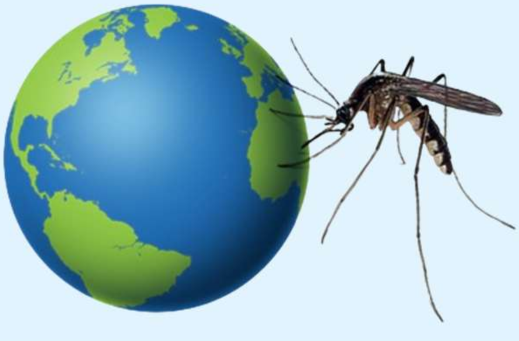
ABSTRACTS
IALS- 2026

Pradhan Mantri Uchchatar Shiksha Abhiyan (PM-USHA)

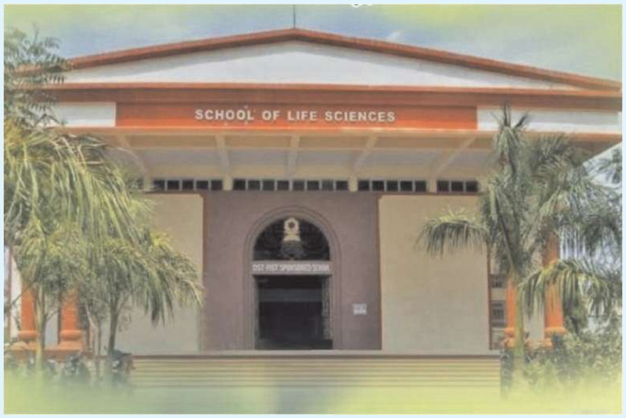
Sponsored

International Conference on Innovations and Applications in Life Sciences: Vector Borne Diseases and Antimicrobial Resistance (IALS-2026)

26th - 27th February, 2026



Organized by
SCHOOL OF LIFE SCIENCES
Swami Ramanand Teerth Marathwada University, Nanded- 431606 (M.S.), India
in Collaboration with CSIR-NCL, Pune.



About School of Life Sciences

The School of Life Sciences had established with inception of Swami Ramanand Teerth Marathwada University at Nanded in 1994. The School of Life Sciences has made remarkable progress within a short period and has an impressive track record in research by the faculty members. The UGC and DST, New Delhi has recognised the School of Life Sciences for continuous support through several levels of assistance such as UGC-DSR (SAP & No SAP), DST-FIST (DRS-1) for major infrastructure & RUSA for promoting research activities in Life Sciences. The School also has received funding from external agencies like USAID, DBT BIRAC, and ICAR etc to undertake research activities, training activities to encourage students and faculty members in cutting edge technologies, collaborative and translational research with National & International organizations etc.

The idea of teaching biology as an integrated discipline was conceived on the campus of this university. The School of Life Sciences has five major ongoing programs: M.Sc. in Basic Sciences (Microbiology, Botany, and Zoology, M.Sc. Biotechnology), B.Sc. in MLT and PGDMLT (One your course).

Major Achievements

- School of Life Sciences has started one UG, five PG and research programs in a short span from is opening viz. Biotechnology, Microbiology, Botany, Zoology, MLT and PGDMLT.
- The students of School of Life Sciences have been placed in various reputed research and education institutes, industries and NGOs. Some are entrepreneurs too.
- The School has attracted students from overseas for the UG, PG and research programs.

Special features

- The School of Life Sciences faculties have completed research projects from various funding agencies of Rs. 2.5 Cr.
- The School of Life Sciences is DST-FIST and UGC-SAP supported. Level-1 of DST- FIST and SAP-1 has been completed whereas level-Il for UGC-SAP and DST-FIST an in progress.

The faculty of SLS is pursuing research in identified trust area and also in various disciplines of Life Sciences viz. enzyme technology, microbial technology, extremophiles biodiversity, platy taxonomy, avian ecology and parasitology, plant tissue culture, phytochemistry and industrially important actinomycetes.

