies and ADMET (cut off score 0.9), nearly 52,000 compounds were selected for molecular docking against the cavity of Rv1422 using AutoDock Vina. Again after re-docking, top ten compounds, bound with Rv1422, were selected for MD simulations, using GROMACS package for 100 ns. Analysis of the dynamics of those protein-ligand complexes has revealed mostly similar binding affinities compared to UDP-N-acetylglucosamine while two ligands have displayed higher binding affinities. These two ligands can be chosen as potential drug compounds for further in-vitro binding study with Rv1422 and in-vivo effects on pathogen in future.

Keywords:
Tuberculosis, Rv1422, Virtual Screening, MD Simulatio

Presentation code: 82

A BIOINFORMATICS EXPLORATION OF DIFFERENTIALLY EXPRESSED GENES AND MOLECULAR MECHANISMS IN THE DEVELOPMENT OF INVASIVE DUCTAL BREAST CARCINOMA

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ABSTRACT

Breast cancer is one of the most common malignancies in women and a major health concern worldwide, involves diverse molecular subtypes and complex gene expression patterns. Early detection through regular screening significantly improves survival rates. This study aimed to explore differential expressed genes and molecular mechanisms that associated with invasive ductal breast carcinoma via an integrated bioinformatics approach. Gene expression profiles of GSE72297 was retrieved from Gene Expression Omnibus database (GEO) to identify common differentially expressed genes (DEGs) using the GEO2R tool led to the identification of 551 differentially expressed genes (DEGs) including 124 up-regulated and 427 down-regulated. Then, Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analyses were performed through Enrichr tool and were able to shed light on the involvement of these DEGs in chemokine activity, collagen-containing extracellular matrix, cellular response to tumor necrosis factor, TNF signaling pathway, Chemokine signaling pathway, IL-17 signaling pathway etc. which are crucial in breast cancer pathogenesis. Moreover, a protein–protein interaction (PPI) network of the DEGs was constructed through String database. On this basis, hub genes from critical PPI sub networks were explored utilizing Cytoscape and Cytohubba software's, revealing densely interconnected gene clusters with potential prognostic significance. The protein–protein interaction network analysis highlighted 10 hub genes: CCL5, CCL2, CXCL1, CXCL8, CXCL6, CXCL5, CXCL2, ELN, LEP and LOXL3. Furthermore, validation of the hub gene expression and their association with overall survival was performed using GEPIA2. Kapplan-Meier analysis results showed that these hub genes were highly related to the overall survival of patients. This study provides a detailed view of the underlying molecular mechanisms in invasive ductal breast carcinoma, suggesting potential biomarkers and therapeutic targets.

Presentation code: 85

STRUCTURAL MODELLING AND BIOINFORMATIC ANALYSIS OF RAS85D IN DROSOPHILA MELANOGASTER

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ABSTRACT

The Ras family of small GTPases plays a central role in regulating cell growth, differentiation and survival. Mutations in Ras genes is strongly associated with tumorigenesis. The Ras85D in Drosophila melanogaster is an ortholog of the Human KRAS onco gene and serves as an important model for studying Ras-mediated signalling pathways. In the present study, an insilico bioinformatics approach was employed to predict and analyze the three-dimensional structure of the Ras85D protein. The amino acid sequence of Ras85D was retrieved from public protein databases and subjected to computational structural modeling using homology based protein modeling tools. The predicted protein model was constructed using structurally related Ras family templates and subsequently refined to obtain a stable confirmation. Structural validation and quality assessment were performed to evaluate stereochemical quality and model reliability. The predicted model revealed conserved GTP-binding domains and structural motifs characteristic of Ras GTPases, indicating strong functional conservation. These findings provide insights into the structural architecture of Ras85D and support the use of Drosophila melanogaster as a model for studying Ras- mediated oncogenic pathways.

Presentation code: 87

IDENTIFICATION OF POTENTIAL NATURAL ACETYLCHOLINESTERASE INHIBITORS THROUGH MOLECULAR DOCKING FOR ALZHEIMER'S DISEASE THERAPY

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ABSTRACT

Alzheimer's disease is a progressive neurodegenerative disorder characterised by cognitive impairment and memory loss, primarily associated with the degeneration of cholinergic neurons. Inhibition of Acetylcholinesterase (AChE) is considered an effective therapeutic strategy to enhance cholinergic neurotransmission and alleviate the symptoms of the disease. In the present study, molecular docking simulations were performed to evaluate the inhibitory potential of eight selected phytochemicals against AChE. The docking analysis was conducted to investigate the binding affinity and interaction patterns of these compounds within the active site of the enzyme. Among the screened phytochemicals, 6,7-Dimethoxy-4-phenylcoumarin exhibited the highest binding affinity with a binding energy of −8.9 kcal/mol, indicating the formation of a stable enzyme–ligand complex. Detailed interaction analysis revealed that the compound forms a hydrogen bond interaction with Tyr72, along with significant hydrophobic interactions involving Tyr341, Trp286, and Leu76 within the active gorge of AChE. These residues play an important role in ligand stabilisation at the peripheral anionic site and within the aromatic gorge of the enzyme. The docking results were further compared with the standard AChE inhibitor Donepezil, which demonstrated a similar binding energy and interaction pattern with key active-site residues, including Tyr72, Trp286, Tyr341, Tyr337, and Val294. In addition to the top-ranked compound, the remaining seven phytochemicals also exhibited favourable binding affinities ranging from −7.3 to −8.9 kcal/mol, indicating significant interaction with the active site of AChE and suggesting their potential inhibitory activity. These findings highlight 6,7-Dimethoxy-4-phenylcoumarin and the other screened phytochemicals as promising natural inhibitors of AChE, which may serve as potential lead compounds for the development of alternative therapeutic agents for the management of Alzheimer's disease. However, further in vitro and in vivo studies are required to validate their pharmacological efficacy and safety.

Keywords: Alzheimer's disease, Acetylcholinesterase (AChE), molecular docking, Donepezil

Presentation code: 91

BIOINFORMATICS DRIVEN INSIGHTS INTO BREAST CANCER: FROM MOLECULAR SIGNATURES TO PERSONALIZED THERAPY

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ABSTRACT

Recent advances in breast cancer research have increasingly integrated bioinformatics to enhance understanding of disease mechanisms and improve therapeutic strategies. Bioinformatics tools facilitate the analysis of large-scale genomic, transcriptomic, and proteomic datasets, enabling the identification of molecular signatures and biomarkers associated with breast cancer subtypes, progression, and treatment response. Emerging trends emphasize the use of machine learning algorithms and networkbased approaches to predict patient prognosis, drug resistance, and potential therapeutic targets with higher accuracy.High-throughput sequencing technologies combined with bioinformatics analyses have revolutionized the characterization of tumor heterogeneity, allowing for more precise molecular classification and personalized treatment plans. Additionally, integrative bioinformatics approaches are employed to decipher complex interactions within tumor microenvironments, including immune cell infiltration and signaling pathways, which are critical for developing immunotherapies and combination treatments. Recent studies also focus on the application of multi-omics data integration to uncover novel regulatory mechanisms and identify key drivers of breast cancer metastasis. The use of bioinformatics pipelines for drug repurposing and virtual screening accelerates the discovery of effective therapeutic agents, reducing the time and cost associated with traditional drug development.Overall, the convergence of bioinformatics and breast cancer research fosters a data-driven paradigm that enhances diagnostic accuracy, prognostic assessment, and therapeutic innovation. This multidisciplinary approach holds significant promise for advancing precision oncology, ultimately improving clinical outcomes and patient management in breast cancer care.

Keywords: Brest Cancer; Bioinformatics; Drug Resistance; Therapeutic innovation; Biomarkers

Presentation code: 93

COMPUTATIONAL SCREENING OF PROBIOTIC STRAINS FOR NEUROTRANSMITTER PRODUCING POTENTIAL IN THE GUT-BRAIN AXIS

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ABSTRACT

Mental health disorders, including anxiety, depression, and cognitive decline, are increasingly recognized as major global public health concerns. Conventional pharmacological treatments often address symptoms only after they appear and may be associated with adverse effects, underscoring the need for preventive and alternative approaches. The gut-brain axis has emerged as a critical pathway linking gastrointestinal microbiota with neurological function. Certain probiotics, referred to as psychobiotics, can influence mental health by producing neuroactive compounds such as gamma-aminobutyric acid (GABA), as well as precursors for serotonin and dopamine. However, many commercially available probiotic strains have not been systematically evaluated for their ability to produce these neurotransmitter-related compounds, limiting their targeted use in mental health interventions. This project applies a computational and bioinformatics-based strategy to screen commonly used probiotic strains for their potential to synthesize neuroactive molecules. Public genomic data from selected strains, including Lactobacillus and Bifidobacterium species were analyzed to identify genes involved in neurotransmitter biosynthesis pathways. Metabolic pathway mapping combined with gene presence and copy number analysis was used to develop a quantitative scoring framework that enables comparative evaluation of different strains. The results were presented through heatmaps and pathway diagrams, offering a visual and analytical method to identify strains with higher predicted psychobiotic potential.

Keywords: Psychobiotics, Gut-brain Axis, Neurotransmitter Production, Computational Screening, Mental Health

Presentation code: 130

INVESTIGATING SHRIMP-CYANOBACTERIA INTERACTIONS: MOLECULAR DOCKING AND PHARMACOKINETIC PREDICTION OF NON-PEPTIDE COMPOUNDS TARGETING ANTI LIPOPOLYSACCHARIDE FACTOR AND ARGININE KINASE

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ABSTRACT

Hypersaline ecosystems, such as solar salterns, remain understudied in a South Asian context. This research investigates the microalgal diversity and ecological interactions within the Marakkanam solar salterns, located in the Villupuram district of Tamil Nadu, India. During the low-production season in December 2022, water and cyanobacterial samples were collected from three distinct ponds. Microalgal community analysis revealed the presence of 18 species, with Bacillariophyta (diatoms) being the most dominant group (40% relative abundance), followed by Cyanophyta (33. 3%) and Chlorophyta (26%). Notably, resident shrimp populations inhabiting waters dominated by cyanobacterial blooms exhibited significant immunological disruption, characterized by the marked up-regulation of C-type lectins (CTLs) and the concurrent down-regulation of major immune signaling cascades. To explore the molecular basis of this interaction, we employed computational methods to assess the binding affinity of cyanobacterial metabolites toward key shrimp proteins. Using Auto Dock, optimized ligand compounds were docked against target proteins, specifically anti lipopolysaccharide factor and arginine kinase. The in-silico analysis identified Crypto phycin B as a potent ligand, demonstrating superior binding efficiency to both targets. Subsequent evaluation of the dynamic receptor-ligand interactions suggests that conformational flexibility is a critical factor governing the stability and efficacy of these binding events. This study provides the first insights into the microalgal composition of the Marakkanam salterns and proposes a mechanistic hypothesis for cyanobacteria-mediated immunosuppression in resident shrimp via specific protein interactions.

Keywords: Cyanobacteria, Molecular Simulations, Non-Peptide Compounds, Anti lipopolysaccharide Factor, Arginine Kinase, Hypersaline Environment

Theme-5:

CELL BIOLOGY, BIOCHEMISTRY AND BIOTECHNOLOGY

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Presentation code: 12

ENVIRONMENTAL BIOLOGY SCIENTIFIC RESEARCH IN VITRO PRODUCTION FROM AXILLARY BUD EXPLANTS OF SOLANUM SEAFORTHIANUM

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ABSTRACT

The number of shoots developed on the axillary bud explants ranged from 1-4 to 2-3 by the addition of BAP at a concentration of 1.0 mg/l or NAA at 2.0 mg/l. Among the concentrations of 0.5 mg/l BAP proved to be ideal for multiple shoot induction. MS medium fortified with 1.0 mg/l BAP or 2.0 mg/l L-Glutamic acid also induced shoot buds on Axillary bud explants. Gupta et al (1983), M. Venkateshwarlu (2020) Komalavalli et al (2000) In vitro production in Solanum seaforthianum axillary bud multiplication Martin (2002). Recent development in MS media with different levels of BAP, NAA, L Glutamic acid, IAA, Kn. The effect of growth regulators on important parameters of callus initiation and plant regeneration M. Venkateshwarlu (2020) Rao et al (1995) Vasil (1980), Kartha (1981), Skoog F (1944). Addition of BAP at 2.0 mg/l and NAA at 3.0 mg/l to the MS basal medium, induced regeneration from the leaf segments. With an increase in the level of BAP Kn, IAA 2.0 – 3.0 mg/l the percentage of explants producing shoots also increased Punga et al (1990) The species has become widely naturalised outside its native range and is an invasive species in Australia, Africa, Indochina, the Pacific Islands and India choking native vegetation and poisoning livestock. The plant is highly heat resistant, but cannot tolerate frost conditions. The plant contains modest amounts of various tropane alkaloids such as atropine scopolamine and hyoscyamine and should be considered mildly toxic and inedible

Key words: Solanum seaforthianum, Axillary bud explants, BAP, Kn & IAA

Presentation code: 15

ASSESSMENT OF GENOTOXICITY IN PERIPHERAL LYMPHOCYTES OF BREAST CANCER PATIENTS UNDER CHEMOTHERAPY

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ABSTRACT

Cancer is a prevalent and serious disease, with breast cancer being common among women. The study investigates the genotoxic effects of various anticancer drugs such as methotrexate, cisplatin, cyclophosphamide, vincristine, vinblastine, bleomycin, Adriamycin, gemcitabine, and 5-fluorouracil. Lymphocytes were cultured using RPMI 1640 medium with supplements like phytohaemoagglutinin, discyristicine, and Human AB serum. Cultures were harvested, and slides were prepared and scored for metaphases. The cytogenetic analysis revealed that patients undergoing combined radiotherapy and chemotherapy showed unstable chromosomal aberrations such as dicentrics, centric rings, and acentric fragments. These aberrations were observed before, during, and after chemotherapy, with a higher frequency of chromosomal damage correlating with increased age and chemotherapy exposure.

Keywords: 5-FU, Lymphocytes, SCE, Chromosome aberrations, Breast cancer patients, chemotherapy, lifestyle.

Presentation code: 26

COMPARATIVE ANALYSIS OF CHLOROPHYLL PIGMENTS AND TOTAL PROTEIN IN HEALTHY AND VIRUS-INFECTED CROP LEAVES

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Plant viral infections significantly alter physiological and biochemical processes, particularly affecting photosynthetic pigments and protein metabolism in crop plants. The present study aims to evaluate the impact of viral infection on chlorophyll pigments and total soluble protein content in healthy and infected crop leaves. Healthy and virus-infected leaves of *Solanum lycopersicum(tomato), Capsicum annuum(chilli), Lagenaria siceraria (bottle gourd),* and *Luffa acutangula* (ridge gourd) were collected for analysis. Chlorophyll pigments were extracted using 80% acetone and quantified spectrophotometrically. The pigment contents of infected leaves were compared with healthy leaves to determine the biochemical impact of viral infection. The study revealed a reduction in chlorophyll content in infected leaves compared to healthy leaves. In tomato plants, chlorophyll-a decreased from 19.27 to 12.93 and chlorophyll-b from 25.60 to 23.31. In chilli, chlorophyll-a reduced from 23.36 to 11.67 and chlorophyll-b from 32.01 to 19.43. Bottle gourd showed a reduction of chlorophyll-a from 15.00 to 12.58 and chlorophyll-b from 27.76 to 21.66, while ridge gourd showed a decrease from 15.66 to 14.06 and 29.50 to 26.19 respectively. Protein estimation also showed variation between healthy and infected plants. Tomato protein OD decreased from 0.33 to 0.056 and chilli from 0.671 to 0.146, whereas bottle gourd increased from 1.071 to 1.278 and ridge gourd from 1.158 to 1.503, indicating possible stress-induced protein responses. The study demonstrates that viral infection significantly alters chlorophyll pigments and protein metabolism in crop plants. Reduction in chlorophyll content indicates impairment of the photosynthetic system, while variation in protein levels suggests activation of plant stress and defense responses. These findings highlight the potential of biochemical markers such as chlorophyll pigments and total soluble proteins for early detection and monitoring of viral stress in crop plants.

Keywords: Chlorophyll pigments, Viral infection, Protein estimation, Crop plants, Plant stress response.

Presentation code: 27

EMERGING BIOTECHNOLOGICAL INNOVATIONS IN GREEN SYNTHESIS OF VITIS VINIFERA PEEL-MEDIATED GOLD NANOPARTICLES: CHARACTERISATION AND BIOLOGICAL APPLICATIONS

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ABSTRACT

The development of sustainable nanomaterials through green synthesis has emerged as a promising strategy in nanobiotechnology, offering an eco-friendly alternative to conventional physicochemical nanoparticle synthesis methods. In the present study, gold nanoparticles (AuNPs) were synthesized using Vitis vinifera peel extract through a facile, cost-effective, and environmentally benign bio reduction process. The bioactive phytoconstituents present in the peel extract, particularly polyphenols, flavonoids, and phenolic acids, functioned as both reducing and stabilizing agents, facilitating the rapid conversion of Au^{3+} ions into stable gold nanoparticles. The formation and physicochemical characteristics of the synthesized AuNPs were systematically investigated using advanced analytical techniques, including UV–Visible spectroscopy, Fourier Transform Infrared Spectroscopy (FTIR), X-ray Diffraction (XRD), and Transmission Electron Microscopy (TEM). Spectroscopic analysis confirmed the surface plasmon resonance characteristic of gold nanoparticles, while structural and morphological evaluations revealed predominantly spherical and crystalline nanoparticles with an average size of approximately 50 nm. FTIR analysis further indicated the involvement of plant-derived functional groups in nanoparticle stabilization and capping. The biosynthesized AuNPs were further evaluated for their biological potential through multiple in vitro assays. The nanoparticles demonstrated significant antibacterial activity against selected pathogenic microorganisms, along with notable antioxidant, antidiabetic, and anti-inflammatory properties. Importantly, the synthesized AuNPs exhibited pronounced cytotoxic and anticancer activity against oat cell small cell lung cancer (SCLC) cell lines, suggesting their potential utility in nanomedicine and targeted cancer therapeutics. Overall, the findings highlight the potential of Vitis vinifera

peel—an abundant agricultural by-product—as a valuable bioresource for the green fabrication of multifunctional gold nanoparticles. This study underscores the integration of plant-based nanotechnology and biomedical research, contributing to the advancement of sustainable nanomaterials with promising applications in drug development, cancer therapy, and biomedical engineering.

Keywords: Green nanotechnology; Vitis vinifera peel extract; Gold nanoparticles (AuNPs); Plant-mediated synthesis; Nanobiotechnology; Physicochemical characterization; TEM; Anticancer activity; Small cell lung cancer (SCLC); Biomedical applications; Sustainable nanomaterials.

Presentation code: 47

INVESTIGATION ON FOMITOPSIS FEEI AND ITS BIOLOGICAL APPLICATIONS ON EXTRACELLULAR ENZYMES

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ABSTRACT

Fomitopsis feei is a wood-decaying basidiomycete fungus belonging to the family Fomitopsidaceae. It plays a vital ecological role in degrading lignocellulosic materials and producing biologically active metabolites. Recent research has focused on macrofungi like Fomitopsis feei due to their ability to synthesize bioactive compounds such as polysaccharides, phenolic compounds, and extracellular enzymes. These metabolites exhibit antimicrobial, antioxidant, and therapeutic properties, making the fungus a promising natural source for medicinal and industrial applications. However, large-scale production and extraction of these compounds remain limited due to the lack of optimized protocols and insufficient understanding of biosafety and molecular mechanisms. This study investigates the biochemical and pharmacological properties of Fomitopsis feei and evaluates its biological applications. Fruiting bodies were collected from natural habitats and identified morphologically. The fungal strain was cultured under laboratory conditions using suitable growth media. Bioactive compounds were extracted with organic solvents and analyzed for biological activity, highlighting the fungus's potential as a source of pharmacologically important compounds.

Keywords: Fomitopsidaceae, malt extract agar medium, proteins, lipids, carbohydrates, bioactive compounds, antimicrobial & antioxidant activities.

Presentation code: 84

SERI BIOTECHNOLOGICAL PERSPECTIVES ON MICROCLIMATE-MEDIATED VARIATION IN POST-COCOON TRAITS OF TASAR SILKWORM, ANTHERAEA MYLITTA DRURY

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ABSTRACT

Tasar silkworm, Antheraea mylitta Drury (Daba BV), is a wild, semi-domesticated, silk producing insect that produces a natural, biodegradable silk of high economic significance and supports the livelihoods of large tribal populations in India. Its silk output and rearing performance are strongly influenced by environmental variables such as temperature, relative humidity, season and host leaf quality, making it an important model for Seribiotechnological interventions aimed at stabilizing productivity under field conditions. In the present study, disease-free layings of A. mylitta were obtained from Mahadevpur and reared on Terminalia arjuna under well-managed plantation conditions at Kakatiya University campus, Warangal, and compared with crops raised on the similar host in natural forest conditions at Chennur and Mahadevpur in Telangana State. These sites differed in rearing temperature, relative humidity, season and altitude, thereby providing distinct microclimatic windows for assessing phenotypic responses. Post-cocoon parameters including cocoon weight, pupa weight, shell weight, shell ratio, filament length, cocoon length and width, reelability and denier were recorded following standard procedures. Cocoons produced at Kakatiya University under winter conditions (27°C, 78% relative humidity) exhibited higher shell and cocoon weights and greater cocoon dimensions, along with slightly lower denier values, indicating improved biomass conversion and better fibre quality compared to Chennur and Mahadevpur. Conversely, Mahadevpur, characterized by higher temperature and humidity during the rainy season (30°C, 87% relative humidity), yielded lighter cocoons but showed higher reelability, which was associated with dried pupal condition due to delayed harvest and reflects an interaction between post-cocoon handling microclimatic stress. Chennur showed intermediate values for most of the recorded traits.

The site-specific variation in these quantitative traits emphasizes the sensitivity of tasar silkworm performance to even modest deviations from optimal microclimate and highlights the scope for Seri biotechnological applications. The data generated can serve as a baseline for selecting and breeding microclimate-tolerant tasar strains, optimizing host-plant management, refining rearing calendars, and designing simple decision-support tools that link environmental monitoring with cocoon quality prediction. Such holistic approaches can contribute to enhanced tasar silk quality, higher and more stable yields and improved livelihood security for tribal rearers under changing environmental scenarios.

Key words: Seri biotechnology; Tasar silk; Antheraea mylitta; microclimate; post-cocoon parameters; Terminalia arjuna; tribal livelihoods

Presentation code: 110

THE ROLE OF VITAMIN C IN IMPROVEMENT OF IRON ABSORPTION, INVITRO STUDY

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ABSTRACT

Iron absorption in the human gut is a critical step in maintaining iron homeostasis. Vitamin C, a potent reducing agent, plays a key role in enhancing iron absorption from dietary sources. This abstract summarizes the mechanisms and evidence supporting Vitamin C's role in improving iron absorption in the human gut. In the gut, Vitamin C reduces ferric iron (Fe^{3+}) to ferrous iron (Fe^{2+}), increasing its solubility and bioavailability. Studies have shown that co-consumption of Vitamin C with iron-rich foods enhances iron absorption by 2-3fold. The duodenum, the primary site of iron absorption, is where Vitamin C exerts its effects, facilitating the uptake of Iron by enterocytes. The mechanisms underlying Vitamin C's effect involve chelation, reduction, and stabilization of iron in the gut lumen, making it more available for absorption. Research suggests that Vitamin C's reducing properties prevent the formation of insoluble iron compounds, maintaining iron in a soluble state. Incorporating Vitamin C-rich foods into meals can be an effective strategy to improve iron status, particularly in populations with high iron requirements. This abstract highlight the importance of dietary Vitamin C in enhancing iron absorption in the human gut, providing insights for developing targeted interventions to combat iron deficiency. By optimizing dietary strategies, we can improve iron bioavailability and reduce the burden of iron deficiency worldwide.

Presentation code: 141

COMPARATIVE EVALUATION OF NUTRITIONAL MEDIA FOR OPTIMIZED CULTURE OF RED-EYED DROSOPHILA MELANOGASTER

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ABSTRACT

The nutritional medium and environmental conditions are critical determinants of growth, survival, and reproductive success in Drosophila melanogaster. This study presents a comparative evaluation of four culture media—Cornmeal–Yeast–Agar–Sugar (CYAS), Banana–Jaggery (BJ), Wheat–Semolina (WS), and Synthetic Agar–Yeast (SAY)—along with the influence of pH and relative humidity (RH) on the optimized culture of red-eyed D. melanogaster. Across four generations, CYAS supported the highest fecundity and survival, BJ accelerated development but showed contamination risks, WS provided cost-effective maintenance with moderate outcomes, and SAY enhanced adult longevity. Further analysis revealed that medium pH significantly affected developmental performance, with slightly acidic to near-neutral conditions (pH 5.5–6.5) yielding optimal larval survival (≈90%), shortest developmental time (≈9.8 days), and highest fecundity (≈45 eggs/female/day). Extreme pH conditions adversely impacted growth and reproduction. Similarly, RH played a crucial role, with 65–75% identified as optimal, ensuring maximum survival and fecundity (≈47 eggs/female/day), while low humidity caused desiccation and high humidity increased fungal contamination. Overall, the study establishes that CYAS medium, pH 5.5–6.5, and RH 65–75% provide ideal conditions for stable and reproducible Drosophila culture, offering valuable guidelines for laboratory maintenance and experimental consistency.

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INTEGRATED ASSESSMENT OF HYDRO-CHEMICAL DRIVERS INFLUENCING PLANKTON COMMUNITY RESILIENCE IN A SEMI-ARID FRESHWATER ECOSYSTEM: IMPLICATIONS FOR BIODIVERSITY SUSTAINABILITY AND SUSTAINABLE DEVELOPMENT GOALS (SDGS)

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ABSTRACT

Freshwater lakes are vital ecosystems providing habitat, nutrient cycling, climate regulation, and freshwater supply while supporting biodiversity and human livelihoods. In semi-arid regions like Telangana, these lakes are highly sensitive to seasonal fluctuations and anthropogenic pressures, emphasizing the need to understand hydrochemical drivers and plankton dynamics for sustainable management.An integrated assessment was conducted in Bommakal Freshwater Lake, Karimnagar District, Telangana, India during June 2022–May 2023 to evaluate the influence of hydrochemical parameters on zooplankton and phytoplankton communities and their role in ecosystem resilience. Seasonal water samples were analyzed for T, pH, EC, TDS, SD (m), DO, BOD, CO_2, TA, TH, Cl^-, NO_3^-, PO_4^{3-}, Na^+, K^+, and NH_4^+ using standard methods. Pearson's correlation revealed significant interdependencies among parameters, highlighting the strong coupling between water chemistry and plankton structure.Zooplankton (Rotifera, Cladocera, Copepoda, Ostracoda) and phytoplankton (Chlorophyceae, Cyanophyceae, Bacillariophyceae, Euglenophyceae) were quantified using dominance, Simpson, Shannon, and evenness indices, revealing clear seasonal trends and community resilience. Rotifers and copepods were sensitive to DO, nutrients, and ionic concentrations, whereas ostracods remained stable across seasons. Phytoplankton diversity responded to nutrient and light availability, reflecting the dynamic interaction between physico-chemical drivers and primary producers.The study has significant implications for the United Nations Sustainable Development Goals. SDG 6 (Clean Water and Sanitation) is addressed through water quality monitoring and early detection of eutrophication or ionic stress. SDG 14 (Life Below Water) is supported by maintaining plankton diversity, which sustains higher trophic levels. SDG 15

(Life on Land) is indirectly promoted via resilient freshwater ecosystems supporting terrestrial-aquatic interactions, habitat connectivity, and nutrient cycling. Overall, seasonal hydrochemical dynamics regulate plankton diversity and ecosystem resilience, providing a framework for adaptive management, biodiversity conservation, and sustainable stewardship of semi-arid freshwater lakes. Bommakal Lake exemplifies an ecologically stable system, yet ongoing monitoring is essential to safeguard its ecological integrity.

Keywords: Bommakal Lake; Hydrochemical parameters; Zooplankton; Phytoplankton; Diversity indices; Ecosystem resilience; Sustainable Development Goals (SDGs)

Presentation Code: 10

DISPER-EEM" MAY BE THE BEST ECOTECNOLOGY OWING TO DIGITAL CATION EXCHANGE CAPACITY IN ENVIRONMENTS THAT DETERMINES EVERY FEATURES IN BIOLOGY

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ABSTRACT

DISPER-EEM" may be the best ecotecnology owing to digital cation exchange capacity in environments that determines every feature in biology DISPER-EEM DISease PERcentage null with EEM environment Editing Model stated that digital CEC is everything in Biology. A digital CEC below 20 meq per 100 g Soils which usually Rocks, Plateau and sands and gravels environments are non-diseases. Any Ecotechnology is algorithmic relations among environmental parameters in nature and in synthetic environmemts to find the esteem godness. This Ecotechnology has strong digital application even in natural, Synthetics in Hydroponics and all mankind. Our Study found Every Inland fish-species can be breedable well within the low TDS viz i.e. Total Dissolved Solids below 100 ppm or alternatively a low Water-Hardness below 150 ppm. Beyond this any higher water Hardness or water TDS results lack of Oxygen causing hazards or may be considered as environmental pollutions to all the young off-springs the same scientific principle is applied in digital Hydroponic as well. Recently we derive dissolved Oxygen can be judged based on water Temperature following Ecotechnology. Not only in water Environmental Soils are having a huge 93 metals and many ions 86 Metals are harmful to every Biology whereas water having 7 dissolved metals and sand is the better and best medium as digital hydroponics than conventional soils. Thus, in agriculture and fisheries Ecotechnology DISPER is used It's apparent that the water hardness or metals contents or digital CEC can be well identified with the Satellite based remote sensed digital data or grey-values also and hence less metals digital hydroponics or any environment is beneficial to Biology and Dissolved Oxygen can be determined remotely as well with water Temperature to benefit fisheries and Hydroponics. Study has been found that and excessive water-hardness results excessive metals in soil, excessive poisonous metals and heavy metals (86) are very harmful and can be controlled with adding Ash and ash also in water the best medium to make water more transparent or a low TDS or low Water-Hardness and make congenial Fishes

to breed and hatch at the same time makes the best environment This communication has applied Ecotechnology namely Digital CEC in sediments or environment is everything to biology, all plants and animals

Keywords: Ecotechnology, Digital CEC is everything Biology, DISPER-EEM to make Environment disease-less, Digital Health & Environment

Presentation Code: 19

FIRE-DRIVEN CHANGES IN NTFP DIVERSITY AND PRODUCTIVITY IN TROPICAL DRY DECIDUOUS FORESTS OF TELANGANA, INDIA: IMPLICATIONS FOR NTFP-BASED LIVELIHOODS

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ABSTRACT

Forest ecosystems provide diverse goods and ecosystem services, among which Non-Timber Forest Products (NTFPs) play a crucial role to support the livelihoods of forest-dependent tribal and rural communities. NTFPs contribute significantly to food security, traditional medicine, shelter, and commerce generation. Though these resources are increasingly threatened by various factors such as habitat degradation, fragmentation, unscientific collection, overexploitation, climate change, and forest fires. Of these, forest fires represent a major ecological disturbance which directly damages NTFP species, alters forest structure and species composition, and disrupts ecological interactions that influence the availability and productivity of these resources. Dry deciduous forests are particularly vulnerable to fire, especially during the pre-monsoon dry season when vegetation becomes highly combustible. Tropical dry deciduous forests are predominant in Telangana state and experiences regular fire incidents every year. Reports indicate that more than 13,000 forest fires occur annually in the state, affecting approximately 3,983.28 sq km of forest area and placing Telangana among the three top states in terms of burned forest area in India. Studies suggest that nearly 80-95% of these fires are human-induced, often associated with activities such as agricultural burning, podu cultivation and deliberate fires set to easy collection of seasonal NTFPs including tendu leaves (Diospyros melanoxylon), mahua corolla (Madhuca longifolia var. latifolia), and gums from species like Firmiana sp., Boswellia sp., Anogeissus sp., and Cochlospermum sp. The present study assesses the ecological impacts of forest fires on NTFP diversity and productivity and discusses potential management strategies to mitigate fire impacts. Effective forest fire management is essential for the conserving forest biodiversity and ensuring the sustainability of NTFP-based livelihoods in Telangana.

Presentation Code: 20

BIOEFFICACY OF SELECTED BIOPESTICIDES AGAINST FALL ARMYWORM IN MAIZE (ZEA MAYS L.) AGROECOSYSTEMS

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ABSTRACT

Maize (*Zea mays* L.) is one of the most important cereal crops cultivated worldwide and plays a crucial role in food security, livestock feed, and industrial applications. However, maize productivity is threatened by several insect pests, among which fall armyworm (Spodoptera frugiperda) has emerged as a major invasive pest. The pest causes severe damage to maize leaves and reproductive structures, leading to significant yield losses. Excessive reliance on chemical insecticides has resulted in environmental pollution, pest resistance, and harmful effects on beneficial organisms. Therefore, eco-friendly pest management strategies are required. The present study evaluated the bioefficacy of selected biopesticides including Bacillus thuringiensis, Beauveria bassiana, Metarhizium anisopliae, and neem-based formulations against fall armyworm in maize agroecosystems. Field experiments were conducted using a randomized block design with four replications. Observations on larval population, leaf damage percentage, and grain yield were recorded. The results revealed that microbial biopesticides significantly reduced fall armyworm infestation compared with untreated control. Among the treatments, Bacillus thuringiensis showed the highest efficacy followed by Beauveria bassiana and Metarhizium anisopliae. Neem-based botanical pesticides also exhibited moderate effectiveness. The study demonstrates that microbial and botanical biopesticides can serve as environmentally safe alternatives for managing fall armyworm in maize production systems.

Keywords: Maize, Fall Armyworm, Biopesticides, Bioefficacy, and Integrated Pest Management

Presentation Code: 21

SUSTAINABLE VERMICOMPOSTING USING EARTHWORMS FOR THE BIODEGRADATION OF AGROCHEMICAL RESIDUES

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ABSTRACT

Earthworms are important biological agents in sustainable waste management and ecological restoration. The present study investigates the role of vermiremediation using selected earthworm species for reducing pesticide residues and heavy metal contamination in biodegradable wastes. During vermicomposting, earthworms convert organic residues into nutrient-rich compost while facilitating the stabilization and transformation of toxic substances. The synergistic interaction between earthworms, associated microbial communities and organic substrates accelerates the breakdown of hazardous pollutants and enhances soil quality. The study emphasizes vermicomposting as an environmentally friendly and economically viable bioremediation approach that supports sustainable agriculture, minimizes environmental pollution, and highlights the ecological importance of earthworms in organic waste recycling systems.The process utilizes earthworms to convert biodegradable agricultural and household waste into nutrient rich vermicompost, which enhances soil fertility, improves crop productivity, and promotes ecological balance. In rural settings, Vermicomposting creates diverse development opportunities by generating supplementary income, providing self- employment, particularly self help groups, and reducing dependence on chemical fertilizers. It also encourages organic farming practices and supports efficient recycling of locally available biomass, there by strengthening rural livelihoods and security. Environmental factors such as temperature and moisture fluctuations affect earthworm survival and productivity, while financial constraints and weak institutional support hinder scaling up of the technology. Targeted capacity- building programs, extension Services, policy support, and improved market linkages can significantly enhance its adoption. Addressing these challenges can established vermicomposting as a viable tool for sustainable agriculture, waste management in rural regions.

Keywords: Earthworms, Biodegradable, Agriculture, Vermocompost, etc**.**

Presentation Code: 22

GREEN ALTERNATIVES TO HARMFUL CHEMICAL REPELLENTS: THE ROLE OF BOTANICAL MOSQUITO REPELLENTS IN AN ECO-FRIENDLY APPROACH

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ABSTRACT

Millions of people rely on chemical-based mosquito repellents to protect themselves from mosquito bites. However, several studies have reported that these synthetic repellents may pose harmful effects on human health, other living organisms, and the environment. In addition, continuous use of chemical insecticides can lead to the development of resistance in insect populations, making each generation of mosquitoes stronger and more tolerant to these chemicals. In this context, natural mosquito repellents derived from plants offer an eco-friendly and sustainable alternative. The present study focuses on locally available plant species with mosquito repellent properties. Information was collected from elders, rural inhabitants, and tribal communities who possess traditional botanical knowledge of plant-based insect repellents. Various plant parts such as leaves, flowers, and aromatic plant extracts are traditionally used to repel or kill insects due to the volatile compounds released from them, which interfere with the insect nervous system. Natural mosquito repellent plants emit distinct odours that mosquitoes tend to avoid. Preparation of natural repellents is simple, cost-effective, and can even be carried out at the household level. Generally, 5–10% essential oil (ca. 10–20 drops) is mixed with carrier oil or alcohol (two tablespoons) and applied to the skin or clothing as a spray or rub. Unused preparations should be stored in dark bottles away from heat or direct sunlight. Several locally available plant species were identified as effective mosquito repellents, including Chrysanthemum sp., Cymbopogon nardus, Melia azedarach, Ageratum conyzoides, Nicotiana tabacum, Rosa indica, Hyptis suaveolens, Tagetes patula, Chloroxylon swietenia, and Eucalyptus globulus. These plant-based repellents represent a promising eco-friendly alternative for mosquito management.

Presentation Code: 45

ENVIRONMENTAL AND ECOLOGICAL FACTORS IN HUMAN ADAPTATIONS OF WARANGAL

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ABSTRACT

Environmental and ecological factors such as climate, water resources, vegetation, soil, and urban development play a significant role in shaping human adaptations. The main objective of this project is to study the influence of environment and ecological factors on human adaptations of people living in regions of Warangal. The Warangal region in Telangana, India, characterized by a tropical, semi-arid climate, experiences significant seasonal variations, including high summer temperatures (often exceeding 42°C), intense dry spells, and moderate monsoon precipitation. As a drought-prone region with red soil and scattered black cotton soil, the environment poses substantial challenges to subsistence, agriculture, and water security. The study was conducted using both primary and secondary data collection. Primary data collection is done by conducting online survey in form of Google form. Secondary data is collected from online source related to environmental and ecological factors on human adaptations studies of warangal region. The study finds that while traditional ecological knowledge provides a basis for survival, strengthening sustainable resource management (such as Cultural adaptaions, water conservation and agroforestry) is essential for mitigating the impacts of climate change, particularly as the region faces a high climate change severity score.

Keywords: Temperature, Ph, Human Adaptations, Soil Moisture, Water M.O's, Cultural Practices.

Presentation Code: 49

EFFECT OF CLIMATE VARIABILITY ON ECONOMIC PARAMETERS OF SILKWORM (BOMBYX MORI L.) UNDER NORMAL REARING

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ABSTRACT

Sericulture is a science of art and silkworm is a queen of textiles, and an important subsistence-supporting activity that contributes to rural economy and is a harbinger in providing employment to women and youth of rural India. The growth, survival, and productivity of the silkworm (Bombyx mori L.) are highly dependent on environmental factors, such as temperature and humidity that plays a critical role in regulating silkworm metabolism, larval development, and cocoon formation. Variability in these climatic parameters may negatively influence the cocoon yield and economic traits associated with silk production. The purpose of the study is to evaluate the influence of climatic variations on important economic parameters of silkworm's cocoon weight, shell weight, shell ratio, and floss weight under normal rearing conditions. Silkworm larvae were reared by following standard rearing practices, and cocoons were collected after completion of the rearing period. The harvested cocoons were weighed using a digital weighing balance, and the economic parameters were calculated using standard formulas. The results indicated that climatic fluctuations exert noticeable effect on the economic traits of cocoon. Variations in temperature and humidity during the larval rearing period affected cocoon weight and shell weight, which are important indicators of silk yield and cocoon quality. Favourable environmental conditions supported better larval growth and cocoon development, resulting in increased silk production. Conversely, unfavourable climatic conditions reduced cocoon quality and economic performance.

Keywords: *Trichoderma*, Secondary metabolites, Biocontrol, Crop production

Presentation Code: 57

THE TRIAD OF SURVIVAL: SYNERGISTIC DYNAMICS OF ECOLOGY, ENVIRONMENTAL BIOLOGY, AND CLIMATE CHANGE IN THE ANTHROPOCENE

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ABSTRACT

The contemporary era, characterized as the Anthropocene, is defined by the profound and accelerating transformation of Earth's systems. This ABSTRACT synthesizes the critical intersections between ecology, environmental biology, and climate change, exploring how their synergistic dynamics dictate the resilience of global biodiversity. Ecology provides the fundamental framework for understanding the complex interactions between organisms and their environments, yet these traditional relationships are being fundamentally altered by anthropogenic pressures. Environmental biology bridges the gap between theoretical ecology and practical conservation, focusing on the physiological and molecular responses of species to pollutants, habitat fragmentation, and resource depletion. However, the most pervasive catalyst for ecological shifts is global climate change. Driven by the unprecedented elevation of atmospheric greenhouse gases, climate change acts as a "threat multiplier." It disrupts phonological synchrony—such as the timing of pollination and migration—leading to trophic mismatches that threaten the stability of entire food webs. Current research indicates that as mean global temperatures rise, species are forced into rapid range shifts toward higher latitudes or altitudes, often outpacing their innate capacity for dispersal. Furthermore, ocean acidification and extreme weather events are pushing ecosystems beyond critical tipping points, resulting in irreversible loss of coral reefs and peat lands. By integrating metabolic scaling theories with climate modeling, environmental biologists are identifying "refugia" that may serve as vital strongholds for biodiversity.

Keyword: Critical intersections. Phonological synchrony, Climate change, unprecedented elevation, anthropogenic, fragmentation

Presentation Code: 59

HYDROLOGICAL PARAMETER DYNAMICS OF CHIPPALERU MANGROVES, ANDHRA PRADESH, INDIA: A CLUSTER ANALYSIS APPROACH

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ABSTRACT

This study investigated the hydrological dynamics of the Chippaleru mangrove estuary in Andhra Pradesh, India, through analysis of physico-chemical parameters across three monitoring stations. Nine key parameters were measured: water temperature, air temperature, dissolved oxygen (DO), nitrates (NO_3-N), turbidity, phosphates (PO_4-P), salinity, transparency, and pH. Cluster analysis revealed consistent grouping patterns across all three stations, with parameters organizing into three distinct clusters. Cluster 1 consistently grouped water and air temperature, demonstrating strong thermal correlation. Clusters 2, the largest cluster, contained DO NO_3-N, PO_4-P, and turbidity, representing interconnected biogeochemical processes. Cluster 3 grouped salinity, transparency, and pH, reflecting water clarity and ionic composition relationships. The similarity was there in clustering patterns across all stations (80% similarity).

Key words: mangroves, hydrology, cluster analysis, estuarine dynamics, Andhra Pradesh, water quality

Presentation Code: 75

ALGAL MICROBIAL FUEL CELLS: INTEGRATING WASTEWATER TREATMENT WITH SUSTAINABLE BIOENERGY PRODUCTION

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ABSTRACT

Algal Microbial Fuel Cells (AMFCs) are an emerging bioelectrochemical technology that combines microbial electrogenesis and algal photosynthesis in a synergistic manner to produce electricity and treat wastewater containing organic matter. In an AMFC system, electroactive bacteria in the anodic compartment oxidize organic matter and release electrons to flow through an external circuit to the cathodic compartment, where oxygenic phototrophic microalgae consume oxygen and produce biomass. This two-chamber system not only produces clean and renewable energy but also addresses critical issues related to wastewater treatment and carbon sequestration on a global scale to mitigate the effects of climate change and fossil fuel depletion. AMFCs have been found to valorize various organic waste feedstocks effectively, converting waste into a valuable resource. The feedstocks used are varied, ranging from domestic sewage, which is rich in carbohydrates and proteins, to agricultural waste such as rice straw, sugarcane bagasse, and manure, which are rich in lignocellulose. The waste is also rich in leachates from municipal waste. The waste is hydrolyzed or subjected to anaerobic digestion to support anodic spp such as Geobacter, which remove COD by 70-90%, generating 1-5 W/m².For the construction of an AMFC at the laboratory scale, cost-effective designs with transparent materials like polycarbonate or glass are used to build dual-chamber H-type or flat-plate reactors with effective volumes ranging between 100 and 500 mL. The inoculum is 5-10 cm². The cathodes of the AMFC consist of algal biofilm with Chlorella vulgaris or Spirulina platensis on similar material, illuminated with LED arrays of 100-500 µmol photons m^{-2} s^{-1}. The proton exchange membranes separate the anodic and cathodic chambers of the cell. Ag/AgCl is used as the reference electrode. The construction of the cell is such that it is airtight with the use of peristaltic pumps. This review aims to highlight the advancements made in the optimization of the AMFC. The optimization is expected to improve the efficiency of the cell for the circular bioeconomy.