Dr. Manohar G. Chaskar
M.Sc. Ph.D., Mombushuo Fellow (Japan)
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NANDED – 431 606 (Maharashtra)
स्वामी रामानंद तीर्थ मराठवाडा विद्यापीठ
नांदेड – ४३१ ६०६ (महाराष्ट्र)

Established by Govt. of Maharashtra on 17th September 1994, Recognized by the UGC U/s 2(f) and 12(B), NAAC Re-accredited with B++ Grade, a State University

23rd February, 2026

Message

It gives me immense pleasure to welcome all the distinguished delegates, scientists, researchers, faculty members, and students to the International Conference on "Innovations and Applications in Life Sciences: Vector-Borne Diseases and Antimicrobial Resistance" organised by the School of Life Sciences, Swami Ramanand Teerth Marathwada University, Nanded, scheduled to be held on 26th and 27th February 2026. I am pleased to note that this conference is supported through PH-USHA funding and is being organised in academic collaboration with CSIR-National Chemical Laboratory, Pune.

The increasing burden of vector-borne diseases and the growing threat of antimicrobial resistance pose serious global public health challenges. Addressing these concerns requires innovative research, interdisciplinary approaches, and strong scientific collaborations. This conference provides an excellent platform for knowledge exchange, research dissemination, and the development of strategic solutions to these pressing issues.

Our University remains committed to promoting excellence in higher education, research, and innovation. Through such academic initiatives, we aim to foster global collaboration, encourage young researchers, and contribute towards socially relevant scientific advancements.

I sincerely congratulate the School of Life Sciences and the organising committee members for their commendable efforts in organising this important conference. I am confident that the deliberations will lead to meaningful academic interactions and significant contributions to scientific research and public health.

I extend my best wishes for the grand success of the conference.

(Manohar Chaskar)

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Dr. Vinod K. Paul
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February 11, 2026

Message

It is a great pleasure and anticipation that I acknowledge this landmark International Conference on **'International Conference on Vector-Borne Diseases and Antimicrobial Resistance'** organized by the Swami Ramanand Teerth Marathwada University, Nanded, Maharashtra—a gathering that addresses some of the most pressing challenges facing global health today.

The conference's dual focus on vector-borne diseases and antimicrobial resistance is timely to address the current pressing challenges, affecting millions of lives across continents and demanding urgent, coordinated action. Vector-borne diseases alone account for more than 17% of all infectious diseases globally, while antimicrobial resistance threatens to undermine decades of medical progress.

This conference embodies a collaborative spirit. By bringing together researchers, clinicians, policymakers, and public health practitioners under one roof, it creates a vital ecosystem for knowledge exchange and partnership building. The innovations and applications discussed here—from molecular diagnostics to surveillance systems, novel therapeutic approaches to community-based interventions will shape the health security architecture of tomorrow.

What distinguishes this gathering is its focus on translating scientific excellence into practical solutions. The deliberations here have the potential to inform national health programs, influence policy frameworks, and contribute substantively to India's global health leadership. More importantly, they can directly impact the lives of vulnerable populations who bear the disproportionate burden of these diseases.

I extend my sincere appreciation to Swami Ramanand Teerth Marathwada University for conceptualizing and hosting this important initiative. To the organizing committee, researchers presenting their work, and all participants, your dedication to advancing health science and improving human well being is truly commendable.

As you engage in discussions over the coming days, I encourage you to think boldly, collaborate generously, and remain focused on actionable outcomes. The challenges before us are formidable, but so too is the collective expertise assembled here.

I wish this conference resounding success and look forward to the trans-formative insights and recommendations that will emerge from your scholarly deliberations.

V K Paul

(Vinod Paul)

सत्यमेव जयते

डॉ. राजीव बहल, एमडी, पीएचडी.
DR. RAJIV BAHL MD, PhD

सचिव, भारत सरकार
स्वास्थ्य अनुसंधान विभाग
स्वास्थ्य एवं परिवार कल्याण मंत्रालय एवं
महानिदेशक
भारतीय आयुर्विज्ञान अनुसंधान परिषद

Secretary, Government of India
Department of Health Research
Ministry of Health & Family Welfare
Director-General
Indian Council of Medical Research

Message

Warmest Greetings and Best Wishes to the organizers, speakers, delegates, and students participating in the International Conference on Innovations and Applications in Life Sciences: Vector-Borne Diseases and Antimicrobial Resistance (ICLS 2026) scheduled on 26th and 27th February 2026.