Key words: Algal Microbial Fuel Cell, Sustainable energy, Organic Wastes, Anode – Cathode.

Presentation Code: 76

HEAVY METAL POLLUTION AND ITS ECOLOGICAL IMPACT ON FRESHWATER ZOOPLANKTON DIVERSITY: INDICATORS OF AQUATIC ECOSYSTEM HEALTH

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ABSTRACT

Freshwater ecosystems are increasingly threatened by pollution caused by heavy metals released from industrial activities, agricultural runoff, and domestic waste. These metals accumulate in aquatic environments and significantly affect aquatic organisms, particularly zooplankton, which play a vital role in aquatic food chains. The present study investigates the impact of heavy metal pollution on the diversity and abundance of freshwater zooplankton. Water samples were collected from selected freshwater bodies and analyzed for heavy metals such as lead (Pb), cadmium (Cd), copper (Cu), zinc (Zn), and chromium (Cr). Zooplankton samples were collected using plankton nets and identified under a compound microscope. Results showed that increased concentrations of heavy metals were associated with a decline in zooplankton diversity and abundance. Sensitive species such as rotifers and cladocerans were significantly reduced in polluted sites compared to relatively clean sites. The study highlights the importance of zooplankton as bioindicators for assessing freshwater ecosystem health and emphasizes the need for pollution control strategies to protect aquatic biodiversity.

Keywords: Heavy metals, freshwater pollution, zooplankton diversity, aquatic ecosystem, bioindicators**.**

Presentation Code: 88

ASSESSMENT OF MICROPLASTIC CONTAMINATION IN SALT

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ABSTRACT

Microplastic pollution in edible salt has become a serious environmental problem which also endangers public health because it creates pathways for human contact and damages ecosystems. The research aims to create a cost-effective biosensing system which can be used in outdoor settings to detect four main microplastic polymers which include polyethylene (PE) and polypropylene (PP) and polystyrene (PS) and polyethylene terephthalate (PET) present in salt samples. The proposed approach integrates chemical dye assisted fluorescence with surface functionalized quantum dots (QDs) as highly sensitive optical signal transducers. The researchers selected quantum dots because these particles provide exceptional photostability together with high quantum yield and adjustable emission properties and they maintain their fluorescent output despite exposure to high salinity environments. The QDs of this system bind with biological components which allow the system to detect specific microplastic materials through direct interactions with target particles. The system detects surface binding through light intensity changes which lead to visible results that do not need advanced instruments for spectroscopy or microscopy. The developed platform allows users to detect multiple substances through its simple testing system which household and environmental users can operate without special training. The research demonstrates that moonlight monitoring can be used to create accessible public awareness programs which enable people to monitor microplastic pollution in saltwater environments.

Keywords: Microplastics, Edible salt, Quantum dots, Fluorescence biosensor, Nanotechnology, saline detection

Presentation Code: 98

INTEGRATED EVALUATION OF WATER QUALITY, FISH DIVERSITY, AND FISHERMEN LIVELIHOODS IN THE KRISHNA RIVER BASIN

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ABSTRACT

Andhra Pradesh and Telangana are recognized as two of the principal inland fish-producing states in India. The Krishna River and its reservoirs provide an important freshwater resource that supports large-scale fish production in both states. Among them, Andhra Pradesh ranks first in national fish production, contributing nearly 40.9% of the country's total fisheries and aquaculture output as of 2025 while Telangana also fast-growing contributor to inland fisheries. Maintaining suitable water quality is essential for conserving aquatic biodiversity and sustaining fisheries. The present study evaluated water quality parameters, fish diversity, habitat availability, and the socio-economic conditions of fishing communities along the Krishna River. Water and fish samples were collected between June 2024 and September 2025, and structured surveys were conducted to assess the income and livelihood status of fishermen and fish traders. The analysis indicated that all measured water quality parameters-pH, Dissolved Oxygen (DO), Biochemical Oxygen Demand (BOD) and Chemical Oxygen Demand (COD) were within Indian and international permissible limits. The pH ranged from 6.8 to 7.9. DO levels exceeding the minimum requirement of 5 mg/L(5.5-9.0) . BOD values were between 1.3 and 5.1 mg/L, remaining below the permissible limit of 6 mg/L. COD ranged from 16 to 23 mg/L, within the accepted international threshold of 23.2 mg/L. Fish diversity showed an increase over the study period, with 36 species documented in 2024 and 42 species in 2025. Economic analysis revealed that the average daily income of local fishermen ranged from ₹300 to ₹1,500 during the off-peak season (June–February) and from ₹700 to ₹3,000 during the peak season (September–November). Fish traders earned between ₹450 and ₹1,500 per day in the off-peak season and ₹200 to ₹500 per day during the peak season. These earnings indicate that fishing and fish trading provide sustainable livelihoods, enabling families to meet their daily needs.

Keywords: Water Quality; Freshwater; Krishna River; Aquatic Biodiversity; Fisherman

Presentation Code: 136

PLANETARY ONE HEALTH IN THE AGE OF MICROPLASTICS: FRESHWATER SNAIL SENTINELS FOR PREDICTING THE NEXT WAVE OF AQUATIC DISEASES

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ABSTRACT

The rapid rise of microplastics in freshwater systems is reshaping pathways of infectious disease emergence, yet their role in host–parasite interactions remain poorly understood. This study introduces a predictive disease-ecology framework that positions freshwater snails as early-warning sentinels for microplastic-driven transmission risk. Unlike conventional bioindicators that reflect environmental degradation retrospectively, snails provide real-time insight into biologically active contamination at the interface of pollution and parasitism, functioning as intermediate hosts for medically and veterinary significant trematodes. We examine how microplastic ingestion influences three interconnected processes: (i) disruption of snail immune and metabolic function, (ii) restructuring of microbial communities via plastisphere formation, and (iii) increased parasite development and infectivity under climate-amplified stress. Evidence suggests that microplastics act not only as toxic particulates but as biological vectors that concentrate pathogens and facilitate their persistence within host systems. This dual role may lower host resistance thresholds while enhancing parasite success, thereby amplifying transmission potential. Building on this, we propose an integrative early-warning model that combines microplastic burden, snail biomarker responses, and parasite prevalence to forecast disease risk in freshwater ecosystems. This approach shifts monitoring from passive pollution assessment to active epidemiological prediction, particularly relevant in densely populated and climate-vulnerable regions with high human–livestock–water interaction. By reframing freshwater snails as dynamic sentinels within a multi-stressor disease system, this work bridges pollution science with predictive epidemiology. It offers a scalable framework for anticipating environmentally mediated disease outbreaks and guiding targeted interventions under the Planetary One Health paradigm.

Keywords: Microplastics, Disease ecology, Freshwater snails, Plastisphere, One Health.

Theme-7:

EMERGING TECHNOLOGIES AND INNOVATIONS IN BIOLOGY

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Presentation Code: 07

ROLE OF IMPLEMENTING ARTIFICIAL INTELLIGENCE (AI) STRATEGIES IN BIOLOGICAL SCIENCES: FUTURE PROSPECTS OF AI IN RESEARCH AND ANALYSIS

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ABSTRACT

Artificial Intelligence (AI) is a term generally thought of as computerized systems that work and react in ways commonly thought to require intelligence. AI technologies, methodologies, and applications can be used throughout the biological sciences and biology research. Artificial Intelligence (AI) has emerged as a transformative instrument in biological sciences, facilitating the analysis of complex biological datasets, predicting molecular interactions, and automating laboratory and field operations. In AI strategies machine learning, deep learning, computer vision, and natural language processing (NLP) and their applications across genomics, proteomics, taxonomy, ecology, and medical diagnostics. Recent advancements in artificial intelligence include the utilization of models such as convolutional neural networks (CNNs) and support vector machines (SVMs). The integration of AI with biological databases accelerates drug discovery, species classification, and environmental assessment. The study highlights future prospects and strategies in biological sciences and implementing AI responsibly for sustainable biological research.

Keywords: Artificial Intelligence, AI technology Machine Learning, Biological research, AI strategies

Presentation Code: 09

ADVANCE IN LIFE SCIENCES: PRESENT AND FUTURE – A RESEARCH PERSPECTIVE

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ABSTRACT

Life sciences represent one of the most dynamic and transformative scientific domains in the modern world. Rapid technological progress, interdisciplinary research integration, and molecular-level understanding of biological systems have revolutionized healthcare, agriculture, environmental protection, and biotechnology. Contemporary life science research is strongly influenced by innovations such as gene editing, artificial intelligence-assisted biology, precision medicine, synthetic biology, and nanobiotechnology. International institutions such as the World Health Organization emphasize the importance of biological science advancement in strengthening global health security. The emergence of tools like the CRISPR-Cas9 gene editing system has transformed genetic engineering, enabling precise modification of genomes. These advancements have created opportunities for treating hereditary diseases, improving agricultural productivity, and understanding cellular mechanisms at an unprecedented depth. Future life science development is expected to focus on personalized healthcare, regenerative medicine, sustainable agriculture, digital biology, and advanced disease diagnostics. This paper examines present achievements in life sciences, technological innovations, emerging research directions, challenges, and future possibilities shaping biological research and human welfare.

Keywords: CRISPR-Cas9, Precision Medicine, Digital Biology, Global Health Security, Synthetic Biology.

Presentation Code: 29

BIOCONVERSION OF SERICULTURE WASTE INTO HIGH-VALUE PRODUCTS: A SUSTAINABLE ECONOMICAL APPROACH

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ABSTRACT

Sericulture is one of the most important agro-based rural cottage industry which provides bread and butter to rural folk, especially women. However, along with production of silk during sericulture practices, substantial quantities of seri waste are generated at different stages, such a moriculture, rearing, reeling, re-reeling, and other post reeling activities, where in this waste include silkworm pupae, reeling effluents, litter, pruning residues, and spun silk waste. Traditionally these wastes are either discarded or kept as unutilized waste material, resulting in environmental pollution and economical loss to the seri farmers. The present study focuses on the conversion of left over seri waste in to valuable products, including protein rich animal feed, bioactive compounds, biofertilizers, and bioenergy through various sustainable bioprocesses like, biochemical extraction, microbial fermentation, composting, and other biological treatments to develop an integrated waste management approach that promotes efficient resources utilization and supports the concept of zero waste sericulture system while increasing the income opportunities.

Keywords: Sericulture, seri waste, valuable products, bio processing, and zero waste.

Presentation Code: 35

A STEP FORWARD IN EMERGING TECHNOLOGIES AND INNOIVATIONS IN BIOLOGY- CRYONICS

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ABSTRACT

As soon as person is legally declared dead, the process of cryopreservation begins. Declaration of decay process is accompolished by cooling the body with ice and maintaining the minimal tissue viability through blood circulation, which is reestablished with the help of a heart-lung resuscitator. subsequently, blood as to be exchanged with a cryoprotectant solution.

Keywords: Cryopreservation, cryoprotectant, liquid nitrogen, vitrification, nanotechnology, organ regeneration

Presentation Code: 56

RECENT ADVANCES IN MULBERRY SERICULTURE: TECHNOLOGIES, CHALLENGES AND FUTURE PROSPECTS

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ABSTRACT

Sericulture is an important agro-based enterprise that integrates agriculture, entomology, and rural livelihood systems. Mulberry sericulture plays a significant role in global silk production and provides employment opportunities for rural communities. In recent decades, advances in life sciences and agricultural technologies have significantly improved mulberry cultivation practices, silkworm rearing methods, and cocoon productivity. Scientific developments such as improved mulberry varieties, climate-controlled rearing systems, biotechnology-based silkworm breeding, and precision agriculture technologies have enhanced the efficiency of sericulture production systems. Despite these technological developments, the sericulture sector still faces challenges including climate change, pest and disease outbreaks, labour shortages, and increasing production costs. The present review paper examines recent advances in mulberry cultivation, modern technological innovations in silkworm rearing, and biotechnology-driven genetic improvements in silkworm breeding. The paper also highlights emerging technologies such as artificial intelligence, IoT-based monitoring systems, drone-assisted agriculture, and smart farming techniques that may transform the future of sericulture production. Understanding these developments is essential for improving productivity and sustainability in the silk industry.

Keywords: Mulberry Sericulture, Silkworm Rearing, Cocoon Production, Biotechnology, Precision Agriculture

Presentation Code: 100

CARICA PAPAYA SEED-MEDIATED SYNTHESIS OF NICKEL OXIDE NANOSTRUCTURES FOR HIGH-PERFORMANCE SUPERCAPACITORS

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ABSTRACT

This study explores the eco-friendly synthesis of Nickel oxide nanoparticles (NiO NPs) using carica papaya seeds extract for supercapacitor applications. The green approach leverages carica papaya's bioactive compounds as reducing and stabilizing agents, eliminating the need for toxic chemicals. The synthesized NiO NPs were characterized using UV-Vis, FTIR, and DLS, confirming their formation, functional groups, and moderate size uniformity. The NiO NPs were integrated into a graphite wax composite electrode doped with glycine to enhance electrochemical performance. Systematic evaluation through cyclic voltammetry (CV), galvanostatic charge-discharge (GCD), and electrochemical impedance spectroscopy (EIS) demonstrated superior charge storage capabilities, excellent cycling stability (5000 cycles with minimal degradation), and low charge transfer resistance. The electrode exhibited optimal performance in 0.1M HCl, highlighting its potential for efficient energy storage. This work highlights the potential of bio-derived NiO NPs for eco-friendly supercapacitors, combining cost-effectiveness with high electrochemical performance, paving the way for sustainable energy storage solutions

Keywords: Green synthesis, Sustainable energy storage, Bio-waste Valorization, graphite composite electrode, Electrochemical performance

Presentation Code: 111

ARTIFICIAL INTELLIGENCE REVOLUTIONIZING LIFE SCIENCES: CURRENT APPLICATIONS AND FUTURE PERSPECTIVES.

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ABSTRACT

The rapid growth of biological data and technological advancements have significantly transformed life science research. Artificial Intelligence (AI) has emerged as a powerful tool capable of analyzing complex biological datasets, identifying patterns, and accelerating scientific discoveries.The integration of AI with life sciences is revolutionizing various fields including genomics, drug discovery, disease diagnosis, and agricultural biotechnology. The present study aims to highlight the current applications of artificial intelligence in life sciences and explore its future potential in advancing biological research.This work is based on the review and analysis of recent scientific literature, research articles, and technological developments related to AI applications in biological sciences. Recent studies indicate that AI-driven systems can predict protein structures, analyze genomic data, assist in early disease detection, and enhance crop monitoring and management. For instance, the AI system AlphaFold developed by DeepMind has significantly advanced structural biology by accurately predicting protein structures. Overall, artificial intelligence has become an essential tool in life sciences, improving research efficiency, accelerating innovation, and supporting solutions to global challenges such as healthcare improvement, food security and sustainable agriculture.

Keywords: Artificial Intelligence, Life Sciences, Machine Learning, Drug Discovery, Genomics.

Presentation Code: 117

SUSTAINABLE MICROWAVE-ASSISTED SYNTHESIS OF COBALT SULFIDE NANOSTRUCTURES USING JATROPHA CURCAS LEAF EXTRACT FOR ENHANCED SUPERCAPACITOR PERFORMANCE

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ABSTRACT

The growing demand for sustainable energy storage devices has driven significant interest in the development of environmentally friendly nanomaterials with superior electrochemical performance. In this study, cobalt sulfide (CoS) nanoparticles were synthesized through a green microwave-assisted method using Jatropha curcas leaf extract as a natural reducing and stabilizing agent. The phytochemicals present in the plant extract play a crucial role in the formation and stabilization of the nanoparticles, offering an eco-friendly and cost-effective synthesis route. The structural, optical, and morphological properties of the synthesized CoS nanoparticles were systematically characterized using various analytical techniques. UV–Visible spectroscopy confirmed the optical absorption behavior of the nanoparticles, while Fourier Transform Infrared (FTIR) spectroscopy identified the functional groups associated with phytochemicals responsible for nanoparticle stabilization. X-ray diffraction (XRD) analysis revealed the crystalline structure of cobalt sulfide, and scanning electron microscopy (SEM) coupled with energy dispersive spectroscopy (EDS) provided detailed insights into the surface morphology, particle distribution, and elemental composition of the synthesized nanoparticles. Furthermore, the electrochemical performance of the CoS nanoparticles was evaluated for supercapacitor applications using cyclic voltammetry (CV) and electrochemical impedance spectroscopy (EIS). The results demonstrated promising capacitive behavior, good electrical conductivity, and low charge transfer resistance, indicating the suitability of

the synthesized material for high-performance energy storage devices. The microwave-assisted green synthesis method provides a rapid, efficient, and environmentally benign approach for the preparation of CoS nanoparticles with potential applications in advanced supercapacitor technologies

Keywords: Green synthesis, Cobalt sulfide nanoparticles, Jatropha curcas leaf extract Microwave-assisted synthesis and Energy storage device.

Presentation Code: 118

LIFE SCIENCES IN TRANSITION: CURRENT BREAKTHROUGHS AND EMERGING HORIZONS

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ABSTRACT

The life sciences are undergoing a transformative era, driven by innovations that bridge molecular biology, biotechnology, and computational sciences. Present advances such as CRISPR-Cas9 gene editing, RNA-based therapeutics, single-cell omics, and artificial intelligence in drug discovery have redefined research and clinical applications. These breakthroughs are enabling precision medicine, sustainable agriculture, and regenerative therapies. Looking ahead, the future of life sciences is poised to expand into in vivo gene and cell therapies, spatial omics with real-time mapping, bioprinted functional organs, and eco-conscious laboratory practices. While these developments promise unprecedented benefits for human health and environmental sustainability, they also raise ethical, regulatory, and accessibility challenges. The integration of global collaboration, responsible innovation, and sustainability will be critical in shaping the trajectory of life sciences. This synthesis highlights the continuum from present achievements to future possibilities, underscoring the discipline's role in addressing complex biological and societal needs

Keyword: Life sciences, CRISPR-Cas9, RNA therapeutics, artificial intelligence, single-cell omics, regenerative medicine, bioprinting, sustainability, precision medicine, future innovations

Presentation Code: 121

EMERGING TECHNOLOGIES IN LIFE SCIENCES: INTEGRATING GENERATIVE AI, SYNTHETIC BIOLOGY, AND ADVANCED THERAPEUTICS FOR FUTURE INNOVATIONS

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ABSTRACT

The recent developments in Emerging Technologies has led to phenomenonal advances in the field of Life Sciences.In the present study,advances in different fields of Life Sciences are studied for better understanding of interdisciplinary application of the the technologies and their impact.Genenerative AI and synthetic biology paved the way for precision editing using Prime editing and Base Editing technologies.Al driven genomics foundation models serve as language models and predict the function of genes and synthesize new functional synthetic DNA sequences.Generative models -Evo2 and Alpha Fold 3 can design synthetic DNA,RNA and enzymes.Organ -on- a -chip and body -on -a- chip technologies simulate the invivo conditions in the organs.This provides an alternative to drug discovery and testing in animals.Synthetic Biological Intelligence merges living cells with digital platforms.This can generate more human centric results by integrating human cognitive model mechanisms with AI for enhancing efficiency of computing platforms .Cell free synthesis allows for the production of desired biomolecules from cell extracts rather than using whole cells.This eliminates the need for maintaining large cultures.CAR T - Cell therapy, Universal T - Cell vaccines and m- RNA based vaccines have shifted the dynamics of disease treatment and recovery.Al based data analytics play a vital role in wild life life monitoring and e - DNA helps in the discovery of the animals without invading the organisms thereby promoting wild life conservation with minimal human interaction.The Brain Computer Interface allows individuals to execute actions by commanding through thought which can improve the life of people with neuro motor disabilities.There is a wide scope for further research in the present emerging technologies in the field of Life Sciences for the welfare of life on the earth and conservation of environment.

Key words: Prime Editing, Base Editing, Evo -2, Alpha Fold -3, organ- on- a -chip, body -on -a chip, e -DNA, Brain computer interface

Presentation Code: 122

BIOLOGICAL INNOVATIONS FOR LIFESPAN AND HEALTH SPAN OPTIMIZATION

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ABSTRACT

Human longevity research is redefining the biological limits of aging by transitioning from passive observation to active intervention within Life Sciences. Rather than merely prolonging survival, contemporary approaches emphasize the optimization of health span, ensuring sustained physiological efficiency and cognitive integrity across extended years. Aging is now conceptualized as a dynamic and plastic process governed by interrelated mechanisms, including Cellular Senescence, mitochondrial decline, and Epigenetic Modification, which collectively drive systemic deterioration. Cutting-edge developments in Regenerative Medicine and Synthetic Biology are enabling precise manipulation of these aging determinants. Senolytic interventions are designed to selectively eliminate senescent cells, thereby mitigating chronic inflammation and enhancing tissue homeostasis. Concurrently, innovations in Stem Cell Therapy offer promising avenues for cellular rejuvenation and organ repair. Central metabolic regulators such as the mTOR Signaling Pathway and Autophagy further represent critical targets for modulating longevity. The integration of Artificial Intelligence is accelerating the identification of aging biomarkers and facilitating predictive, personalized therapeutic strategies. As longevity science advances, it not only challenges traditional perceptions of aging but also necessitates careful consideration of ethical, social, and accessibility dimensions. Ultimately, the extension of the human timeline is evolving into a deliberate scientific endeavor aimed at achieving prolonged vitality, resilience, and enhanced quality of life.

Presentation Code: 134

BIO-ASSISTED SONOCHEMICAL PREPARATION OF CEO_2 NANOPARTICLES USING CENTELLA ASIATICA AND THEIR PHOTOCATALYTIC ACTIVITY TOWARD METHYL RED DYE

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ABSTRACT

The development of environmentally friendly synthesis methods for nanomaterials has gained significant attention in recent years due to increasing concerns regarding environmental sustainability and green chemistry. In this study, pure cerium oxide (CeO_2) nanoparticles were synthesized via a green sonochemical approach using the leaf extract of Centella asiatica as a natural reducing and stabilizing agent. The bioactive phytochemicals present in the plant extract facilitated the formation and stabilization of CeO_2 nanoparticles without the use of toxic chemicals. The synthesized nanoparticles were characterized using various analytical techniques such as X-ray diffraction (XRD), Fourier transform infrared spectroscopy (FTIR), UV–visible spectroscopy and scanning electron microscopy (SEM) to determine their structural, morphological, and optical properties. The results confirmed the formation of crystalline CeO_2 nanoparticles with nanoscale dimensions and good dispersion. The photocatalytic performance of the synthesized nanoparticles was evaluated through the reduction of methyl red dye under light irradiation. The CeO_2 nanoparticles exhibited excellent photocatalytic activity, leading to significant degradation of methyl red dye within a short reaction time. The enhanced photocatalytic efficiency is attributed to the high surface area, improved charge separation, and the presence of phytochemical

residues from Centella asiatica that facilitate electron transfer. This green sonochemical synthesis method offers a simple, cost-effective, and eco-friendly route for producing CeO_2 nanoparticles with promising applications in wastewater treatment and environmental remediation.