This conference, a pivotal collaboration between the School of Life Sciences, Swami Ramanand Teerth Marathwada University, Nanded, and CSIR-NCL, Pune, under the visionary PM-USHA initiative arrives at a critical juncture. The twin challenges of vector-borne diseases and antimicrobial resistance represent two of the most significant threats to global public health and sustainability.

I extend my best wishes for an insightful discourse that fosters groundbreaking collaborations and drives innovative solutions toward a healthier nation. May this platform successfully bridge the gap between cutting-edge research and practical applications, contributing profoundly to the "One Health" paradigm.

I wish you a highly productive, enlightening, and successful conference.

Rajiv Bahl

(Dr. Rajiv Bahl)

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प्र-कुलगुरू

SWAMI RAMANAND TEERTH MARATHWADA UNIVERSITY,
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स्वामी रामानंद तीर्थ मराठवाडा विद्यापीठ,
नांदेड-४३१ ६०६, महाराष्ट्र राज्य

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Date : 20/02/2026

MESSAGE

It gives me great pleasure to convey my best wishes on the occasion of the International Conference on *"Innovations and Applications in Life Sciences: Vector-Borne Diseases and Antimicrobial Resistance"* being organised by the School of Life Sciences, Swami Ramanand Teerth Marathwada University, Nanded, scheduled to be held on 26th and 27th February 2026.

Vector-borne diseases continue to pose serious public health challenges, particularly in tropical and subtropical regions, while antimicrobial resistance has emerged as a silent global pandemic threatening decades of medical progress. Addressing these complex challenges requires sustained scientific innovation, robust surveillance mechanisms, and effective translation of research outcomes into public health practices.

Conferences of this nature play a vital role in fostering constructive dialogue among researchers, healthcare professionals, academicians, and policymakers. Such academic platforms not only promote interdisciplinary scientific collaboration but also help in shaping evidence-based strategies for disease prevention, control, and management. They further strengthen research culture and inspire young scholars to contribute towards addressing critical global healthcare challenges.

I sincerely congratulate the organising team for selecting a highly relevant and impactful theme. I am confident that this conference will facilitate meaningful deliberations, encourage collaborative research initiatives, and contribute significantly to advancements in public health and life sciences.

I extend my heartfelt best wishes for the grand success of the conference.

(Pro. Ashok M. Mahajan)

"Dnyanteerth", Vishnupuri, NANDED-431 606 (Maharashtra), India [ज्ञानतीर्थ, विष्णुपूरी, नांदेड - ४३१ ६०६ (महाराष्ट्र) भारत]
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Message

It is a pleasure to extend my greetings on the occasion of the International Conference addressing key challenges in vector-borne diseases and antimicrobial resistance, being organised by the School of Life Sciences, Swami Ramanand Teerth Marathwada University, Nanded.

Vector-borne diseases continue to remain a significant public health concern in many parts of the world, necessitating continuous and focused research in epidemiology, vector biology, diagnostics, and effective control strategies. The growing challenge of antimicrobial resistance further underscores the urgent need for integrated, multidisciplinary, and innovative scientific approaches to safeguard global health.

This conference provides a valuable platform for researchers, academicians, and public health professionals to share knowledge, exchange experiences, deliberate on emerging trends, and strengthen collaborative research efforts. Such academic engagements are vital for translating scientific research into practical and sustainable disease control programmes.

I sincerely appreciate the dedicated efforts of the organising committee in conceptualising and conducting this important academic event.

I congratulate the organizers and wish the conference a successful and impactful outcome.

Dr. M. K. Patil

Dean,
Science & Technology Faculty
S.R.T.M. University
Nanded - 431 606 (M.S.)

International Conference on

"Innovations and Applications in Life Sciences: Vector-Borne Diseases and Antimicrobial Resistance"

IALS-2026

26th and 27th February 2026

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KEYNOTE SPEAKER

Role of *Anopheles* vectors of Non-human primate malaria in the Greater Mekong Subregion: A zoonotic disease and One Health approach

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Abstract

Non-human primate malaria has been reported in most Southeast Asian countries, particularly Malaysia, Indonesia, and the Philippines. In Thailand, Non-human primate malaria cases have increased notably, particularly among patients visiting border areas, although they still represent a small proportion of total malaria cases in endemic regions with macaque populations. Nevertheless, the rising incidence of Non-human primate malaria in humans poses a significant threat to the national malaria elimination program. *Plasmodium knowlesi* is currently the most common simian malaria species infecting humans in Thailand, while *P. cynomolgi* and *P. inui* have also been reported. Mosquitoes belonging to the *Anopheles leucosphyrus* Group, which are forest-dwelling species, serve as the primary vectors of Asian Non-human primate malaria. However, limited information is available regarding the role of vectors responsible for simian malaria transmission in Thailand.