Keywords: Green synthesis, Cerium oxide nanoparticles, Centella asiatica, Sonochemical synthesis, Photocatalysis, Methyl red dye degradation.

Presentation Code: 138

PHARMACEUTICALLY OPTIMIZED GREEN SYNTHESIS OF GOLD NANOPARTICLES USING KALANCHOE PINNATA: A MULTIVARIATE STATISTICAL APPROACH

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ABSTRACT

The development of efficient and stable nanomaterials is critical for advancing pharmaceutical applications. This study focuses on the statistically optimized, green synthesis of gold nanoparticles (Au NPs) using aqueous Kalanchoe pinnata leaf extract, targeting their potential in drug delivery and theranostics. A hybrid experimental strategy, transitioning from one-factor-at-a-time screening to a 5-factor Box–Behnken design, was employed to model and simultaneously optimize critical synthesis parameters governing the nanoparticles' pharmaceutical-grade properties. Multi-response optimization via a desirability function was used to minimize the surface plasmon resonance peak (λmax) for smaller particle size while maximizing absorbance intensity for enhanced plasmonic yield—both key for biological efficacy. Highly predictive quadratic models (R2 >0.97) identified an optimized synthesis condition (0.44 mM precursor 3.50% v/v AKPLE, pH 7.2, 80.6℃, 66.7 min). Characterization confirmed that synthesis under these conditions produced spherical, crystalline, and monodisperse Au NPs (average TEM size: 26.3 ± 4.1 nm) with excellent colloidal stability (zeta potential: –30.45 mV), a pre-requisite for pharmaceutical formulation. This validated, multivariate framework establishes a precise method for producing biocompatible Au NPs with tailored physicochemical properties. The resulting nanoparticles exhibit ideal characteristics for diverse pharmaceutical applications, including targeted drug delivery, photothermal therapy, and as contrast agents in bioimaging, offering a scalable and sustainable alternative to conventional synthesis methods.

Keywords: Pharmaceutical Nanotechnology, Green Synthesis, Gold Nanoparticles, Kalanchoe pinnata, Response Surface Methodology, Drug Delivery.

Theme-8:

MICROBIOLOGY, PARASITOLOGY AND IMMUNOLOGY

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106	T. Rajyalaxmi, J. Mounika, G. Shamitha	Isolation and Morphological Characterization of Leaf-Associated Fungi from Terminalia arjuna
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Presentation Code: **5**

MOLECULAR CHARACTERIZATION OF EMERGING BACTERIAL PATHOGENS AND AMR GENES IN TELANGANA AQUACULTURE SYSTEMS

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ABSTRACT

Aquaculture has emerged as one of the fastest-growing food-producing sectors in India, with Telangana representing a major inland fish-producing state. However, intensification of farming practices, indiscriminate antibiotic usage and environmental stressors has contributed to the emergence of bacterial diseases and antimicrobial resistance (AMR) in aquaculture systems. The present study focuses on the molecular characterization of emerging bacterial pathogens and the detection of antimicrobial resistance genes in aquaculture farms across Telangana. Fish samples exhibiting clinical signs such as fin rot, gill necrosis, hemorrhages and ulcerative lesions, along with pond water and sediment samples were collected from major aquaculture districts. Bacterial isolates were identified through phenotypic characterization and confirmed using 16S rRNA gene sequencing. Predominant pathogens included species of Aeromonas, Vibrio, Edwardsiella, Pseudomonas and Flavobacterium. Molecular screening for AMR determinants was performed using PCR-based detection of resistance genes, including β-lactamase genes (bla_TEM, bla_SHV), tetracycline resistance genes (tetA, tetM), sulfonamide resistance genes (sul1, sul2) and quinolone resistance genes (qnrA, qnrS). The study revealed a high prevalence of multidrug-resistant (MDR) isolates with several strains harboring multiple resistance determinants. Biofilm-forming ability was also observed in selected isolates, potentially enhancing persistence and horizontal gene transfer in aquatic environments.

Keywords:
Molecular characterization, Emerging bacterial pathogens, Antimicrobial resistance (AMR), Multidrug resistance, Aquaculture, 16S rRNA sequencing, AMR genes, Biofilm formation.

Presentation Code 28

DENGUE FEVER: THE WORLDWIDE IMPACT OF A MOSQUITO-BORNE DISEASE

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ABSTRACT

Dengue fever is a mosquito-borne viral illness that is quickly spreading over the globe, with significant death and morbidity rates. Dengue fever is an acute viral infection transmitted by Aedes mosquitos and caused by an RNA virus from the Flaviviridae family. For the past ten years, the number of dengue cases has gradually increased in India. Dengue is driven by complex interactions among host, vector and virus that are influenced by climatic factors. During the second half of the twentieth century, dengue became the most widespread vector-borne viral disease of humans, with current estimates of between 50 and 100 million cases of dengue fever per annum worldwide. The most typical symptoms include acute-onset high fever, muscle and joint pain, myalgia, cutaneous rash, hemorrhagic episodes, and circulatory shock. Even though oral symptoms are rarely the main presenting symptom of dengue infection, this can happen in some situations. To reduce mortality, an early and precise diagnosis is essential. The symptoms might vary from asymptomatic fever to life-threatening complications including hemorrhagic fever and shock. Although dengue virus infections are normally self-limiting, the disease has become a public health concern in tropical and subtropical countries. Dengue fever is a major public health concern owing to its rapid worldwide spread, and its burdens are now unmet due to a lack of accurate therapy and a simple diagnostic approach for the early stages of illness.

Keywords: Dengue fever, Aedes (Ae), Clinical symptoms, Pathogenesis, Laboratory Diagnosis, Treatment.

Presentation Code 36

TITLE: FUNCTIONAL CHARACTERIZATION OF BACTERIAL STRAINS FOR BIOSORPTION AND ENZYMATIC RESPONSE UNDER HEAVY METAL STRESS

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ABSTRACT

Soil contamination with heavy metals is considered a major threat to microbial diversity and plant growth. Some bacterial strains have evolved survival strategies to cope with heavy metal stress. The objective of this study is to assess the Biosorption potential of selected bacterial species and to study the enzymatic profile of selected bacterial strains on varying levels of heavy metal toxicity. Bacterial strains showing potential to tolerate heavy metals were grown on nutrient broth with varying concentrations of selected heavy metals. Growth response of bacterial strains to heavy metals has been studied, and enzymatic response has been carried out to assess the impact of heavy metal toxicity on bacterial strains. From the results of this study, it has been found that exposure to heavy metals has a major impact on enzymatic response of bacterial strains. Bacterial strains showed an increase in antioxidative enzymes such as catalase to cope with oxidative stress caused by heavy metal toxicity. The differential enzymatic responses observed among bacterial strains highlight their varied tolerance capabilities and potential mechanisms of resistance under heavy metal stress. Strains exhibiting stable or enhanced enzymatic activities under elevated metal concentrations may serve as promising candidates for bioremediation and environmental management strategies. Overall, the findings of this study provide insights into the biochemical adaptations of bacteria under heavy metal stress and contribute to understanding their potential role in mitigating metal toxicity in contaminated environments.

Keywords: Heavy metal toxicity, Bacteria, Antioxidant enzymes, Mitigation, Biosorption

Presentation Code 39

THE MICROBIOLOGY OF ACTINOMYCETES ORGANISMS KNOWN TO CAUSE FARMER'S LUNG DISEASE AND THEIR OCCURRENCE FROM COAL MINES OF TELANGANA

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ABSTRACT

Farmer's Lung Disease (FLD) is a form of hypersensitivity pneumonitis, an allergic inflammatory disease caused by the inhalation of thermophilic Actinomycetes, a cluster of Gram-positive, filamentous, spore-forming, branching bacteria that flourish in high humidity, high-temperature environments such as moldy silage, grain and manure. FLD incidence is highly variable and depends on multiple factors such as intensity, frequency and duration of exposure, type of farming and climate change. The findings suggest that ecological samples were collected from coal mines of Telangana operated by SCCL, focusing on core and buffer zones to assess thermophilic Actinomycetes, particularly the Streptomyces genus. Research in the region of Kothagudem such as Streptomyces felleus strain confirms the presence of Actinomycetes species that possess strong durable spore structures potentially leading to respiratory and allergic inducing risks similar to FLD. The presence of these organisms in coal dust suggests that pneumoconiosis miners will be at risk for hypersensitivity reactions, highlighting the need to recognize these microbial threats in the industrial environment. This research focuses on the occurrence and distribution of these organisms within the unique ecological niche of the coal mines in Telangana. As a result of these studies, implementing appropriate control measures including personal protective equipment (PPE), proper engineering, environmental controls and safe work practices helps reduce exposure to Actinomycetes and protects farmers' respiratory health.

Keywords: FLD, SCCL, Actinomycetes, thermophilic, fungi, Telangana, coal mines microbiology.

Presentation Code 42

SECONDARY METABOLISM WITH SPECIAL REFERENCE TO ACTINOMYCETES ISOLATED FROM COAL MINES OF TELANGANA AND OCCURRENCE OF ANTIBIOTIC PRODUCTION

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ABSTRACT

Secondary metabolism in microorganisms plays a crucial role in the production of bioactive compounds, particularly antibiotics. Among various microorganisms, Actinomycetes are well known for their ability to synthesize a wide range of secondary metabolites with pharmaceutical importance. Actinomycetes isolated from coal mines of Telangana (Bhupalapally) soils exhibit significant metabolic diversity due to the extreme environmental conditions, including high pressure, limited nutrients, and varying temperatures. These stress conditions often stimulate the production of secondary metabolites, especially antibiotics. These isolates can produce antibiotics with activity against both Gram-positive and Gram-negative bacteria. Starch Casein Agar (SCA) is often considered the best medium for isolating soil-borne actinomycetes, as they efficiently utilize complex carbohydrates like starch. Temperature: 20–30°C (mesophilic). pH: generally neutral (around pH 7.0–7.2). Incubation time: 7 to 14 days (slow-growing). The exploration of coal mine ecosystems therefore represents a promising approach for discovering novel antibiotic-producing microorganisms. Actinomycetes from coal mines may contribute to the development of new antimicrobial agents and help address the growing problem of antibiotic resistance. Hence, coal mine actinomycetes represent an important resource for future pharmaceutical research and drug discovery.

KEYWORDS:
Secondary metabolism, Actinomycetes, Starch Casein Media, Coal mines.

Presentation Code 46

THE MICROBIOLOGY OF ACTINOMYCETES ORGANISMS KNOWN TO CAUSE FARMER'S LUNG DISEASE AND THEIR OCCURRENCE FROM COAL MINES OF TELANGANA

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ABSTRACT

Farmer's Lung Disease (FLD) is a hypersensitivity pneumonitis caused by inhalation of thermophilic Actinomycetes. These are Gram-positive, filamentous, spore-forming bacteria that thrive in environments with high humidity and temperature. The incidence of FLD varies depending on exposure intensity, farming practices, and climate change. This study reports findings from ecological samples collected from coal mines in Telangana operated by SCCL, focusing on thermophilic Actinomycetes, particularly the Streptomyces genus. Research in Kothagudem confirmed the presence of Streptomyces felleus, which produces durable spores capable of causing respiratory and allergic reactions similar to FLD. The study emphasizes the occupational risk to miners from these organisms and highlights the importance of recognizing microbial threats in industrial settings. It advocates for control measures such as personal protective equipment (PPE), engineering solutions, environmental controls, and safe work practices to reduce exposure and protect respiratory health.

Keywords: FLD, SCCL, Actinomycetes, thermophilic, fungi, Telangana, coal mines, Microbiology.

Presentation Code 52

ENTAMOEBA HISTOLYTICA INFECTIONS IN PATIENTS FROM TELANGANA: CULTURE METHODS AND RESPONSE TO ANTIAMOEBIC DRUGS

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ABSTRACT

Entamoeba histolytica is an important protozoan parasite responsible for amoebiasis, which remains a major public health problem in many developing regions including Telangana, India. The present study focuses on the isolation and culture of E. histolytica from patients presenting with gastrointestinal symptoms and evaluates the response of clinical isolates to commonly used antiamoebic drugs. Stool samples collected from suspected cases were examined microscopically for the presence of cysts and trophozoites and were subsequently cultured using suitable xenic and axenic culture media to obtain viable parasite isolates. The cultured trophozoites were maintained under controlled laboratory conditions and subjected to drug susceptibility testing against commonly used antiamoebic agents such as metronidazole, tinidazole, chloroquine, and emetine. The response of the isolates was assessed by measuring growth inhibition and determining inhibitory concentration values. The findings indicate that most clinical isolates show susceptibility to standard antiamoebic drugs, although slight variations in sensitivity were observed among different isolates. Continuous monitoring of drug response is essential to detect emerging resistance and to ensure effective treatment strategies for amoebiasis in endemic regions like Telangana. This study also to determined the tolerance and efficacy of two antiamoebic drugs against these two clinical isolates. Minimum Inhibitory Concentration of Metronidazole and Auranofin of drug were determined by Invitro sensitivity assay, using the microtiter plates. Cell scoring was given by microscopic observation under an inverted microscope. The results show that the isolates were able to tolerate metronidazole at high concentration however Auranofin showed efficacy at low concentration against the clinical isolate of Entamoeba histolytica grown in Xenic cultures.

Keywords: Metronidazole, Auranofin, Clinical isolates, Entamoeba histolytica, Axenic culture, Xenic culture

Presentation Code 72

SCREENING OF PESTICIDE-DEGRADING BACTERIA AND THEIR BIOREMIDIATION EFFICIENCY IN AGRICULTURAL SOILS

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ABSTRACT

The heavy use of pesticides in the agricultural is causing severe risks to soil health, and environment, making it necessary to introduce eco-friendly remediation strategies. The study mainly aims in the isolation and screening of pesticide-degrading bacteria from agricultural soils and also to evaluate their potential for bioremediation. Soil samples will be collected from the selected farming sites and the analysis of the microbial communities will be done to assess diversity and abundance. In this study the main focus will be on identifying the bacterial strains capable of degrading commonly used pesticides. These are then subjected to screening and evaluation of efficiency under controlled lab conditions. The comparative analysis will be carried out mainly to understand the variation occurred in microbial populations due to different farming practices. The findings of the study are expected to contribute to eco-friendly and sustainable bioremediation strategies. This promotes the use of native soil bacteria, which intends to enhance soil fertility, reduce accumulation and support long-term agricultural sustainability.

Keywords
Pesticide-Degrading Bacteria, Bioremediation, Agricultural Soil, Soil Microbial Communities, Sustainable Agriculture, Environment

Presentation Code 80

EXPLOITING INDIGENOUS GUT PROBIOTICS OF ANTHERAEA MYLITTA FOR NUTRITIONAL FORTIFICATION: A COMPARATIVE STUDY WITH SPIRULINA ON LARVAL GROWTH AND POST COCOON TRAITS

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ABSTRACT

The tropical Tasar silkworm, Antheraea mylitta Drury, is an economically important wild sericigenous insect responsible for the production of valuable Tasar silk. Nutritional enhancement of host plant leaves is considered an effective strategy for improving silkworm growth and silk productivity. The present study aimed to comparatively evaluate the influence of Spirulina supplementation and probiotic gut bacterial fortification on larval performance and cocoon characteristics of A. mylitta. Spirulina, a nutrient-rich microalga, was applied to Terminalia arjuna leaves through foliar spraying, while gut bacteria isolated from the silkworm were screened for probiotic potential using acid tolerance and hemolytic assays. The selected probiotic isolate was subsequently used for fortification of host plant leaves and both spirulina-treated and probiotic-fortified leaves were fed to silkworm larvae during the fourth and fifth instars of crop-1 (August) under natural rearing conditions. Key larval and post-cocoon parameters including larval weight, larval length, cocoon weight, shell weight, and filament length were recorded. Both treatments exhibited positive effects on silkworm growth and silk-related traits; however, probiotic bacterial fortification resulted in comparatively higher improvement in several parameters. The findings suggest that probiotic gut bacteria may serve as a promising eco-friendly bio-supplement for enhancing productivity and cocoon quality in Tasar sericulture.

Key words: Tasar, Antheraea mylitta, Gut bacteria, Spirulina, Post cocoon characters.

Presentation Code 106

ISOLATION AND MORPHOLOGICAL CHARACTERIZATION OF LEAF- ASSOCIATED FUNGI FROM *TERMINALIA ARJUNA*

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ABSTRACT

Terminalia arjuna is a medicinally important plant widely recognized for its rich phytochemical composition and associated microbial diversity, particularly endophytic fungi that serve as potential sources of bioactive compounds with significant biological potential. The present study aimed to isolate and characterize fungal endophytes from the leaves of Terminalia arjuna and evaluate their morphological features. Healthy leaf samples were collected, surface sterilized, and inoculated on suitable culture media under aseptic conditions to promote fungal growth. Microscopic observations revealed the presence of characteristic features of the genus Fusarium. The isolate exhibited typical features consistent with Fusarium species, suggesting its occurrence as an endophytic fungus within the leaf tissues. The findings indicate that Terminalia arjuna harbours potentially beneficial fungal endophytes, which may contribute to plant health and serve as a promising source of bioactive compounds.

Key words: Terminalia arjuna, Endophytic fungi, Characterization, Fusarium.

Presentation Code 109

ISOLATION AND IDENTIFICATION OF ENDOPHYTIC FUNGI FROM *TERMINALIA CHEBULA*

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ABSTRACT

Terminalia chebula is a medicinal plant known for its rich bio-active compounds. Endophytic fungi present inside plant tissues are important as they can produce useful secondary metabolites. In the present study, endophytic fungi were isolated and identified from different parts of Terminalia chebula, including raw fruits, medium-aged leaves and dried fruits. The plant samples were collected and surface sterilized, followed by inoculation on culture media to obtain pure fungal isolates. The isolates were identified based on their cultural and morphological characteristics. This study helps in understanding the diversity of Endophytic fungi present in Terminalia chebula.

Key words: *Terminalia chebula*, Endophytic fungi, Inoculation.

Presentation Code 123

BIOPROSPECTING OF MICROORGANISMS FOR NOVEL ENZYMATIC DEGRADATION OF POLLUTANTS

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ABSTRACT

Environmental pollution caused by synthetic organic compounds has emerged as a major global concern due to their persistence, toxicity, and resistance to conventional treatment methods. Microorganisms, owing to their metabolic diversity and adaptability, represent a promising resource for the degradation of such pollutants. The present study focuses on the bioprospecting of diverse microbial populations from contaminated environments for their potential to produce novel enzymes capable of degrading recalcitrant pollutants. Samples are proposed to be collected from various ecological niches, including industrial effluents, wastewater treatment sites, and polluted soils. Isolation and screening of microorganisms will be carried out using selective enrichment techniques to identify strains exhibiting significant degradative potential. Emphasis will be placed on detecting enzyme-mediated degradation mechanisms, particularly those involved in the breakdown of complex organic compounds. Selected microbial isolates will be further characterized based on morphological, biochemical, and molecular parameters. Enzymatic assays will be performed to evaluate the activity and efficiency of pollutant-degrading enzymes. Additionally, optimization of environmental conditions such as pH, temperature, and substrate concentration will be undertaken to enhance enzymatic performance. The study aims to uncover novel microbial strains and enzymatic systems with potential applications in sustainable bioremediation strategies. The findings are expected to contribute to the development of eco-friendly and cost-effective approaches for mitigating environmental pollution. This research highlights the significance of microbial diversity as a valuable tool in addressing current and future environmental challenges.

Keywords: Bioprospecting, Microorganisms, Enzymatic degradation, pollutants, and Enzymatic assays

Presentation Code 125

GUT BACTERIA CAN INJECTED PROTEIN INTO THE HUMAN CELLS

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ABSTRACT

Protein Injection by Gut Bacteria into Human Cells. The human gut hosts a complex and diverse community of microorganisms that play essential roles in digestion, immunity, and overall health. Among these microorganisms, certain bacteria have evolved specialized mechanisms to interact directly with human cells. One such mechanism is the Type III secretion system, a needle-like molecular structure used by some pathogenic bacteria to inject proteins into host cells. This process is primarily observed in harmful bacteria such as Salmonella, Escherichia coli, and Shigella. These bacteria deliver effector proteins directly into human intestinal cells, allowing them to manipulate cellular functions. The injected proteins can alter the host cell's structure, suppress immune responses, and facilitate bacterial survival and replication. As a result, this interaction often leads to infections and gastrointestinal diseases. Despite the harmful effects associated with pathogenic bacteria, it is important to note that not all gut bacteria possess this ability. Beneficial microorganisms, commonly known as probiotics, contribute positively to human health and do not use such invasive mechanisms. Understanding the differences between harmful and beneficial bacteria is crucial for developing targeted therapies and improving gut health. In conclusion, protein injection by certain gut bacteria represents a significant aspect of host–microbe interaction, highlighting both the complexity of microbial behaviour and its impact on human health. This knowledge provides valuable insights for medical research, disease prevention, and therapeutic advancements.

Keywords: Gut microbiota, Type-III secretion system, Effector proteins, Pathogenic bacteria, Host–microbe interaction, Gastrointestinal infections

Presentation Code 126

PARASITIC INFECTION LINKED WHITE SPOT DISEASE (ICHTHYOPHTHIRIUS MULTIFILIIS) MODULATING BEHAVIOUR ALTERATIONS, FEEDING AND STRESS RESPONSE IN MALE BETTA SPLENDENS (REGAN 1910)

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ABSTRACT

The Betta splendens (Regan, 1910) commonly known as fighting fish, the male reproductive success is strongly reliant on energetically costly parental commitment. It has been extensively researched that parasitic infections have a major impact on host physiology, behaviour, and ecological relationships. This study examines the effects of Ichthyophthirius multifiliis-caused White Spot Disease on eating habits, stress reactions, and behavioural changes in Betta splendens (Regan, 1910). In order to determine changes in aggression, activity levels, territoriality, and food response, experimental groups of infected and non-infected individuals were monitored in a controlled laboratory setting. Significant behavioural abnormalities, such as decreased locomotors activity, decreased territorial aggression, and increased erratic movements, were present in infected individuals and were suggestive of physiological discomfort. When compared to controls, the feeding response was much reduced in infected fish, indicating a reallocation of energy toward immune function. Diseased specimens showed much higher levels of stress markers, which were deduced from behavioural indicators including surface gasping and seclusion inclinations. The results emphasise how a major ecological element influencing host behaviour and resource use is parasite infection. Niche dynamics and competitive interactions in aquatic ecosystems may be impacted by changes in aggression and eating behaviour. This research advances our knowledge of host-parasite interactions and their wider consequences for behavioural ecology and fish health management.

Keyword: Betta splendens (Regan 1910), Ichthyophthirius multifiliis, White Spot Disease, Aggression, Feeding and Stress Response.

Theme-9:

MOLECULAR BIOLOGY, GENETICS AND GENOMICS

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Presentation Code: 23

BASELINE PROTEOMIC SIGNATURES OF AQUEOUS HUMOUR AND LENS PROTEINS IN NATIVE SHEEP: IMPLICATIONS FOR EARLY OCULAR DISEASE DIAGNOSIS

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ABSTRACT

Early diagnosis of ocular diseases in sheep requires a clear understanding of the molecular constituents of intraocular fluids and lens tissues. The aqueous humour (AH) and lens proteins play critical roles in maintaining ocular clarity, and their compositional changes can serve as early indicators of ocular pathology in commercial broiler chickens. This study aimed to characterize and purify the major protein fractions of AH and lens tissues to establish baseline molecular signatures of the healthy broiler eye. Eye samples (n = 10) were collected from healthy commercial broilers immediately after slaughter under aseptic conditions. AH was aspirated, and lens tissue was dissected and homogenized in phosphate-buffered saline (0.025 mM). Preliminary protein profiling was performed using SDS-PAGE. To obtain purified protein fractions for better molecular resolution, column chromatography was conducted using Sephadex G-75, enabling effective size-based separation of AH and lens proteins. Electrophoretic analysis revealed major protein bands between ~10 kDa and 55 kDa. AH contained distinct albumin-like, globulin-like, and low molecular weight proteins, whereas lens extracts showed dominant crystallin-rich bands. Chromatographic purification enhanced band sharpness and resolution, allowing precise identification of key protein fractions. Notably, a conserved and prominent 18 kDa protein was consistently detected in both AH and lens samples, suggesting its potential as a reliable molecular marker. Additional fractions, including proteins around 50 kDa and 20–21 kDa, were distinctly separated following purification and may hold diagnostic value. These findings provide a foundational proteomic profile of AH and lens tissues in broiler chickens and highlight candidate proteins that may serve as biomarkers for the early diagnosis of ocular diseases. Further proteomic validation and clinical correlation are needed to develop a rapid field-level diagnostic tools for poultry ophthalmic health management.

Keywords: Aqueous humour, Lens Proteins, Biomarkers, Ocular diseases, sheep

Presentation Code: 50

MOLECULAR AND GENOMIC INNOVATIONS IN NON-MULBERRY SILKWORMS

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ABSTRACT

Non-mulberry sericulture plays a vital role in the rural economy of India by providing sustainable employment, reducing rural migration, and supporting eco-friendly livelihood opportunities. India holds a unique position as the only country producing all four major types of silk: mulberry and non-mulberry varieties. Among the non-mulberry silks, the tropical tasar silkworm, Antheraea mylitta, is a semi-domesticated wild sericigenous insect widely reared in North and Central India, while Antheraea assama (Muga) and Philosamia ricini (Eri) are primarily cultivated in the North-Eastern region. Despite its socio-economic importance, the sector requires significant improvement in rearing practices, cocoon productivity, and effective marketing strategies. Advancements in molecular biology have opened new avenues for understanding the genetic architecture and improving desirable traits such as silk yield and quality, fecundity, emergence, oviposition, behavior, voltinism, and disease resistance. Molecular characterization through DNA-based markers has become an essential tool for identifying and conserving valuable genetic resources. Techniques such as Simple Sequence Repeat (SSR), Inter-Simple Sequence Repeat (ISSR) and Expressed Sequence Tags (ESTs) are widely used to study genetic diversity and identify target traits in silkworm populations. Genetic diversity studies among geographical races of A. mylitta facilitate hybridization programs for the development of economically superior strains. Additionally, genomic databases such as WildSilkbase provide valuable EST resources for comparative genomics, evolutionary studies, and functional analysis. The study of non-mulberry silkworms and their host plants in the lines of DNA profiles, protein profiles, population genetics, geographic distribution, comparative genomics suggest an increased scope of improvement in non mulberry sericulture

Keywords: genetic studies, *A.mylitta*, *A.assama*, *P.ricini*, Biotechnological

Presentation Code: 74

MOLECULAR REGULATION OF ENDOMETRIAL RECEPTIVITY IN CAPRA HIRCUS: INTERFERON-T MODULATES IMPLANTATION-ASSOCIATED GENE EXPRESSION

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ABSTRACT

Successful embryo implantation requires a receptive endometrium characterized by coordinated molecular and cellular changes within the uterine microenvironment. In ruminants such as cattle, buffalo, sheep and goats, ovarian hormones such as estradiol (E2) and progesterone (P4), along with embryo-derived interferon-tau (IFN-τ), mediate endometrial receptivity and maternal recognition of pregnancy. However, the molecular mechanisms underlying these interactions in goats remain poorly understood. In the current study, the goat endometrial epithelial cells (GEEC) were isolated and characterised for their molecular signatures. In brief, GEECs were treated with luteal phase levels of E2 and P4, followed by IFN-τ stimulation to mimic the peri-implantation uterine microenvironment. Quantitative real-time PCR was carried out to evaluate the expression of implantation-associated genes, using GAPDH as the reference gene. Results revealed that IFN-τ treatment distinctly upregulated the interferon-stimulated gene 15 (ISG15), confirming activation of interferon signalling pathways in GEEC. In contrast, luteolytic mediator COX2 was significantly downregulated following IFN-τ stimulation, hinting that IFN-τ protects corpus luteum from luteolysis. These findings suggest that IFN-τ, in synchronization with ovarian hormones, regulates key genes involved in immune signalling and epithelial remodelling in GEEC, providing insights into embryo–maternal communication and the molecular mechanisms governing implantation in goats.

Keywords: Epithelial Cells, Goat, IFN-T, ISG15, Pregnancy

Presentation Code: 77

TISSUE-SPECIFIC EXPRESSION OF ESTERASES IN CATFISH (HETEROPNEUTES FOSSILIS) AND THEIR ROLE IN XENOBIOTIC METABOLISM

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ABSTRACT

Fresh water ecology is constantly under stress due to continuous use of agrochemicals especially the pesticides (The pesticide residues in fresh water system). Pesticide have been widely used all over the world to control insects, pests and other disease vectors. The fish Heteropneustes fossilis was used as test organism in aquatic environment. Esterases are the enzymes catalysing the formation and break down of carboxylic acid esters of alcohols. They preferentially hydrolyse the triglycerides and esters of long chain fatty acids. Esterases are used as a bioindicators to measure the toxic potency of pesticide residues usually applied in agriculture. The Organophosphates, carbamates and the pyrethroids are extensively used across the world to protect agriculture crops, animals and human health and in preservation of materials against the insect damage. Pesticide toxicity to fish has been investigated in several studies. These studies investigates the study of esterase enzymes and the role of detoxification in the Heteropneustes fossilis at molecular level i.e., protein. The proteins are fractionised into soluble and insoluble fractions after extracting them into physiological buffer solutions. Both soluble and insoluble fractions are quantified by lowrys method and by colorimetric absorption at 650 nm.Biochemical analysis of Proteins and Lipids were also performed The results will be presented during the seminar.

Keywords: Xenobiotic, Bioindicators, Esterases, Detoxification

Presentation Code: 86

THE EFFLUX GATEKEEPER: STRUCTURAL DYNAMICS AND THERAPEUTIC TARGETING OF ABC TRANSPORTERS IN MULTIDRUG RESISTANCE

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ABSTRACT

One of the major groups of protein molecules bound to membranes consists of ATP-binding cassette (ABC) transporters. They participate in the transportation of various chemical compounds. These proteins use ATP hydrolysis as a driving force to move substrates across the membrane against a concentration gradient. ABC proteins serve as critical physiological and pharmacological gatekeepers, transporting lipids, bile salts, and toxins. These efflux pumps function as innate defense mechanisms, directly modulating drug bioavailability and excretion. Central to this phenomenon is the overexpression of ATP-Binding Cassette (ABC) transporters, a superfamily of transmembrane proteins—most notably P-glycoprotein (ABCB1), MRP1 (ABCC1), and BCRP (ABCG2) — that actively extrude a chemically diverse array of therapeutic agents. the molecular architecture of ABC transporters and evaluates the transition from traditional competitive inhibitors to modern, "stealth-based" pharmacological interventions. cryo-EM data supports an 'alternating access' model, where ATP binding at the Nucleotide-Binding Domains (NBDs) drives a conformational flip from an inward- to an outward-facing state, effectively purging cytotoxic substrates from the cell. The energy expenditure is governed by the hydrolysis reaction:

$$ATP + H2O \longrightarrow ADP + Pi + \text{Solute Extrusion}$$

While conventional chemosensitizers suffer from blood-brain barrier toxicity, lipid nanoparticles and 'collateral sensitivity agents effectively restore drug efficacy by bypassing efflux or exploiting the high metabolic demands of ABC transporters. Future therapies must evolve from simple pump antagonists to sophisticated genetic and nano-delivery platforms. A deep understanding of ABC transporter structural dynamics remains the foundation for developing more effective, next-generation drugs for cancer and superbugs.

Keywords: Multidrug resistance, ATP-binding cassette, P-glycoprotein, Cryo-Electron Microscopy, Nucleotide-Binding Domains, Efflux Pumps

Presentation Code: 103

TARGETING MITOCHONDRIAL, METABOLOMIC AND EPIGENETIC SIGNATURES IN TRIPLE NEGATIVE BREAST CANCER: A NOVEL THERAPEUTIC STRATEGY.

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ABSTRACT

Triple negative breast cancer (TNBC) is an aggressive, highly metastatic, chemoresistant molecular subtype with poor prognosis features by absence of estrogen (ER), Progesteron (PR) and human epidermal growth factor 2 (HER2) expressions. It accounts for 15-20% of all breast cancers, posing a challenge to therapeutic interventions. Emerging evidences implicates the mitochondrial dysfunction, altered metabolomics and aberrant epigenetic regulators are key drivers in TNBC pathogenesis offering a targetable molecular signatures. TNBC cells show upregulated DRP1, NDUFS, MFNS, and pink proteins with elevated Reactive oxygen species (ROS) and shows a metabolomic shift towards oxidative phosphorylation (OXPHOS) and majorly depends on glutamine metabolism. These metabolomic hallmark signatures fuels epigenetic remodelling through S- Adenosylmethionine (SAM), α-Ketoglutarate and Acetyl Co-A bioavailability. 2- hydroxyglutarate, a oncometabolite modulates the activity of histone demethylases and TET enzymes and bridges the cross-talk loop between epigenetic silencing of tumor suppressor genes and metabolomic reprogramming. Inhibitors of mitochondrial complex-I (Rotenone, Metformene) , DNMT inhibitors (5-Azacytidine), HDAC inhibitors (Vorinostat, entinostat) and EZH2 antagonists have shown synergistic anti-tumor activity in TNBC In-vitro and In-vivo models by exhibiting more than 70% cell death. The mechanistic interplay among the Mitochondria-Metabolomic- Epigenetic axis indicates a mechanistically integrated and clinically significant therapeutic landscape in TNBC. Co-targeting of these multi-faceted interdependent pathways in synergistic approach may pave a promising path to overcome chemo resistance and improve survival outcomes in the high-risk TNBC patient population.

Keywords: TNBC, Triad- targetable molecular signatures, chemoresistance, Mitochondrial-Metabolomic- Epigenetic Cross-talk. Biomarkers.

Presentation Code: 113

UNRAVELLING THE HETEROGENEITY OF TRIPLE NEGATIVE BREAST CANCER BY INTEGRATIVE MULTI-OMIC ANALYSIS

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ABSTRACT

The highly heterogeneous, aggressive, clinically challenging subtype of Breast Cancer accounting for 15-20 % of Breast cancer cases characterized by the absence of estrogen, Progesteron and HER 2 receptors is Triple Negative Breast Cancer. Very high potential of metastasis, chemo resistance, lack of targeted therapies combined with its high recurrence rate is leading to substantial mortality in TNBC patients. Complex signaling networks and the molecular heterogeneity of TNBC remains obscure despite of extensive research. The molecular heterogeneity of TNBC is revealed by the recent advancement in Multi-Omic Technologies by integrating Genomics, Transcriptomics, Proteomics and Metabolomics along with emerging techniques such as Single cell and Spatial transcriptomics which acts as transformative approaches providing valuable insights about tumor heterogeneity that can be utilized for targeted therapies and identification of potential biomarkers of TNBC. The Multi-omic analysis from genome to metabolome revealed critical insights about Copy Number Alterations, Structural Variants in BRCA 1/ 2, RB1, TP 53, PIK3CA genes, Non coding RNA Networks, Alternative Splicing, Dysregulated Gene Expression, Post Translational Regulatory Mechanisms and Reprogrammed Metabolic Pathways. The Tumor cellular diversity and Tumor Microenvironment interaction understanding is further enhanced by advanced Single Cell and Spatial Transcriptomic techniques. The complex heterogeneous molecular architecture of TNBC can be unraveled by Integrative Multi-Omic Analysis, an indispensable paradigm converging potential insights from Tumor progression to Drug Resistance. Ultimately, Advances in Integrative Multi-omic analysis holds the potential to revolutionize Triple Negative Breast Cancer diagnostics, personalized targeted treatment and precision medicine.

Keywords: TNBC, Integrative Multi-Omic Analysis, Single Cell Transcriptomics, Spatial Transcriptomics, Personalized therapy.

Presentation Code: 135

CRISPR-CAS9 MEDIATED FUNCTIONAL ANALYSIS OF RAS ONCOGENE HOMOLOGS IN DROSOPHILA MELANOGASTER: IMPLICATIONS FOR COLORECTAL CANCER

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ABSTRACT

Colorectal cancer (CRC) is driven by aberrant activation of RAS oncogenes, including NRAS, KRAS, and HRAS, which regulate critical signaling pathways involved in cell proliferation and survival. Due to the high evolutionary conservation of these genes, Drosophila melanogaster serves as a robust model for investigating RAS-mediated oncogenic mechanisms. The present study integrates comparative homology analysis with CRISPR-Cas9–mediated functional validation to elucidate the conserved role of RAS signaling in CRC. Initially, sequence retrieval and multiple sequence alignment were performed to assess homology between human RAS genes and the Drosophila homolog RAS64B. Phylogenetic and conserved domain analyses revealed significant sequence identity, particularly within GTP-binding and effector regions, indicating strong evolutionary conservation. Structural modeling further confirmed similarity in protein conformation and functional motifs. To validate functional conservation, CRISPR-Cas9 gene editing was employed to target the RAS64B locus in Drosophila melanogaster. Guide RNAs were designed to induce site-specific mutations, including knockout and targeted modifications mimicking oncogenic variants. Edited lines were screened and subjected to PCR-based validation and gene expression analysis. CRISPR-mediated perturbation of RAS64B resulted in observable phenotypic alterations and dysregulation of downstream signaling pathways, consistent with oncogenic transformation. Comparative expression profiling demonstrated parallels between modified Drosophila models and human CRC-associated RAS activity. These findings confirm the functional equivalence of RAS homologs across species. In conclusion, this study highlights the integration of computational and genome-editing approaches to investigate conserved oncogenic pathways. The results establish Drosophila melanogaster as a powerful in vivo system for modeling RAS-driven colorectal cancer and provide a foundation for future translational and therapeutic research targeting RAS signaling.

Theme-10:

PHARMACEUTICAL APPLICATIONS IN BIOLOGICAL SCIENCES

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Presentation Code: 08

SNAKE VENOMS AS A NOVEL SOURCE OF ANTIVIRAL AGENTS: MECHANISMS, THERAPEUTIC POTENTIAL, AND BIOMEDICAL APPLICATIONS

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ABSTRACT

Snake venoms are emerging as a promising reservoir of antiviral agents due to their diverse composition of bioactive molecules, including proteins, peptides, enzymes, and toxins. These components exhibit unique biological activities that can inhibit viral replication, modulate immune responses, and induce cytotoxic effects in infected cells. Notably, peptides from snake venoms have demonstrated inhibitory activity against HIV and SARS-CoV-2 by targeting viral proteases and capsid glycoproteins. L-amino acid oxidases (LAAOs), phospholipases A_2, and other venom-derived enzymes show antimicrobial and cytotoxic properties, with potential antiviral implications. Detoxified neurotoxins from elapid snakes have been shown to enhance the expression of gamma interferon, a key antiviral cytokine, highlighting their role in immune stimulation. While much of the current literature emphasizes antimicrobial and anticancer properties, increasing evidence supports the potential of venom-derived compounds as broad-spectrum antiviral agents. These molecules can also be optimized for reduced immunogenicity and enhanced specificity, making them attractive candidates for drug development. Biomedical applications include their use in novel drug formulations, immune therapeutics, and potential alternatives to antiviral vaccines. Despite challenges related to toxicity and complex venom composition, advances in venom research and biotechnological tools continue to unveil new therapeutic avenues. This review underscores the untapped potential of snake venoms in antiviral therapy and the need for further clinical investigations.

Keywords: Snake venom; Antiviral agents; Bioactive peptides; L-amino acid oxidase (LAAO); Immune modulation; Drug discovery; Viral inhibition; COVID-19; HIV; Therapeutic applications

Presentation Code: 24

GREEN NANOMEDICINE: PHARMACEUTICAL HORIZONS WITH GOLD AND SILVER NANOPARTICLES

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ABSTRACT

The advent of nanotechnology has revolutionized pharmaceutical sciences, offering innovative solutions for drug delivery, diagnostics, and therapeutics. Among various nanomaterials, gold and silver nanoparticles have attracted significant attention due to their unique physicochemical properties, biocompatibility, and multifunctional applications. Conventional synthesis methods, however, often involve toxic chemicals and energy-intensive processes, raising concerns about sustainability and safety. Green synthesis, employing biological resources such as plant extracts, microbes, and biomolecules, provides an eco-friendly alternative that aligns with the principles of sustainable development. This approach not only reduces environmental impact but also enhances the biological functionality of nanoparticles through natural capping agents. Green-synthesized gold and silver nanoparticles exhibit promising pharmaceutical applications, including antimicrobial, anticancer, anti-inflammatory, and targeted drug delivery activities. Their ability to interact with biomolecules at the cellular and molecular levels opens new horizons in nanomedicine, particularly in precision therapeutics and regenerative medicine. Furthermore, the integration of traditional ecological knowledge with modern nanotechnology fosters a holistic framework for sustainable healthcare innovations. This review highlights the current progress, challenges, and future prospects of green-synthesized gold and silver nanoparticles in pharmaceutical sciences, emphasizing their potential to bridge biological sustainability with advanced medical applications.

Keywords:
Green synthesis, Gold nanoparticles, Silver nanoparticles, Nanomedicine, Pharmaceutical applications, Sustainable biotechnology, Drug delivery, Antimicrobial activity, Biocompatibility, Eco-friendly nanotechnology.

Presentation Code: 69

THE ANTI-INFLAMMATORY PROPERTY OF ALGAE-BIOMOLECULES IN GUT HEALTH MANAGEMENT

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ABSTRACT

The biomolecules that were isolated through the application of algae have a substantial potential of being novel agents that are utilized to improve gut health since they contain a high anti-inflammatory effect. This abstract sheds the light on the emerging facts where most of the algae species; brown, green as well as red synthesize bioactive compounds such as polysaccharides, polyphenols and unique lipids that can affect the inflammatory pathways involved in gut disorders like inflammatory bowel disease (IBD). Research shows that algal metabolites such as fucoidans, laminarins, as well as special lipids can reduce pro-inflammatory cytokines and oxidative stressive markers and help to restore intestinal barrier functions and promote beneficial microbiota. The mechanisms offer an alternative that is not pegged on the conventional medicines that could be employed to counter the different inflammatory activities of the gut by the natural and low-toxicity compounds. The novelty of this review is to offer the overview of the latest findings that show how algae-derived biomolecules can be utilized as an alternative or as a supplement to the existing anti-inflammatory drugs and underline which types of algae species and molecular groups are most promising. All this evidence supports the use of algae-derived agents as good and next-generation alternatives to the strategic management and prevention of gut inflammatory disorders.

Keywords: Inflammatory Bowel Disease, Polysaccharides, Anti-inflammatory, Biomolecules of algae.

Presentation Code: 70

FORMULATION AND EVALUATION OF AN HERBAL HYDROGEL CONTAINING GINGER, COLEUS FORSKOHLII AND GARCINIA CAMBOGIA FOR THE MANAGEMENT OF LOCALIZED OBESITY

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ABSTRACT

Obesity is a worldwide health issue linked to metabolic disorders and cardiovascular problems. Besides affecting health, localized fat deposits in areas like the abdomen, thighs, and arms also spoil one's physical appearance. Conventional approaches of treatment, such as oral drugs and surgical interventions, sometimes lead to side effects, and therefore, there is a demand for safe and efficient alternatives. Herbal medicines, because of their natural origin. Therapeutic benefits and low side effects have become popular.This study is aimed at making and assessing an herbal hydrogel with extracts of Z.officinale, Coleus forskohlii, and Garcinia cambogia for controlling localised obesity. The plant materials were cleaned, dried, and powdered, and then solvent extraction methods were used to get then subjected to preliminary phytochemical screening to ascertain major bioactive constituents. After that, the extracts were added to the hydrogel base to make the herbal formulation.
Physiochemical parameters such as appearance, pH, viscosity, and spreadability were the criteria for evaluation of the prepared hydrogel. The data indicated good physical characteristics and suitable properties for tropical applications. According to the research, the herbal hydrogel that has been designed could be a good topical obesity, but pharmacological studies are necessary

Keywords: Herbal hydrogel, localized obesity, Medicinal plants, Phytochemical screening, Topical formulation.