Keywords: Non-human primate malaria, *Plasmodium knowlesi*, Mosquito, Thailand.

Plenary session

Vector control in the age of global challenges: From reactive approaches to innovative and proactive management

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Abstract

Vector control is central to reducing the burden of vector-borne diseases (VBDs), yet its impact is increasingly constrained by climate change, rapid urbanization, insecticide resistance, vector adaptation, and persistent funding gaps. In many endemic settings, control strategies remain largely reactive, responding to outbreaks rather than anticipating risk.

This presentation calls for a policy shift towards proactive and innovation-driven vector control. It highlights how climate-informed surveillance, resistance monitoring, molecular diagnostics, and predictive modelling can strengthen decision-making and improve the timing and effectiveness of interventions. Emerging tools and digital innovations, including data-driven risk assessment, offer opportunities to move from short-term response to sustained impact.

The talk emphasizes the importance of Integrated Vector Management and One Health approaches to align health, environmental, and development sectors. Strengthening domestic financing, cross-sectoral coordination, and equitable access to new tools is essential for building resilient vector control systems capable of addressing current and future global challenges.

Keywords: Vector-borne diseases, Vector control, Climate change, Insecticide resistance, One Health, Integrated Vector Management, Policy and governance.

Metagenomics and AMR environmental surveillance

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Abstract

Environmental surveillance involves the systematic monitoring of microorganisms, pathogens, and antimicrobial resistance (AMR) in environmental reservoirs such as water, soil, air, and wastewater to assess potential public health risks. By tracking these systems, it offers early warning signals for disease outbreaks, aids in understanding transmission pathways, and supports evaluation of public health interventions. Within the One Health framework, which recognizes the interconnectedness of human, animal, and environmental health, environmental surveillance helps identify shared disease sources and informs coordinated responses to emerging threats. Metagenomics-based surveillance provides a powerful, culture-independent approach for detecting and characterizing microbial communities in diverse environments. Through high-throughput sequencing of environmental DNA and RNA, it enables the identification of both known and novel organisms, offering comprehensive insights into microbial diversity, functional potential, and AMR patterns.

We have applied nucleic acid-based genomic and metagenomic strategies to identify pathogens and genetic variants of relevance. Our earlier studies demonstrated the utility of such approaches for monitoring viruses and AMR genes in wastewater from sewage treatment plants and open drainage systems, revealing several previously uncharacterized microbial elements.

These strategies enhance understanding of microbial dynamics influenced by natural and anthropogenic factors, supporting environmental management and disease prevention. As sequencing technologies continue to advance and become more accessible, genomic surveillance is expected to play an increasingly central role in global efforts to protect environmental and public health.

Keywords: Antimicrobial resistance (AMR), Environmental, Genomics, Metagenomics, One Health, Surveillance.

Plant-derived mosquito repellents in Thailand: Evidence and excitorepellency (ER) screening

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Abstract

Mosquito-borne diseases continue to pose a serious public-health burden across tropical and subtropical regions. However, heavy dependence on synthetic insecticides and repellents is increasingly challenged by insecticide resistance, concerns about non-target effects, and broader environmental impacts. Plant-derived repellents—such as botanical extracts, essential oils, and purified natural compounds—represent a promising and more sustainable alternative. This presentation synthesizes recent evidence from Thailand and international studies on the effectiveness of these botanicals against major vector genera, including *Anopheles*, *Aedes*, and *Culex*. A key focus is the excitorepellency (ER) assay, which captures mosquito behavioural responses through both contact irritancy and spatial avoidance, making it a sensitive screening approach for identifying strong candidate repellents. Notably, several locally available Thai plant species demonstrate ER responses comparable to DEET while potentially offering lower environmental burden. Integrating validated plant-based repellents into integrated vector management could help reduce chemical inputs without sacrificing control performance. Moving forward, interdisciplinary work linking entomology, phytochemistry, formulation science, and public-health implementation is essential to harmonize testing protocols, improve formulation stability, evaluate field persistence, and support regulatory pathways. With rigorous evaluation and appropriate deployment, plant-derived repellents could become a practical, community-oriented component of sustainable mosquito control strategies.