Presentation Code: 79

DESIGN, SYNTHESIS, AND SCREENING OF PHARMACOPHORE-BASED MOLECULES AGAINST CANCER TARGETS USING *IN SILICO* METHODS.

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ABSTRACT

The JAK–STAT signaling pathway plays a critical role in regulating cellular processes such as proliferation, differentiation, apoptosis, and immune responses. Dysregulation of this pathway is closely associated with the progression of various cancers and inflammatory diseases. Among the key proteins involved in this pathway are Janus Kinase (JAK) and Signal Transducer and Activator of Transcription (STAT), which serve as important therapeutic targets for drug development. In the present study, different signaling pathways related to cancer progression were analyzed, and the JAK–STAT pathway was selected due to its significant role in tumor development.
Molecular docking studies were performed to identify potential pharmacophore molecules that could inhibit JAK and STAT proteins. The three-dimensional structure of the JAK protein (PDB ID: 3LXK) was used as the target receptor for docking analysis. Several ligand molecules werescreened using Auto Dock to evaluate their binding affinity and interaction patterns with the active site residues of the protein. The docking results revealed that the selected ligand exhibited a binding energy of −6.14 kcal/mol with the JAK protein (3LXK), indicating a stable interaction and potential inhibitory activity. Analysis of the ligand–protein complex highlighted key molecular interactions responsible for binding stability, suggesting important pharmacophore features for effective inhibition. These findings provide insights into the structural requirements of JAK inhibitors and may support the development of novel therapeutic agents targeting the JAK–STAT pathway for cancer treatment.

Presentation Code: 92

NANOPARTICLE-MEDIATED TARGET DRUG DELIVERY SYSTEMS FOR PULMONARY NEOPLASM THERAPY

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ABSTRACT

Pulmonary neoplasm remains one of the leading causes of cancer-related death worldwide. Nanoparticle-mediated target drug delivery methods have shown promise in improving the effectiveness and reducing the negative effects of traditional treatment against cancer. While nanoparticle-based formulations for the management of pulmonary neoplasms. It is crucial to consider the design principles that underpin these systems, such as the composition, surface, size, and targeting ligands of nanoparticles. Strategies like taking advantage of the enhanced permeability and retention effects, active targeting with particular ligands, or stimuliresponsive release mechanisms triggered by the tumor microenvironment are probably some of the ways by which nanoparticle-based drug delivery systems accomplish selective delivery to pulmonary cancer cells. This review discusses the preclinical and clinical studies that show how a nanoparticle-based drug delivery system can improve pulmonary neoplasm patients' therapeutic outcomes. The study also discusses the benefits and drawbacks of several kinds of nanoparticles, polymeric nanoparticles, liposomes, and inorganic nanoparticles. We have discussed the data from preclinical and clinical research showing how nanoparticle-based drug delivery systems can improve pulmonary neoplasm patients' therapeutic outcomes. Thus, this review work addresses the potential of nanoparticle-based target drug delivery approaches that have addressed the enormous shortcomings of conventional chemotherapy.

Keywords: Pulmonary neoplasm, Targeted drug delivery, Liposomes, Nanoparticles, Preclinical and clinical studies.

Presentation Code: 95

ANTIDIABETIC ACTIVITY AND LIPID PROFILES IN DIABETIC INDUCED WISTAR RATS TREATED WITH PLANT EXTRACTS AND COMPARATIVE STUDIES.

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ABSTRACT

Diabetes mellitus is a chronic metabolic disorder, characterized by hyperglycemia resulting from defects in insulin secretion, insulin action or both. This investigation was designed to study the antidiabetic activity and lipid profiles was investigated in diabetic induced Wistar rats treated with plant extracts and comparative studies. Diabetes was induced after a single intra peritoneal injection of Alloxan drug (120 mg/ kg). Rats were divided into seven groups with 6 rats in each group: 1. Normal control rats, 2. Diabetic Control rats (Untreated, Alloxanized), 3.Diabetic rats administered with Glybenclamide drug (600µg/kg/bw) as reference standard drug while, 4.Diabetic rats administered with Hemedesmus indicus leafextract (11mg/bw), 5.Diabetic rats administered with Cassia auriculataflower extract (7 mg/bw), 6. Diabetic rats administered with Chloroxylon swietenia bark extract (8 mg/bw), 7.Diabetic rats administered with Tinosporacordifolia leaf extract (10 mg/bw). The parameters studied were lipidprofile like Total cholesterol (TC), Triglyceride (TG), High-density lipoprotein (HDL), Low-density lipoprotein (LDL). The result of test drug was compared with diabetic control. Glibenclamide (600µg/kg/bw) was selected as standard hypoglycaemic drug. Administration of plant extracts shows the antidiabetic activity and reduction in blood glucose level at 7thday. Administration of plant extracts also shows decreased in serum TC, TG, ,HDL, LDL in diabetic induced wistar rats. The results obtained from the present study revealed the potential Antidiabetic activity of selected plant extracts *Hemedesmusindicus, Cassia auriculata, Chloroxylon swietenia* and *Tinospora cordfiolica.*

Keywords: Traditional healers, Medicinal plants, Ethnobotanical survey, diabetes milletus, lipid profile.

Presentation Code: 116

RATIONAL DESIGN AND SYNTHESIS OF THE LACTONE NATURAL PRODUCT PASSIFETILACTONE B

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ABSTRACT

The total synthesis of structurally complex natural products continues to be a central challenge in modern organic chemistry due to their significant biological potential and synthetic intricacy. Passifetilactone B is a bioactive lactone-containing natural product characterized by a unique molecular framework and promising pharmacological relevance. Developing efficient synthetic strategies for such molecules is crucial for enabling further biological investigations and structural modifications. In this study, a concise and strategically designed synthetic route toward the construction of Passifetilactone B was investigated. The synthetic pathway was developed through a sequence of carefully optimized organic transformations, including key carbon–carbon bond forming reactions, functional group interconversions, and stereoselective steps leading to the formation of the lactone core. Particular emphasis was placed on improving reaction efficiency, yield optimization, and minimizing the number of synthetic steps. The developed strategy demonstrates a practical and reliable approach for assembling the complex molecular architecture of Passifetilactone B. This work highlights the importance of rational synthetic planning in natural product synthesis and provides insights that may facilitate the preparation of structurally related bioactive molecules. The methodology reported here may serve as a useful platform for future studies in synthetic and medicinal chemistry.

Presentation Code: 119

GC-MS BASED PHYTOCHEMICAL PROFILING OF TINOSPORA CORDIFOLIA ETHANOLIC EXTRACT: IDENTIFICATION OF BIOACTIVE COMPOUNDS.

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ABSTRACT

Tinospora cordifolia (Giloy) is a highly valued medicinal plant in the Ayurvedic system of medicine, traditionally used for its immunomodulatory, anti-inflammatory and antidiabetic properties. Despite its therapeutic applications, comprehensive phytochemical profiling of its bioactive constituents using modern analytical techniques are essential for scientific validation. The present study aimed to investigate the phytochemical composition of the ethanolic extract of Tinospora cordifolia leaves through Gas Chromatography-Mass Spectrometry analysis to identify the major bioactive compounds responsible for its therapeutic potential. The leaves material of T. cordifolia was subjected to maceration using ethanol as the solvent. The resulting extract was analysed by GC-MS, separated compounds were compared with the library for identification. The Total Ion Chromatogram (TIC) was examined, and the relative percentages of the identified compounds were calculated based on peak area. The ethanolic extract of Tinospora cordifolia contains a rich and diverse profile of bioactive phytoconstituents, with sterols and terpenes as the predominant classes. The identification of immunomodulatory sterols and anti-inflammatory triterpenes provides scientific evidence supporting the traditional therapeutic applications. This comprehensive phytochemical profiling contributes to the phytochemical database of *T. cordifolia* and establishes a foundation for future isolation, characterization, and pharmacological evaluation of individual bioactive compounds.

Keywords: *Tinospora cordifolia*, Giloy, GC-MS analysis, phytochemical profiling, bioactive compounds

Presentation Code: 120

NANO-OINTMENT FORMULATION FOR BROAD-SPECTRUM ANTIMICROBIAL APPLICATIONS USING THE BACTERIAL RED PIGMENT PRODIGIOSIN

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ABSTRACT

The emergence of multidrug-resistant pathogens necessitates the exploration of novel bioactive compounds and nanotechnology-based formulations for effective antimicrobial therapies. Prodigiosin, a red pigment produced by certain bacteria, exhibits diverse biological properties, including antimicrobial activity. This study aimed to synthesize silver nanoparticles (AgNPs) using prodigiosin as a biogenic reducing and stabilizing agent, and to formulate a prodigiosin-based nano-ointment. The synthesized nanoparticles were identified by color change and by UV-Vis spectroscopy. The formulated nano-ointment exhibited significant antibacterial activity against Staphylococcus aureus and Escherichia coli, Pseudomonas aeruginosa, Bacillus subtilis and antifungal activity against different strains of Candida. Compared to control formulations, the prodigiosin-AgNP nano-ointment demonstrated enhanced and broad-spectrum antimicrobial efficacy. Prodigiosin acts as a promising biogenic agent for the eco-friendly synthesis of silver nanoparticles. The developed nano-ointment shows potent broad-spectrum antimicrobial activity, highlighting its potential as a novel therapeutic formulation against bacterial and fungal infections.

Keywords: Prodigiosin, silver nanoparticles, nano-ointment, green synthesis, antibacterial, antifungal.

Presentation Code: 124

SPECTRAL ANALYSIS OF ANTIBIOTIC STAUROSPORINE AND ITS ANTIMICROBIAL ACTIVITY

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ABSTRACT

In the current study, twenty soil samples were collected from coalmine sites of Telangana, India. The isolates were identified based on their culture characterization on glycerol asparagine agar, yeast extract-malt extract agar, inorganic salt starch agar, and starch casein agar medium. The supernatant of all the isolates was tested for antimicrobial and antifungal activities. The biochemical and microscopic studies of isolated strains results indicate the potential isolate strains belongs to Streptomyces genus. Among all the strains the biological activity of BHPL-KSKU5 showed higher anti-bacterial and anti-fungal activity. The molecular characterization of BHPL-KSKU5 16s rDNA gene sequence and phylogenetic tree showed that is mostly related to the Streptomyces champavatii strain. This isolate was submitted to gene bank NCBI with accession number MH553077. Based on the spectral analysis like GC-MS, FTIR and NMR (1H and C13) the antimicrobial compound showed similarity to antibiotic compound Staurosporine from S. champavatii (KSKU5).

Presentation Code: 132

PHYTOCHEMICAL PROFILING AND IN SILICO TOXICOLOGICAL ASSESSMENT OF TINOSPORA CORDIFOLIA LEAF EXTRACTS: AN INTEGRATED APPROACH FOR DRUG DISCOVERY

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ABSTRACT

This study investigates the phytochemical profile of Tinospora cordifolia, a plant traditionally valued for its therapeutic properties. Correctly classified under the Menispermaceae family—a key taxonomic distinction from the often-confused Crassulaceae—the plant was analyzed using Gas Chromatography-Mass Spectrometry (GCMS). The primary objective was to create a biochemical blueprint of an aqueous methanol leaf extract and identify its constituent bioactive compounds. The GCMS profiling revealed a diverse array of phytochemicals, including notable compounds like Ferruginol and various phenanthrenol derivatives. Significantly, the extract contained "organo-toxophores"—organic molecules with structural moieties that imply both biological activity and potential toxicological considerations. Recognizing that understanding safety is as critical as identifying efficacy, this research integrated an in silico toxicological assessment using the Toxtree platform. This Quantitative Structure-Activity Relationship (QSAR) tool estimates toxic hazard by determining a compound's Cramer class. By combining empirical analytical chemistry with predictive toxicology, this study outlines a robust framework for evaluating natural therapeutics. The utility of this approach is demonstrated through discussing the predicted toxicity classes of selected anti-cancer and antiviral compounds from T. cordifolia in the context of regulatory decision-making. This integrated methodology offers a powerful, initial filter for prioritizing lead compounds and streamlining the development of safer, nature-inspired pharmaceuticals.

Keywords: *Tinospora cordifolia,* Organo-toxophore compounds, GC-MS, Methanol, Tox-tree.

Presentation Code: 137

B-NAPHTHOFLAVONE AS A POTENT TELOMERASE INHIBITOR IN CERVICAL CANCER CELLS: INSIGHTS FROM IN VITRO ANALYSIS AND MOLECULAR DOCKING STUDIES

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ABSTRACT

Cervical cancer impacts many women globally, with over 500,000 diagnoses and over 300,000 fatalities annually. Cancer treatment generally encompasses many modalities, including surgery, radiation, and chemotherapy, to excise malignancies. Chemotherapy often induces adverse effects, prompting an ongoing quest for novel pharmaceuticals to mitigate them. Telomerase activity is essential for maintaining telomeres and averting senescence, while the suppression of telomerase may induce cellular senescence in cancer cells for therapeutic purposes. Some synthetic and natural compounds function as telomerase inhibitors, although the comprehension of their effects on cervical cancer cells remains insufficient. Our present work investigated the impact of β-Naphthoflavone (BNF), a synthetic flavonoid molecule, on HeLa cell senescence and its interaction with telomerase both in vitro and in silico. Cytotoxic assessment indicated the lack of hemolysis in blood cells at BNF doses of up to 100µM/mL. BNF significantly reduced TA and cell proliferation at initial time points while simultaneously inducing senescence in a dose-dependent manner at a subsequent time point in the cells. Molecular docking experiments revealed strong contact with the active site of telomerase, yielding a Piecewise Linear Potential (PLP) score of -58.55, comparable to the positive control curcumin (-68.55). Our results highlight the complex relationship between telomerase suppression, anti-proliferative effects, and senescence, providing essential insights for the development of innovative telomerase-targeted therapeutics in the future.

Presentation Code: 142

STABILITY INDICATING RP-HPLC METHOD DEVELOPMENT AND VALIDATION FOR THE ESTIMATION OF MOLNUPIRAVIR IN PURE AND MARKETED PHARMACEUTICAL DOSAGE FORM

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ABSTRACT

A novel, simple, rapid, precise, and robust RP-HPLC method was developed for the quantitative estimation of Molnupiravir in both bulk drug and marketed pharmaceutical formulations. Chromatographic separation was successfully achieved using a Develosil ODS HG-5 RP C18 column (15 cm × 4.6 mm, 5 µm) under isocratic conditions. The mobile phase consisted of Methanol and Phosphate buffer (pH 5) in the ratio of 40:60 % v/v, delivered at a flow rate of 1.0 mL/min, with detection carried out at 231 nm. The developed method was validated as per ICH guidelines for parameters such as linearity, accuracy, precision, specificity, robustness, limit of detection (LOD), and limit of quantification (LOQ). The method exhibited excellent linearity over the concentration range of 12–28 µg/mL with a correlation coefficient of 0.999. The LOD and LOQ were found to be 5.004 µg/mL and 15.164 µg/mL, respectively. Accuracy studies demonstrated good recovery, indicating the reliability of the method. The specificity results confirmed that there was no interference from excipients, ensuring selective estimation of the analyte. Overall, the proposed method is efficient, reproducible, and suitable for routine quality control analysis of Molnupiravir in pharmaceutical dosage forms.

Keywords: Molnupiravir, RP-HPLC, Method Development, Validation, Accuracy, Precision, Robustness, Ruggedness, Specificity, ICH Guidelines.

Theme-11:

TOXICOLOGY AND ENVIRONMENTAL HEALTH

CODE NO.	NAME	TITLE
6	CHANDRA SHEKAR CH & V. PRANITHA	HEAVY METAL POLLUTION AND REMEDIATION THROUGH BIOREMEDIATION AND PHYTOREMEDIATION
25	P. ROHINI	ENVIRONMENTAL TOXICOLOGY: MODERN APPROACHES FOR RISK ASSESSMENT
31	ARUN KUMAR AMBASTHA	CYANOBACTERIUM IMPACT ON HEALTH IN CAMPUS WATER TANKS
34	DR. RAVULA SWAPNA	TOXICOLOGY AND ENVIRONMENTAL HEALTH
40	SILIVERU POOJITHA	TOXICOLOGY AND MANAGEMENT OF FUSARIUM TOXINS
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Presentation Code: 06

A COMPREHENSIVE REVIEW ON HEAVY METAL POLLUTION AND ITS REMEDIATION THROUGH BIOREMEDIATION AND PHYTOREMEDIATION APPROACHES

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ABSTRACT

Heavy metal contamination in the environment has become a major concern due to its toxic effects on soil, water, plants, and living organisms. Industrialization, mining, and agricultural activities contribute significantly to this pollution. Conventional remediation techniques are often expensive and environmentally invasive. In contrast, bioremediation and phytoremediation are eco-friendly, cost-effective, and sustainable alternatives. This review explores the sources, impacts, and toxicological effects of heavy metals and critically examines the biological strategies for remediation, with special focus on the role of microbes and plants in detoxifying polluted environments.

Keywords: Heavy metals, Bioremediation, Phytoremediation, Environmental pollution, Detoxification, Hyperaccumulator plants, Microbial remediation

Presentation Code: 25

ENVIRONMENTAL TOXICOLOGY: MODERN APPROACHES FOR ASSESSING ECOLOGICAL AND HUMAN HEALTH RISKS

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ABSTRACT

Environmental toxicology has advanced significantly to address the increasing complexity of pollutants that affect both ecosystems and human health. The emerging contaminants such as microplastics and endocrine disrupting chemicals present significant risks due to their potential for bioaccumulation and biomagnification within food chains. These pollutants can induce significant physiological disturbances including oxidative stress, hormonal imbalance and other cellular alterations. Furthermore, climate driven changes such as temperature fluctuations and extreme weather events influence the distribution, persistence and toxicity of environmental contaminants. These factors often interact with biological stressors, intensifying ecological impacts and emphasising the need for adaptive environmental management strategies. Environmental toxicology is witnessing a paradigm shift from conventional animal- based testing to innovative methodological approaches. High - throughput in vitro screening, organ - on - a chip technologies that mimic tissue level interactions and computational toxicology are transforming toxicological research. Artificial Intelligence and Machine Learning are increasingly used to predict toxicant fate, identify exposure pathways, and evaluate long - term ecological consequences. These technologies help prioritise chemicals for testing, while reducing research costs, and ethical concerns associated with animal experimentation. Modern risk assessment frameworks now integrate genomics, proteomics and metabolomics with agent- based ecological modelling to enable the identification of system level biological responses, including epigenetic modifications associated with pollution related diseases. Such integrative approaches support evidence-based regulatory decisions, guiding emission control policies and promoting sustainable bioremediation strategies for safeguarding ecosystems and public health. The integration of data-driven technologies, non-animal experimental models, and multi-scale ecological modelling is redefining environmental toxicology. These advances enhance the ability to anticipate and mitigate emerging environmental threats, ultimately contributing to the protection of ecosystem integrity and public health in a rapidly changing global environment.

Presentation Code: 31

CYNOBACTERIUM ARE IMPACT ON THE HEALTH OBSERVED IN MAGADH UNIVERSITY CAMPUS WATER TANKS, SITUATED IN BODHGAYA IN PRESENT SCINARIO

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ABSTRACT

Cynobacteria is found in the water tank kept on the wall in Magadh University Quarters, which is very toxic in water. Actually, the reason behind this is blue green algae or cyanobacteria & also called microcystic algae. Which can be seen floating and bubbling on the top of the water tank, which is making the drinking water are poisonous. It's very harmful for the residents of Magadh University quarter. Algae can be identified by a green, somewhat thick, paint-like layer, which can be seen floating on the water of the tank. Due to which the water gets polluted. The levels of nitrogen and phosphorus increases in the water and the amount of O2 For example, a species of algae called Microcystis aeruginosa is poisonous the water, causing liver and brain damage in swamp dwellers. Its effects are also seen in rats, birds, and other domestic animals. When the algae becomes ineffective or dies, it starts floating on the water. The toxic effects, lack of oxygen, excess of nitrogen and phosphorus, which when mixed with rice, pulses, vegetables and other vegetarian and non-vegetarian food besides drinking, produce highly toxic poison which can be seen in the number of victims here.

Keywords: Microcystic Algae, Microcystis Aeruginos, Paint-Like Layer, Vegetarian And Non-Vegetarian

Presentation Code: 34

TOXICOLOGY AND ENVIRONMENTAL HEALTH

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ABSTRACT

Toxicology and environmental health are closely related fields that study the effects of harmful substances on living organisms and ecosystems. Toxicology focuses on understanding the nature, sources, exposure pathways, and toxic effects of chemicals, pollutants, and biological agents on human health and the environment. Environmental health deals with how environmental factors such as air, water, soil pollution, and chemical contaminants influence human well-being and ecological balance. Rapid industrialization, urbanization, and the excessive use of chemicals in agriculture and industry have increased the release of toxic substances into the environment. These toxicants can enter the human body through inhalation, ingestion, or skin contact, leading to various health problems such as respiratory disorders, neurological damage, reproductive issues, and even cancer. Environmental toxicology studies the behavior, transformation, and accumulation of these substances in ecosystems and their long-term impacts on biodiversity and human populations. Understanding toxicological mechanisms and environmental risk assessment is essential for developing effective pollution control strategies, regulatory policies, and sustainable practices. Public awareness, proper waste management, and the use of eco-friendly alternatives can help minimize toxic exposure and protect environmental and human health.

Presentation Code: 40

THE STUDIES ON TOXICOLOGY AND MANAGEMENT OF FUSARIUM TOXINS IN TELANGANA REGION

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ABSTRACT

Fusarium species are important phytopathogenic fungi widely distributed in agricultural ecosystems and are major producers of harmful mycotoxins contaminating cereals, ground nuts and stored grains. In the Telangana region, due to favorable environmental conditions such as high temperature, intermittent rainfall and improper storage practices enhance the growth of Fusarium species, leading to toxin accumulation in food and feed contamination. Major Fusarium toxins include deoxynivalenol (DON), nivalenol (NIV), zearalenone (ZEA), and T-2 toxin, which possess serious risks to human and animal health. Fusarium toxins exhibit cytotoxic, immunosuppressive and estrogenic effects through oxidative stress, mitochondrial dysfunction and apoptosis induction in biological systems. Management of Fusarium toxins mainly focuses on preventing fungal growth and reducing toxin contamination. Initial work was organized on isolation, screening and identification of maximum production of lignolytic enzymes by cereals, ground nuts and stored grains. Confirmation of the choice of hyper-secretory fungal strain was based on qualitative and quantitative tests. These samples were collected from various places like Bheemaram, Waddepally, Gopalpuram, Arepally and Kakatiya University. The pure cultures were maintained in slants and plates. These pure cultures were used to estimate lignolytic enzymes qualitatively and quantitatively in the studies on toxicology and management of Fusarium toxins.