Keywords: Excitorepellency (ER), mosquito repellent, Mosquito control, Public health.

Scrub typhus in India: An emerging neglected vector-borne zoonosis

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Abstract

Scrub typhus is a resurgent health threat in India that can no longer be ignored. Caused by *Orientia tsutsugamushi* and transmitted by larval trombiculid mites, the pathogen demonstrates remarkable ecological adaptability, thriving across rural, peri-urban, and urban environments. Seasonal outbreaks establish scrub typhus as a major contributor to acute febrile illnesses, yet the disease remains underdiagnosed and underreported due to nonspecific symptoms, clinical overlap with other tropical infections, and inadequate surveillance systems.

Diagnostic limitations including insensitive or inaccessible tools in endemic regions further delay recognition, leading to severe complications and increased mortality rates. Clinically, scrub typhus often presents as an undifferentiated febrile illness, complicating timely detection and management. Addressing this challenge requires strengthened surveillance to define true prevalence, affordable and accurate diagnostics for early recognition, and heightened clinical vigilance to reduce misclassification. Preventive strategies such as vector control, community education, and rapid case detection are critical to curbing transmission. Concurrently, advancing research into mite ecology, antigenic diversity of *O. tsutsugamushi*, and regional distribution patterns will provide essential insights into transmission dynamics and guide targeted interventions. The path forward is clear: India must invest in stronger surveillance to reveal the true scale of the problem, expand access to affordable and accurate diagnostics, and train clinicians to spot scrub typhus early.

The clock is ticking. Without swift, coordinated action across research, medicine, and public health, scrub typhus risks becoming a silent killer. With decisive leadership, however, India can turn this looming crisis into a public health success story.

The time to ACT IS NOW.

Keywords: Scrub typhus, Neglected tropical disease, Zoonotic infection, Surveillance and diagnostics, Public health in India.

Plasmodium falciparum histidine-rich domain-containing secretory protein as a novel diagnostic biomarker for the malaria detection and its role in immunomodulation

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Malaria Biology Group, International Centre for Genetic Engineering and Biotechnology (ICGEB), New Delhi-110067, India

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Abstract

Malaria caused by *Plasmodium falciparum* remains a major global health challenge, requiring timely and accurate diagnosis for effective control and elimination. Current rapid diagnostic tests (RDTs) predominantly rely on HRP2 detection; however, increasing *pfhrp2/3* gene deletions threaten their reliability. This study aims to identify and evaluate a novel HRP2-independent antigen, *P. falciparum* histidine-rich domain-containing secretory protein, as a potential diagnostic biomarker for malaria.

Histidine-rich domain-containing secretory protein (HDCSP) was analyzed using bioinformatics and phylogenetic tools to assess conservation and species specificity. Recombinant HDCSP fragments were expressed, purified, and used to generate polyclonal antibodies. Expression across parasite stages was assessed by Western blot and immunofluorescence. Patient sera reactivity was evaluated using ELISA and Western blot, while circulating antigen presence was confirmed by immunoprecipitation coupled with LC–MS/MS. Immunogenicity was assessed through flow cytometry of murine splenic and pulmonary lymphocytes.

HDCSP contains conserved histidine-rich motifs similar to HRP2/HRP3, is highly conserved among *P. falciparum* isolates, and shows limited similarity to non-human infecting Plasmodium species. It is expressed across all asexual blood stages and secreted into circulation. Malaria patient sera strongly recognized HDCSP, and circulating peptides were confirmed by LC–MS/MS. HDCSP also bound to $CD4^+/CD8^+$ T cells, NK cells, and macrophages, eliciting robust pro-inflammatory cytokine responses, demonstrating its immunogenic potential.

HDCSP is a secreted, immunogenic, HRP2-independent antigen detectable in patient sera. Its conserved expression, circulating presence, and immune recognition make it a promising diagnostic biomarker to enhance malaria detection, particularly in regions affected by *pfhrp2/3* deletions, supporting improved surveillance and control strategies.

Keywords: Malaria, *Plasmodium falciparum*, Diagnostic biomarker, HRP2-independent antigen, Histidine-rich domain-containing secretory protein (HDCSP).

Decentralizing Molecular Diagnostics: From innovation to impact

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Abstract

This platform addresses a critical need in modern healthcare by demonstrating the feasibility of scalable, decentralized molecular diagnostics in resource-constrained environments. By combining portability, rapid turnaround, and programmatic integration, it strengthens disease surveillance, enhances case detection, and supports resilient public health systems. Furthermore, through the EDGE program, we engage with innovators to accelerate go-to-market traction and expand access to innovative solutions in underserved settings.

Keywords: Molecular diagnostics, Healthcare, innovation.

Nation-wide analysis of malaria distribution in India between 2018 and 2023 and its potential drivers

Harish C. Phuleria*
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Abstract

With less than two years remaining from 2027—the year which the government has targeted to achieve zero Indigenous cases, we mapped the malaria indicators across the 700+ districts during 2018 to 2023, identified the hotspots and assessed the potential drivers of malaria transmission in different regions. District-wise data on malaria was obtained from NCVBDC while socio-economic variations, meteorological factors and land-use land-cover changes were sourced to other publicly accessible sources to assess the impact of covariates on the malaria transmission using an ensemble of Random Forest and Poisson regression models. The *P. falciparum* affected regions are widespread in North-eastern and Central India. However, after the pandemic, an emerging geographical expansion into the north-eastern parts is observed for the *P. vivax*. Population belonging to scheduled castes and scheduled tribes and those economically marginalised are among the most vulnerable, but lifestyle habits such as drinking water practices, maternal education, and healthcare accessibility are also associated with malaria transmission.

Keywords: Indigenous cases, NCVBDC, *P. falciparum*, *P. vivax*.

My Journey as Plant Biologist: From Tailor to Tailoring Plant Metabolism

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Abstract

Lessons from working as a tailor in my parents' business in my village (Kari District, Beed) helped me adopt and/or correlate molecular biology techniques such as complementary shapes and tags, to cutting and stitching. I will initially introduce science, research approaches and plant metabolism, followed by specialized metabolites and modern techniques in biological chemistry. These small molecules are indispensable for plant growth and development, as well as for coping with various biotic and abiotic stresses. These specialized active molecules are produced by all plant species and possess diverse structural and functional properties. Four major classes of plant specialized metabolites—namely phenylpropanoids, terpenoids, alkaloids, and peptides— are known to date. Using advanced multi-omics such as next-generation sequencing, proteomics, metabolomics (mass spectrometric/NMR techniques), and bioinformatics, we discovered biosynthetic pathways of important metabolites from potato, tomato and mango. I will discuss three major ongoing projects in the group: (i) insights into plant-insect interactions, emphasizing the role of plant metabolites in plant defenses; (ii) a comparative gene co-expression analysis of tomato and potato coupled with metabolite profiling, which revealed the function of several uncharacterized genes in steroidal glycoalkaloid biosynthesis; and (iii) the metabolism programming in mango fruit ripening to blend distinct aroma compounds in Hapus. Thus, it is clear that several such metabolites have great significance in sustainable crop protection in agriculture, increasing the nutritional value of food, etc. The insights from these investigations will be discussed in my presentation.

Coordinated approaches of USM (Unani System of Medicine) in addressing AMR

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Abstract

Antimicrobial resistance (AMR) is one of the top global public health and development threats. It is estimated that bacterial AMR was directly responsible for 1.27 million global deaths in 2019 and contributed to 4.95 million deaths**.** Antimicrobial resistance (AMR) is a natural process among bacteria, viruses, fungi, helminths, ectoparasites, protozoa that occur due to mutations of genetic changes in pathogens but may be nosocomial or healthcare-associated infections caused by misuse or over use of antimicrobial drugs.

Contributing factors: improper access to clean water, sanitation and hygiene (WASH) for both humans and animals, poor prevention and control, **substandard and counterfeit** vaccines, diagnostic tools and drugs, lack of awareness, knowledge, legislations, misuse and overuse of Antimicrobials among human infections, agricultural and veterinary practices, waste discharges containing AMR bacteria, etc.