Keywords: Mycotoxins, Fusarium, cereals, ground nuts, stored grains, DON, NIV, T-2 toxin, toxicology, management

Presentation Code: 55

IMPACT OF CYANOBACTERIAL CONTAMINATION ON RESIDENT HEALTH: A CASE STUDY OF WATER STORAGE SYSTEMS IN MAGADH UNIVERSITY, BODHGAYA

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ABSTRACT

This study investigates the presence and health impacts of toxic Cyanobacteria (blue-green algae) found in elevated water storage tanks within the Magadh University residential quarters. Observation reveals a significant proliferation of "microcystic algae," specifically Microcystis aeruginosa, characterized by a thick, green, paint-like layer and surface bubbling. This infestation has rendered the local drinking water supply hazardous. The biological activity of these organisms leads to severe water quality degradation, marked by increased levels of nitrogen and phosphorus and a critical reduction in dissolved oxygen. The primary concern is the production of microcystins—potent hepatotoxins and neurotoxins. These toxins are known to cause significant liver and brain damage in humans and have shown lethal effects in local fauna, including rats, birds, and domestic animals. Furthermore, the study notes that the toxicity persists even during the decomposition phase of the algae. Residents are exposed not only through direct consumption of water but also through the preparation of daily meals (rice, pulses, and vegetables), where the toxins remain stable and potent. The increasing number of reported health issues among the campus residents underscores an urgent need for intervention and improved water sanitation protocols.

Keywords: Microcystis aeruginosa, Cyanobacteria, water toxicity, hepatotoxins, Magadh University, public health.

Presentation Code: 60

TOXICOLOGICAL STUDIES OF NUVAN IN THE INTESTINE OF FRESHWATER AIR-BREATING FISH ABABAS TESTUDINEUS (BLOCK)

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ABSTRACT

Toxicological studies of Nuvan on freshwater air-breathing fish Anabas testudineus (Bloch) using bioassay experiments to determine acute toxicity and prolong toxicity by evaluating histopathological aspects has been done. 90 hrs LC50 value was 1.57 ± 0.0276 mg l^{-1}. For the histopathological studies the concentration was selected 1/15 and 1/10 (0.10 and 0.16) of 90 hrs LC50 value. After exposure to 0.10 mg l^{-1} for 10 days enlargement and increase in number of mucous cells in the villi and for 20 days exposure. The epithelium cell also lost their regular appearance. An exposure to 0.16 mg l^{-1} for 10 days tensions in intestinal epithelium was observed at certain places. For 20 days the epithelium cells of intestinal villi lost their cellular integrity and were marked by their nuclei only.

Keywords: Nuvan, Anabas Testudineus, Organophorus Pesticide.

Presentation Code: 62

ENVIRONMENTAL DIABETOGENS AND METABOLIC DISRUPTION: AN ECO- TOXICOLOGICAL REVIEW OF CHEMICAL STRESSORS ON PANCREATIC HOMEOSTASIS IN FAUNAL MODELS

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ABSTRACT

An alarming connection between anthropogenic contaminants and the increased prevalence of metabolic illnesses worldwide has been found at the nexus of environmental science and zoology. This article examines how "Environmental Diabetogens" chemical stressors such heavy metals like arsenic and cadmium and persistent organic pollutants (POPs) can cause diabetes mellitus by upsetting pancreatic homeostasis. Modern life sciences emphasise the influence of the environment on endocrine function, whereas traditional diabetes research concentrates on heredity and food. In faunal models, the study investigates the physiological mechanisms by which environmental pollutants cause oxidative stress and systemic inflammation. Reactive Oxygen Species (ROS) produced by exposure to these pollutants specifically target the susceptible Beta-islets of Langerhans, impairing insulin production and increasing insulin resistance. This study demonstrates how chemical discharge into nearby ecosystems serves as a stimulus for metabolic failure by examining data from terrestrial and aquatic bio-indicators. Additionally, the study incorporates phytochemical innovation as a mitigation technique, assessing the ability of antioxidants derived from plants to counteract oxidative damage caused by pollutants. This multidisciplinary method connects zoological physiology and environmental monitoring. The results highlight the Present and Future need to include eco-toxicological information in public health regulations. Zoology provides important insights for maintaining human metabolic integrity and animal health in increasingly contaminated environments by comprehending the environmental causes of diabetes

Keywords: Environmental Diabetogens, Eco-toxicology, Pancreatic Homeostasis, Oxidative Stress, Endocrine Disrupting Chemicals (EDCs)

Presentation Code: 64

EFFECT OF MALATHION (AN ORGANOPHOSPHATE) ON BIOCHEMICAL CONSTITUENTS OF FRESHWATER FISH LABEO ROHITA (HAMILTON)

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ABSTRACT

The present study was carried out to investigate the effect of Malathion an organophosphate compound (OP), on biochemical constituents of freshwater fish Labeo rohita. The fish were exposed to sub lethal concentration of the toxicant malathion and the variations were observed in biochemical constituents in different tissues i.e., gill, liver, intestine, brain and muscle of the fish. The quantitative Variations were observed proteins, carbohydrates and ninhydrine positive substances at different time intervals i.e., 24, 48, 72 and 96 hours. The results revealed that the components of proteins, carbohydrates and ninhydrine positive substances were found to be significantly at 24, 48, 72 and 96 hours time interval of malathion exposure on different tissues of fish compared to control. The maximum decrease in proteins followed by carbohydrates and ninhydrine positive substances (free amino acids) was observed at 72 hours and 96 hours compared to 24 and 48 hours time interval in different tissues of Labeo rohita on exposure to malathion. The results will be present during the seminar.

Keywords: Carbohydrates, Ninhydrine positive substances, Malathion, Proteins

Presentation Code: 65

TOXICOLOGY: UNDERSTANDING THE IMPACT OF TOXIC SUBSTANCES ON HUMAN HEALTH AND THE ENVIRONMENT

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ABSTRACT

Toxicology is a vital scientific discipline that examines the adverse effects of chemical, biological, and physical agents on living organisms. With the rapid growth of industrialization, pharmaceutical development, and environmental pollution, the study of toxic substances has become increasingly important for protecting human health and maintaining ecological balance. Toxicology integrates knowledge from biology, chemistry, medicine, and environmental science to understand how toxins enter the body, interact with biological systems, and produce harmful effects. In the present context, toxicological research plays a crucial role in evaluating the safety of pharmaceuticals, food additives, pesticides, and industrial chemicals. Modern approaches in toxicology involve advanced analytical techniques, molecular toxicology, and computational modeling to predict toxicity and reduce the risk associated with exposure to harmful substances. Emerging areas such as nanotoxicology, environmental toxicology, and genetic toxicology are expanding our understanding of how new materials and environmental contaminants influence cellular and molecular processes. These developments help scientists identify potential hazards earlier and support the development of safer products and regulatory guidelines. urthermore, toxicology contributes significantly to public health by guiding risk assessment, establishing exposure limits, and supporting policies that minimize human and environmental harm. As global challenges such as chemical pollution, climate change, and increasing chemical production continue to grow, toxicology will remain essential in addressing these issues through scientific research and preventive strategies. In the coming years, advances in biotechnology, high-throughput screening, and artificial intelligence are expected to transform toxicological research by enabling more precise and ethical testing methods, reducing reliance on animal experimentation, and improving the prediction of toxic effects in humans. Ultimately, the continued development of toxicology will play a key role in ensuring safer medicines, healthier ecosystems, and improved quality of life.

Keywords: Toxicology, chemical toxicity, environmental toxicology, risk assessment, human health, toxic substances, public health, molecular toxicology.

Presentation Code: 66

EFFECT OF DIMETHOATE (AN ORGANOPHOSPHATE) ON BIOCHEMICAL CONSTITUES OF FRESH WATER FISH MYSTUS SEENGHALA (SYKAS)

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ABSTRACT

The present study was carried out to investigate the effect of Dimethoate, a synthetic pyrethroid pesticide, is widely used in agricultural and domestic pest control, an organophosphate compound (OP), on biochemical constituents of freshwater fish Channa punctatus. The fish were exposed to sub lethal concentration of the toxicant Dimethoate and the variations were observed in biochemical constituents in different tissues i.e. gill, liver, intestine, brain and muscle of the fish. The quantitative variations were observed proteins, carbohydrates and ninhydrine positive substances at different time intervals i.e., 24, 48, 72 and 96 hours. The results revealed that the components of proteins, carbohydrates and ninhydrine positive substances were found to be significantly at 24, 48, 72 and 96 hours time interval of fenvalerate exposure on different tissues of fish compared to control. The maximum decrease in proteins followed by carbohydrates and ninhydrine positive substances (free amino acids) was observed at 72 hours and 96 hours compared to 24 and 48 hours time interval in different tissues of C.punctatus on exposure to fenvalerate. The results will be present during the seminar.

Keywords: Mystus seenghala, Carbohydrates, Ninhydrine positive substances, Dimethoate, Proteins.

Presentation Code: 67

ZEBRAFISH-THE FAST, ETHICAL KEY TO UNDERSTANDING POLLUTION'S THREAT TO HUMAN HEALTH

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ABSTRACT

Environmental pollution is a big problem for rivers and freshwater everywhere. Every day, huge amounts of untreated wastewater, chemicalsfrom farms and factories, heavy metals, and drug residues from medicinesflow straight into these waters. Experts say over 80% of the world's wastewater gets released without proper treatment, mixing pollutants like pesticides, industrial waste, heavy metals, and pharmaceuticals into rivers and lakes. This makes the water unsafe for nature and people. These harmful substances can cause serious health problems, like cancer, birth defects, hormone changes, damage to organs, and even antibiotic-resistant bacteria that make infections harder to treat. Testing toxic effects directly on humans isn't right or possible, so we really need a good model organism — something safe, quick, and close to how humans work — to study these dangers and predict what might happen. Zebrafish (Danio rerio) has become one of the most widely used model organisms in research today. Its embryos are transparent, which allows researchers to directly observe how toxic substances affect development under a microscope. Zebrafish produce a large number of eggs quickly and develop rapidly, with embryos hatching in about three days. Interestingly, zebrafish share nearly 70% of their genes with humans, making them a valuable model for studying human-related biological processes. Because of these advantages, zebrafish are widely used to study the toxic effects of environmental pollutants and to better understand potential risks to ecosystems and human health.

Keywords: Environmental Pollution, Aquatic Pollutants Heavy Metals, Pesticides, Pharmaceuticals, Zebrafish, Toxicity screening, Model organism.

Presentation Code: 83

EVALUATING THE TOXICITY EVALUATION OF NANO EMULSION DERIVED FROM CITRUS LIMETTA FRUIT PEEL AGAINST *TRIBOLIUM CASTANEUM* (COLEOPTERA : TENEBRIONIDAE)

Shanthi Ajmeera

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ABSTRACT

Citrus fruits produced as essential oils, (EOs), were obtained through the peels, from Citrus sinensis (sweet orange), into hydro distillation, a concentration method that uses a Clevenger-type apparatus for 3 to 4 hours. These EOs and their flavonoids, have various biological activities, such as antioxidant, antimicrobial, and cytotoxic effects, and they are also widely used as food Flavors and cosmetic ingredients. This work aims are to produce as Nano emulsions, through citrus EO from non-used orange peels, and to be study their biological effect as antioxidant, antimicrobial, and cytotoxic agents. The citrus limetta peels were detached (removed), air-dried, powdered (mixture), and extracted by hydro distillation. The EOs of the samples were to be analysed by gas chromatography–mass spectrometry (GC-MS), Fourier-transform infrared spectroscopy (FT-IR), dynamic light scattering (DLS), and zeta potential measurements.

Keywords: Citrus Nano Emulsion, Insecticidal Activity, *Tribolium Castaneum, Citrus Limetta* Peel

Presentation Code: 97

IMPACT OF AGRICULTURAL PESTICIDES ON THE BIOCHEMICAL PHYSIOLOGY OF FRESH WATER FISH

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ABSTRACT

Agricultural pesticides are widely used in modern farming to control pests and increase crop productivity. However, the extensive use of pesticides has resulted in contamination of freshwater ecosystems through agricultural runoff, leaching, and spray drift. Such contamination poses serious threats to aquatic organisms, particularly fish, which are highly sensitive to chemical pollutants. The present study investigates the impact of agricultural pesticides on the biochemical physiology of freshwater fish in selected water bodies of Karimnagar District, Telangana, India. Water and fish samples were collected from Lower Manair Dam and irrigation tanks around Huzurabad during the period June 2023 to March 2024. Physicochemical parameters of water were analyzed and biochemical parameters such as carbohydrate content, protein levels, and enzyme activity were examined in fish tissues. The results revealed elevated nutrient levels in contaminated sites, behavioral abnormalities in fish, and significant alterations in carbohydrate and protein metabolism. Enzyme activity was also affected, indicating physiological stress in fish exposed to pesticide-contaminated environments. The findings suggest that agricultural pesticides can significantly affect the biochemical physiology and survival of freshwater fish. Continuous monitoring of pesticide pollution and adoption of sustainable agricultural practices are essential to protect freshwater ecosystems.

Keywords: Agricultural pesticides, freshwater fish, biochemical physiology, aquatic toxicology, environmental pollution

Presentation Code: 101

ENVIRONMENTAL IMPACT OF AIR PARTICULATE MATTER POLLUTION IN OPENCAST COAL MINES OF SATHUPALLY

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ABSTRACT

Coal mining plays an important role in economic development. Coal is widely used for electricity generation and contributes to more than 40% of the electricity production in the country. Although coal mining provides significant economic and energy benefits, it also has negative environmental impacts. In opencast coal mining, explosives are used to blast rocks, and activities such as drilling, blasting, excavation, and transportation of coal release large amounts of dust and particulate matter into the air. This air pollution affects the surrounding environment and may cause various health problems for people living near mining areas. Therefore, it is important to study the level of particulate matter pollution and its impact on the environment and human health. The present study focuses on measuring particulate matter (dust) levels in and around the opencast coal mining areas of Sathupally and understanding their possible effects on the surrounding environment and public health.

Keywords: Coal Mine, Open Cast, Particulate Matter, Health Problems, Environment and Public Health.

Presentation Code: 114

STUDY OF GANJA (CANNABIS) SUPPLY, VICTIM IMPACT, AND POLICE RESPONSE IN TELANGANA–ANDHRA PRADESH–ODISHA BORDER: A DATA-DRIVEN ANALYSIS

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ABSTRACT

The illegal cultivation, trafficking, and consumption of ganja (cannabis) have emerged as critical socio-economic and law enforcement challenges in the tri-border regions of Telangana, Andhra Pradesh, and Odisha. This study presents a data-driven analysis of cannabis supply chains, victim impact, and police response mechanisms. Primary data were collected through structured questionnaires, interviews, and case studies, while secondary data were obtained from police records and government reports. Findings reveal that organized trafficking networks, socio-economic vulnerabilities, and geographical challenges facilitate the persistence of cannabis trade. The study also highlights the adverse psychological, social, and economic impacts on individuals and families, alongside gaps in law enforcement coordination. The Bhadrachalam check post plays a key role in controlling inter-state trafficking. The research recommends policy interventions, awareness programs, and technology-driven policing strategies to mitigate the problem effectively.

Keywords: Cannabis, Ganja Trafficking, Drug Abuse, Victim Impact, Police Response, Data Analysis, Bhadrachalam

Presentation Code: 115

ACCUMULATION OF HEAVY METALS IN MUSI RIVER WATER AND THEIR IMPACT ON FISHES

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ABSTRACT

The content and effects of six heavy metals—copper (Cu), zinc (Zn), lead (Pb), cadmium (Cd), chromium (Cr), and manganese (Mn)—in fish tissue samples taken from the Musi River are examined in this study. The analysis's goal was to assess the possible consequences that heavy metal contamination poses to human health and the environment. When compared to the permitted limits set by the World Health Organization (WHO), the results showed a substantial difference in metal concentrations. All samples had levels of copper and zinc that were safe. Zinc varied from 0.640 to 0.676 mg/L and copper between 0.061 and 0.076 mg/L, all of which were significantly below the WHO standards of 3.00 mg/L and 1.00 mg/L, respectively. Despite being crucial micronutrients for fish, these two metals are normally well-regulated in biological systems and did not provide a serious risk in this investigation. The quantities of the remaining four metals—lead, cadmium, chromium, and manganese—were found to be significantly higher than acceptable limits. Lead levels were far higher than the WHO standard of 0.01 mg/L, ranging from 0.241 to 0.471 mg/L. Cadmium also surpassed the allowable limit of 0.003 mg/L, despite being found in lesser amounts (0.012 to 0.028 mg/L). In comparison to the standard limit of 0.05 mg/L, chromium was very high (0.928 to 1.686 mg/L). The acceptable 0.40 mg/L criterion was also exceeded by manganese levels, which ranged from 0.678 to 0.705 mg/L. These high levels suggest that industrial sources of contamination include tannery effluents, battery disposal, mining operations, fertilizers, and paints.The chemical results were corroborated by histopathological analysis of fish liver tissues, which showed structural damage such as cellular swelling and disarray, which are typical signs of oxidative stress and metabolic dysfunction caused by metals. Because they are constantly in contact with water and sediment, fish are sensitive bio-indicators of aquatic pollution. Because they are not biodegradable, heavy metals build up in fish tissues through bioaccumulation and bio-magnification, mostly impacting the muscles, liver, gills, and kidneys. Fish populations and aquatic biodiversity are eventually at risk due to these harmful consequences,

which also hinder essential biological processes and decrease growth and reproduction. All things considered, eating tainted fish puts people at risk for major health issues, such as organ damage, neurological conditions, developmental issues, and an elevated chance of cancer. To lessen the negative effects of heavy metal contamination on the environment and public health, the study emphasizes the critical need for regular monitoring of heavy metals in aquatic systems, enhanced pollution management strategies, and community awareness.

Keywords: WHO permissible limits, Ecological risk, Human health risk, Contamination Sources, Histo-pathological Examination, Organ damage, Biomagnification, Neurological disorders.

Presentation Code: 127

BIO MAGNIFICATION: THE EXPONENTIAL INCREASE OF PERSISTENT ORGANIC POLLUTANTS (POPS)

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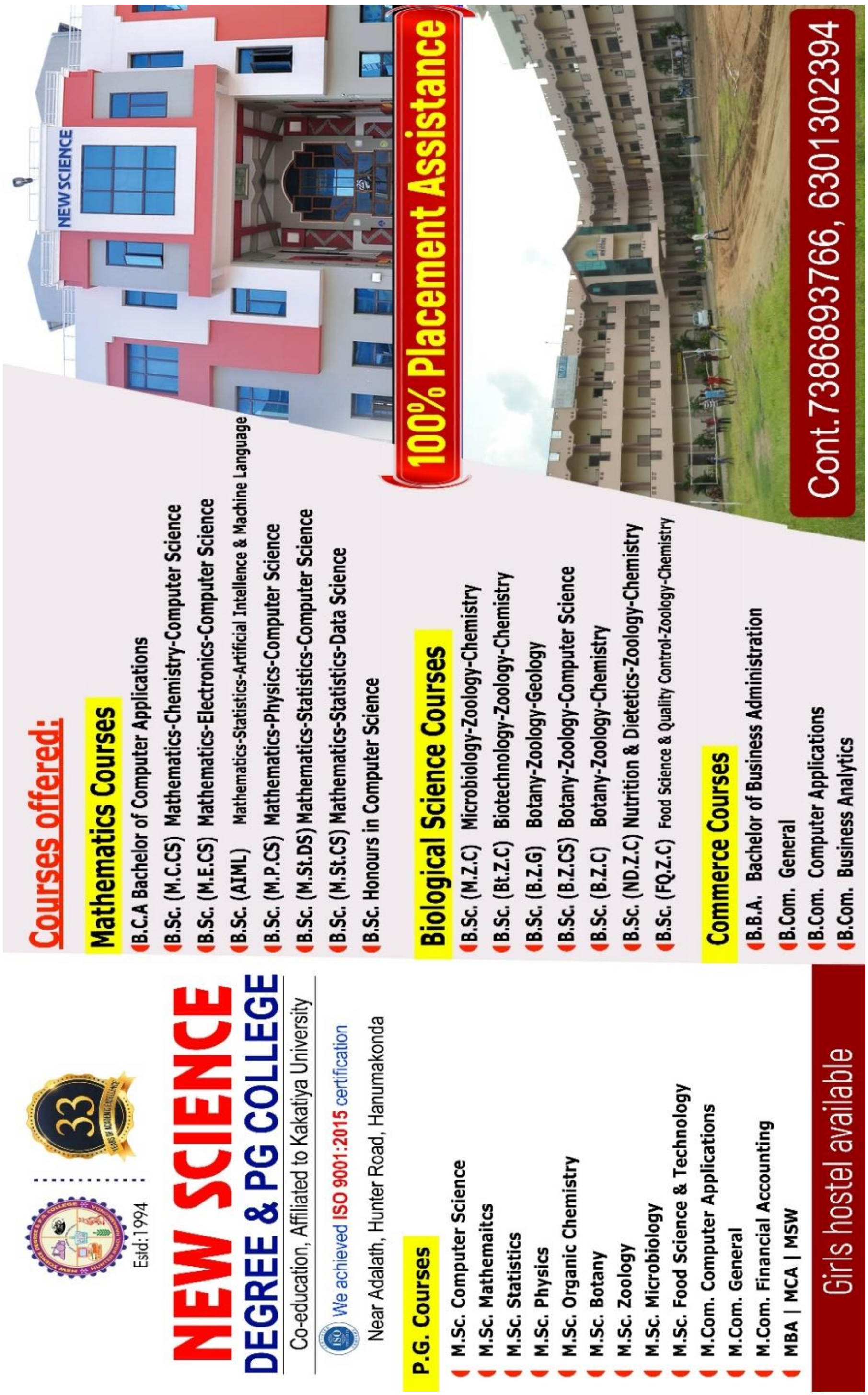
ABSTRACT

Bio magnification represents one of the most significant ecological threats posed by industrial and agricultural pollutants. This paper examines the mechanism of tropic transfer regarding Persistent Organic Pollutants (POPs), such as DDT, PCBs, and dioxins. Unlike water-soluble substances, POPs are highly lipophilic (fat-soluble) and resistant to environmental degradation, allowing them to bypass standard metabolic excretion. Through an analysis of various food webs, this study demonstrates that while the concentration of these pollutants may be negligible in the surrounding environment, they undergo exponential increases as they move from primary producers to apex predators. The data suggests that concentration factors can increase by several orders of magnitude at each successive tropic level, often reaching levels that trigger reproductive failure, neurological damage, and immune suppression in top-tier species. By synthesizing current toxicological research, this paper concludes that the long-range transport and longevity of POPs necessitate more stringent international regulations to prevent irreversible damage to global biodiversity and human health.

Keywords: Biomagnification, Tropic Levels, Persistent Organic Pollutants (POPs), Bioaccumulation, Lipophilic, Apex Predators.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Presentation Code: 143

QUANTITATIVE ESTIMATION AND IDENTIFICATION OF GENERAL TYPE OF LIPIDS IN GILL, LIVER, INTESTINE, MUSCLE, BRAIN TISSUE OF FRESH WATER FISH *CHANNA PUNCTATUS* (BLOCH) IN THIN LAYER CHROMATOGRAPHY (TLC) SPRAYED WITH IODINE REAGENT

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ABSTARCT

Lipids were quantified and observed in different tissues i.e. gill, liver, intestine, muscle and brain tissue of fresh water fish Channa punctatus through Thin Layer Chromatography (TLC). Gill, liver, intestine, muscle and brain tissues of Channa punctatus punctatus dissected and homogenated in chloroform and methanol mixture (2:1 ratio) and centrifuged. The supernatant homogenate was used for the experiment. The sample tissue is loaded in TLC plate and dipped in a beaker which consists of mixture of chloroform and methanol (2:1 ratio) that works as mobile phase. TLC is a sheet of aluminum foil which is coated with a thin layer of adsorbent that works as a stationary phase. The various lipids present in the sample tissue travels across the TLC plate. The distance travelled by the lipid substance is divided by the distance travelled by the mobile phase is called as Retardation factor (Rf Value). After the experiment, the TLC plate is drawn from the beaker and dried, sprayed with Iodine vapors. Spots with yellow color were appeared on the TLC plate. Rf values and individual spots were marked with pencil and calculated. Our test results revealed that Gill tissue has shown three yellow colour spots with Rf value 90 ±0.5were moderately stained, Rf value, 40±0.5; 50±0.5 were unclear. Liver tissue has shown five yellow colour spots with Rf value 50±0.5 and 60±0.5 were highly stained with yellow colour, Rf value 10±0.5; 20±0.5; 80 ±0.5 were moderately stained. Intestine tissue has shown five yellow colour spots with Rf value 10±0.5 and 90±0.5 were moderately stained, Rf value 30±0.5; 40±0.5 and 50 ±0.5 were unclear. Muscle tissue has shown four yellow colour spots with Rf value 90±0.5 were highly stained, Rf value 30±0.5 and 50±0.5 were moderately stained, Rf value 70 ±0.5 were unclear. Brain tissue has shown six

yellow colour spots with Rf value 10±0.5; 40±0.5; 80±0.5 and 90±0.5 were very darkly stained, Rf value 30±0.5 and 60±0.5 were moderately stained. Hence the staining pattern and intensity of spots staining it is observed that general lipids were highest present in brain tissue, followed by liver, gill, muscle and intestine respectively.

Keywords: General lipids; Channa punctatus; TLC; Iodine vapors; Rf value; chloroform- methanol mixture.

Presentation Code: 144

HACCP: A QUEST FOR QUALITY, A SYSTEMATIC APPROACH FOR FOOD SAFETY MANAGEMENT WITH REFERENCE TO SCOMBROID FAMILY IN MACKEREL. R. KANAGURTA

Nandita Ashok More, Sanjay Shamrao Nanware, Suman Pawar

Patuck Jr. College, Mumbai University
Department of Zoology, Yeshwant Mahavidyalaya, Nanded, SRTMU
Department of Zoology, Institute of Science, Mumbai University

ABSTRACT

Food is foundational element and not just a commodity of human health. It is the essential source of energy. Though food is the major requirement for good health, it should be hygienically sound. Safe and nutritious food is a key to promoting good health. Perishable items like fish and meat rapidly deteriorate and need prompt preservation to prevent spoilage. All fish species suffer from enzymatic breakdown and microbial contamination on improper handling. However, mackerel belonging to scombridae family is more vulnerable to spoilage because it contains high level of histidine. Ensuring consumer safety to promote international trade it is essential to comply with regulatory food hygiene standards. Instead of detecting hazards after they occur it focuses on preventing hazards at critical points during production, which is imperative. It significantly reduces the risk of food borne hazards including microbial contamination and improper storage temperature. This preventive approach for the food safety assurance is accomplished by following HACCP (Hazard analysis critical control point) guidelines, which shows commitment to safety and building trust with consumer, thus improving overall business efficiency,

Key words- HACCP, hazards, food safety, quality control, Mackerel,

Presentation Code: 145

FROM MOLECULES TO SYSTEMS: TECHNOLOGICAL TRANSFORMATIONS DRIVING THE FUTURE OF LIFE SCIENCES

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Department of Zoology, TGSWRDC (W), SIDDIPET

ABSTRACT

Life sciences are at a critical moment of transformation, fueled by the rapid pace of technological, interdisciplinary, and international advances. This paper will examine the current status and prospects in life sciences, especially in critical areas like genomics, biotechnology, bioinformatics, and personalized medicine. Gene editing technologies, especially CRISPR-Cas, have completely transformed the way we understand and control genetic information, providing potential answers to genetic diseases, agricultural needs, and preventive medicine. Furthermore, the integration of artificial intelligence and big data analytics in life sciences has expedited drug discovery, disease modeling, and personalized medicine. New disciplines like synthetic biology and systems biology have completely redefined the way we understand complex biological systems, allowing the creation of new biological systems, which can be applied in medicine, energy, and environmental sustainability. However, there are still challenges to overcome in the field. These challenges include the ethical issues that come with these developments, data privacy, and access to these technologies. This is a crucial area that must be considered to ensure the advancement of science. In the future, the life science sector is expected to converge with other fields such as computational sciences, engineering, and nanotechnology. This convergence is expected to bring about innovations that will not only benefit humanity in terms of health but also ensure sustainable development. The future and present of life science have shown immense potential in redefining the limits of science and enhancing the quality of life.

Keywords: Life Sciences, Genomics, Biotechnology, Bioinformatics, Gene Editing, Artificial Intelligence, Personalized Medicine.

Presentation code:146

STEM CELL THERAPY: THE FUTURE REGENERATIVE MEDICINE.

N. Shivathimka

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ABSTRACT

Despite significant advancements in modern medicine, effective treatments for several chronic and degenerative diseases, including diabetes, Parkinson's disease, and Alzheimer's disease, remain limited. Stem cell therapy has emerged as a promising approach within regenerative medicine, offering potential solutions for tissue repair and functional restoration. Stem cells are undifferentiated cells characterized by their capacity for self-renewal and differentiation into specialized cell types. The isolation of human embryonic stem cells in 1998 by James Thomson marked a pivotal milestone in stem cell research. Stem cell therapy involves the use of autologous or allogenic cells to repair or replace damaged tissues, thereby reducing dependence on donor organ transplantation. Under in vitro conditions, stem cells can be directed to differentiate into specific cell types such as cardiomyocytes, neurons, and hematopoietic cells, which can then be transplanted into patients. Emerging evidence suggests that stem cell–based interventions can contribute to tissue regeneration, particularly in cardiac repair. Recent advancements, including induced pluripotent stem cells (iPSCs), enable the reprogramming of somatic cells into pluripotent states, minimizing immunogenic complications and ethical concerns associated with embryonic stem cells. Furthermore, innovative strategies such as tissue engineering, decellularization–recellularization techniques, and blastocyst complementation are being explored for whole-organ regeneration. Future directions integrating gene editing, immune modulation, and bioengineering approaches hold significant promise. Collectively, stem cell therapy represents a transformative paradigm in personalized medicine, with the potential to revolutionize treatment strategies for currently incurable diseases.

Keywords: pluripotent stem cell technology, Decellurization and recellurization of bio- scaffold,combinatorial technique, Tissue engineering, Bio- engineering synergy.

Presentation code:147

RECOMBINANT SPIDER SILK PRODUCTION IN TRANSGENIC CAPRINES

Kandi Akshaya

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ABSTRACT

Spider silk is a remarkable biomaterial known for its exceptional tensile strength, elasticity, and biocompatibility, making it highly valuable for applications in biomedicine, textiles, and defense. However, large-scale production of natural spider silk is limited due to the territorial and cannibalistic nature of spiders. Recombinant DNA technology offers a viable alternative for scalable production. This study explores the generation of transgenic caprines (goats) as bioreactors for the expression of recombinant spider silk proteins. The silk-producing genes, primarily encoding spidroin proteins, are genetically engineered into the caprine genome under the control of mammary gland-specific promoters. This enables the secretion of recombinant silk proteins in milk, from which they can be efficiently purified. Compared to microbial and cell culture systems, transgenic caprines provide higher yield, proper protein folding, and cost-effective scalability. The expressed recombinant spider silk proteins are further processed into fibers and evaluated for their mechanical and structural properties, demonstrating similarities to native spider silk. This approach highlights a sustainable and economically viable platform for producing high-performance biomaterials. The study underscores the potential of transgenic livestock in industrial biotechnology and opens new avenues for the development of advanced biomaterials for medical sutures, tissue engineering scaffolds, and high-strength fibers.

Keywords: Recombinant spider silk, transgenic caprines, spidroin proteins, mammary gland expression, bioreactors, biomaterials, genetic engineering, tissue engineering.

Presentation code:148

MICRO PLASTIC POLLUTION AND THE ROLE OF PLASTIC EATING MICROBES

Koyyada Ravali

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ABSTRACT

Microplastic pollution has emerged as a critical environmental challenge of the 21st century. Microplastics, defined as plastic particles smaller than 5 mm, originate from primary sources such as microbeads, synthetic textile fibers, and tire abrasion, as well as secondary sources involving the fragmentation of larger plastic debris. Their pervasive presence across marine, freshwater, and terrestrial ecosystems poses significant threats to biodiversity and ecological stability. Microplastics have been detected in human biological samples, raising concerns about their potential health impacts, including inflammatory, neurological, and reproductive toxicity through food chain transfer. In aquatic systems, ingestion of microplastics by organisms leads to reduced feeding efficiency, impaired energy metabolism, and biomagnification across trophic levels. While conventional management strategies such as reduction, reuse, and recycling (3Rs) remain essential, they are insufficient to address the existing burden of plastic waste. Microbial remediation has emerged as a promising complementary approach. Certain microorganisms, including Ideonella sakaiensis and Thermobifida fusca, as well as fungi like Aspergillus tubingensis, can colonize plastic surfaces forming a "plastisphere" and secrete enzymes such as PETase and MHETase that depolymerize plastic polymers into simpler compounds. These intermediates are subsequently metabolized into less harmful end products. Although still in developmental stages, microbial degradation offers a sustainable strategy for mitigating microplastic accumulation. Advancing this approach through biotechnology and environmental engineering could significantly contribute to long-term plastic pollution control.

Keywords: Microplastics, plastic pollution, microbial remediation, plastisphere, PETase, Ideonella sakaiensis, biodegradation, environmental sustainability.

Presentation code:149

TINY PARASITE CAN CAUSE BIG DISEASE

Thotla Pravalika

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ABSTRACT

Toxoplasmosis is a globally prevalent zoonotic disease caused by the obligate intracellular protozoan Toxoplasma gondii, first described in 1908 by Charles Nicolle and Louis Manceaux. Felids serve as the definitive hosts, while a wide range of warm-blooded animals, including humans, act as intermediate hosts. Transmission primarily occurs through ingestion of contaminated food, particularly undercooked meat, or exposure to oocysts from cat feces. The infection is of significant public health concern, causing severe complications such as congenital defects, abortion, and neonatal mortality, especially in immunocompromised individuals and pregnant women. In India, seroprevalence rates exceed 20%, facilitated by favorable climatic conditions. Recent advances in molecular parasitology have identified critical targets for therapeutic and vaccine development. Notably, CRISPR-based genetic manipulation studies have demonstrated that depletion of the essential splicing factor TgCDC5 disrupts RNA processing in T. gondii, leading to impaired parasite replication. The parasite's intron-rich genome necessitates precise RNA splicing, making TgCDC5 indispensable for survival. Experimental studies in murine models indicate that splicing-deficient parasites induce a strong protective immune response, suggesting their potential as live-attenuated vaccine candidates. Current treatment relies on a combination of pyrimethamine, sulfadiazine, and clindamycin; however, preventive strategies, including food safety and hygiene practices, remain critical. Targeting molecular pathways such as RNA splicing offers promising avenues for improved disease control.

Keywords: Toxoplasmosis, Toxoplasma gondii, zoonotic infection, TgCDC5, RNA splicing, CRISPR, vaccine development, seroprevalence, public health.

Presentation code:150

BIOPHILIC AND REGENERATIVE DESIGN APPROACHES FOR SUSTAINABLE AND ENERGY-EFFICIENT BUILT ENVIRONMENTS

A. Sumanya

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ABSTRACT

The increasing environmental challenges of the 21st century necessitate innovative approaches to sustainable architecture and resource management. This study explores the principles of biophilic and regenerative design as frameworks for creating environmentally responsible and energy-efficient built environments. The concept of biophilia, introduced by Erich Fromm and later popularized by Edward O. Wilson, emphasizes the inherent human affinity toward nature and its positive impact on health and well-being. Biophilic design integrates natural elements such as light, vegetation, and spatial patterns into architectural practices to enhance occupant comfort and productivity. In contrast, regenerative design adopts a holistic approach that goes beyond sustainability by aiming to restore and enhance ecological systems. It focuses on the co-evolution of human and natural systems, promoting buildings that function as integral components of their surrounding ecosystems. This paper examines the conceptual frameworks, operational mechanisms, similarities, and differences between these two approaches. The findings suggest that while biophilic design prioritizes human-nature interaction, regenerative design extends this perspective to ecological restoration and long-term environmental resilience. Integrating both approaches can significantly contribute to sustainable development by improving energy efficiency, resource utilization, and ecosystem health. These strategies offer a pathway toward designing built environments that are not only less harmful but actively beneficial to both humans and nature.

Keywords: Biophilic design, regenerative design, sustainable architecture, energy efficiency, ecological restoration, human–nature interaction, built environment, environmental sustainability.

Presentation code:151

ARTIFICIAL INTELLIGENCE IN DRUG DISCOVERY

Sushmitha

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ABSTRACT

Artificial Intelligence (AI) is rapidly transforming the drug discovery landscape by addressing the limitations of traditional drug development, which is time-consuming, costly, and often inefficient. Conventional approaches typically require over a decade and substantial financial investment to bring a drug from discovery to market. AI-driven methodologies, particularly machine learning and deep learning, enable the rapid analysis of large-scale biological and chemical datasets, facilitating accelerated identification of potential drug candidates.AI plays a critical role across multiple stages of drug discovery, including target identification, virtual screening, de novo drug design, and prediction of pharmacokinetic and toxicological properties. Advanced algorithms can model complex protein–ligand interactions, optimize lead compounds, and predict biological activity with high accuracy. Furthermore, AI integration with cheminformatics and bioinformatics enhances the ability to uncover novel therapeutic targets and repurpose existing drugs. Despite these advancements, challenges such as limited availability of high-quality datasets, algorithm interpretability, and data privacy concerns remain significant barriers. Additionally, effective implementation requires interdisciplinary expertise spanning computational science, biology, and medicinal chemistry. Overall, AI has the potential to significantly reduce drug development timelines, lower costs, and improve success rates. Continued advancements in AI technologies are expected to revolutionize pharmaceutical research and contribute to the development of safer and more effective therapeutics.

Keywords: Artificial Intelligence, drug discovery, machine learning, virtual screening, drug design, pharmacokinetics, bioinformatics, cheminformatics.

Presentation code:152

BIOINFORMATICS AND COMPUTATIONAL BIOLOGY

Sumera

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ABSTRACT

Bioinformatics and computational biology are interdisciplinary domains that integrate biology, computer science, mathematics, and statistics to analyze and interpret complex biological data. The exponential growth of high-throughput technologies, such as next-generation sequencing and proteomics, has generated vast datasets, necessitating advanced computational approaches for efficient data processing and analysis. Bioinformatics primarily focuses on the development and application of algorithms, software tools, and databases to manage and analyze biological sequences and structural data. It plays a crucial role in genome annotation, sequence alignment, structural prediction, and biological data management. In contrast, computational biology emphasizes the use of mathematical modeling, statistical frameworks, and simulations to understand biological systems and dynamic processes, including gene regulation, molecular interactions, and evolutionary mechanisms. These fields are integral to diverse applications such as genomics, proteomics, drug discovery, disease diagnostics, and personalized medicine. They also contribute significantly to agricultural biotechnology through crop improvement and stress-resistance studies. Overall, bioinformatics and computational biology have transformed life sciences by enabling data-driven insights into complex biological systems. Their continued advancement is essential for accelerating innovation in biomedical research, biotechnology, and precision medicine.

Keywords: Bioinformatics, computational biology, genomics, proteomics, sequence analysis, systems biology, data analysis, personalized medicine.

Presentation code:153

GREEN SYNTHESIS AND CHARACTERIZATION OF DOPED AG-ZNO NANOPARTICLES USING NOTHAPODYTES NIMMONIANA LEAF EXTRACT AND EVALUATION OF THEIR ANTIBACTERIAL ACTIVITY

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ABSTRACT

The increasing demand for environmentally sustainable nanomaterials has encouraged the development of green synthesis approaches using biological resources. In the present study, silver- doped zinc oxide (Ag–ZnO) nanoparticles were synthesized using the aqueous leaf extract of Nothapodytes nimmoniana, a medicinal plant known for its rich phytochemical composition. Plant-derived biomolecules such as phenolics, proteins, and flavonoids act as natural reducing and stabilizing agents, enabling the eco-friendly production of nanoparticles. The synthesis process involved the reaction of leaf extract with silver nitrate and zinc acetate solutions under alkaline conditions, followed by heating and calcination. The formation of Ag–ZnO nanoparticles was visually confirmed by the appearance of a creamy color in the reaction mixture. The synthesized nanoparticles were characterized using multiple analytical techniques including UV–Visible spectroscopy, X-ray diffraction (XRD), Fourier Transform Infrared spectroscopy (FTIR), Scanning Electron Microscopy (SEM), and Energy Dispersive X-ray spectroscopy (EDX). UV–Visible spectroscopy revealed a surface plasmon resonance peak around 550 nm, confirming nanoparticle formation. XRD analysis demonstrated the crystalline nature of the Ag–ZnO nanocomposite with an average crystallite size of approximately 18 nm. FTIR analysis identified functional groups responsible for the reduction and stabilization of nanoparticles, while SEM images showed predominantly spherical morphology. EDX analysis further confirmed the presence of silver, zinc, and oxygen elements in the synthesized nanostructure. The antibacterial activity of the Ag–ZnO nanoparticles was evaluated against Gram-positive (Bacillus subtilis, Bacillus sphaericus) and Gram-negative (Escherichia coli, Proteus vulgaris) bacteria using the agar well diffusion method. The results demonstrated significant antibacterial activity, particularly against Bacillus sphaericus, indicating the potential biomedical applications of green-synthesized Ag–ZnO nanoparticles.

Keywords: Green synthesis, Ag-ZnO nanoparticles, Nothapodytes nimmoniana, Nanoparticle characterization, Antibacterial activity.

Presentation code:154

ANALYSIS OF PHYSICOCHEMICAL PARAMETERS OF KONDAPOCHAMMA SAGAR RESERVOIR

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2. Department of Zoology, Tara Government College, Sangareddy, Telangana

ABSTRACT

Kondapochamma Sagar, a 15.8 Km long Reservoir with a capacity of 15 TMC, was built in Siddipet district by the Government of Telangana as a part of the Kaleshwaram Project. The reservoir is 618 M above the sea level. The main purpose of the reservoir is to provide irrigation facility to 2,85,280 acres. River Godavari water is lifted through three pump houses into Kondapochamma Sagar which is 227 KM away. A study was conducted on the physico-chemical parameters of the Kondapochamma Sagar from June 2021 to May 2023. Six sites were selected in the reservoir for the collection of water samples. Samples collected on a monthly basis were analyzed in the laboratory by standard methods (APHA, 1995) to determine the physical parameters such as water colour, odour, Turbidity, and temperature, and chemical parameters such as pH, TDS, carbonates, bicarbonates, total hardness, Ca Hardness, Mg hardness, chlorides, nitrates, sulphates, phosphates, dissolved oxygen, BOD, and COD.
The results of the present study indicate that all the parameters showed slightly higher values during the pre-monsoon seasons than the post-monsoon seasons. This may be due to the aeration of the lake during summer and higher salt concentration. Overall, all the tested physicochemical parameters fall slightly above the permissible limits as per APHA (American Public Health Association) and AWWA (American Water Works Association) standards. Telangana Government has future plans to supply drinking water to Hyderabad city from Kondapochamma Sagar. But these waters must be treated before they are supplied for drinking purposes.

Keywords: Godavari River, Kaleshwaram Project, Water quality, Telangana Irrigation Project, water quality

Presentation code:155

IMPACT OF CLIMATE CHANGE ON ANIMAL BIODIVERSITY: CHALLENGES AND CONSERVATION STRATEGIES.

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ABSTRACT

Climate change represents a critical global threat to animal biodiversity, driven by rising temperatures, altered precipitation patterns, and an increased frequency of extreme weather events. These environmental changes disrupt natural habitats, leading to shifts in species distribution, altered migration routes, and changes in reproductive cycles. Many species lack the adaptive capacity to respond rapidly, increasing their risk of decline and extinction. Vulnerable ecosystems, including forests, marine environments, and polar regions, are particularly affected. Additionally, climate change accelerates the spread of invasive species and zoonotic diseases, further destabilizing ecological balance. This study examines the major challenges posed by climate change to animal biodiversity and underscores the urgent need for effective conservation strategies. Approaches such as habitat preservation, sustainable resource management, and targeted wildlife conservation programs are essential to mitigate these impacts and ensure long-term ecosystem stability. Understanding these dynamics is crucial for developing sustainable solutions to safeguard biodiversity for future generations.

Keywords: Climate change, Animal biodiversity, Species distribution, Habitat loss, Ecosystem imbalance, Conservation strategies, Global warming, Wildlife protection.