Coordinated approach of USM: Usage of Unani Adjuvants in reducing side effects of allopathic drugs, drug-drug interaction, adverse drug reactions, adverse effects, and toxicities in common cause of therapies like ART, ATT, anti-cancerous drugs, pain killer, and other long-term therapies like osteoarthritis, steroid therapies can be beneficial in reducing AMR. USM have number of single and compound drug formulations that are anti-inflammatory, anti-oxidants, immune boosters and immuno modulators that also have antimicrobial activities like *Curcuma longa*, Cinnamon, Giloy, Afsanteen, or ***Artemisia absinthium*** (Wormwood) and Qurs Afsanteen, Qurs Qaranjwa, Qurs Sartaan Kafoori.

These drugs that are common in century old practices and also being observed in research trials of NIs of Mo Ayush and reputed Unani medical colleges like AKTC, AMU, Jamia Hamdard, Nizamia College, Hyderabad and National Institute of Unani Medicine, Bangalore and Ghaziabad, National Institute of Unani Medicine for Skin disorders, etc. can be used as adjuvants in combination with multi drug allopathic regimes and can be mainstreamed healthcare delivery system. Standardisation techniques, preclinical, clinical, epidemiological, and field trials together with collaborative approaches are required to strengthen, validate, and re-validate the traditional treasures of Unani system of Medicine.

Key words: USM, Adjuvants, AMR, Drug-drug interactions, ADR, SE, AE.

EcoBiotraps: An innovative adjunct vector control device

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Abstract

Vector-borne diseases such as dengue, chikungunya, and malaria, exacerbated by climate change and urbanization, pose ongoing threats in densely populated low-resource settings worldwide. EcoBio, a social organisation, partnered with the Brihanmumbai Municipal Corporation's SMILE Council to evaluate EcoBioTraps (EBTs)—100% green lethal ovitraps designed for broad-spectrum mosquito control—via a 12-month longitudinal cohort study in Dharavi, Mumbai, India. Covering 200,000 residents across 18 clusters and 9 sites, the trial adhered to WHO mosquito surveillance protocols over 13 cycles.

EBTs achieved a 97% reduction in active larval breeding sites, attracting *Aedes*, *Anopheles*, and *Culex* species and diverting oviposition from primary habitats. Community interventions using information, education, and communication (IEC) plus behaviour change communication (BCC) fostered high acceptance, improved knowledge and practices, and demonstrated cost-effectiveness in economically disadvantaged urban slums.

A key innovation was a 15-day early warning system for pre-outbreak detection, shifting paradigms from reactive to proactive source reduction. These outcomes validate EBTs for integrated vector management (IVM) in endemic regions.

Building on this, MoviTraps (MVT)—a sustainable retail-adapted indoor version—aims to scale deployment from community to household levels across India and similar global contexts, promoting eco-friendly, community-driven mosquito control.

Keywords: Lethal ovitrap, Vector control, *Aedes*, *Anopheles*, *Culex*, Green solution, Sustainable MVT, Urban slums, Integrated vector management.

ORAL PRESENTATION

Oral-01

A novel molecular mechanism driving macrophage phenotypic switching during colorectal cancer progression

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Abstract

Colorectal cancer (CRC) is one of the deadliest cancer types and is characterized by a complex tumor microenvironment (TME), which includes cancer and immune cells engaging in intricate signaling crosstalk. TME is dependent on the CRC stage and contributes to cancer aggressiveness and therapy resistance. It has been established that tumor-associated immune cells can support cancer progression. However, the underlying mechanisms are not fully elucidated. Here, we provide evidence that communication between CRC and immune cells, particularly tumor-associated macrophages (TAMs), occurs through the release of soluble factors and extracellular vesicles (EVs), such as exosomes. Our study reveals that TAMs initially recognize exosomes as foreign entities, triggering a pro-inflammatory response. Over time, however, the contents of these phagocytosed exosomes reprogram the TAMs into an anti-inflammatory, tumor-supportive phenotype. To target the mechanisms that drive this switching of macrophages may provide a novel therapeutic strategy to maintain macrophage pro-inflammatory activity and inhibit tumor-supportive functions during colorectal cancer progression.

In conclusion, this study demonstrates that CRC cell-derived EVs orchestrate macrophage inflammatory signaling and immune checkpoint responses through NF–κB-dependent induction of PD-L1, thereby contributing to an immunosuppressive TME. Modulation of EVs-driven signaling using a natural inhibitor highlights a potential adjunct strategy to limit cancer cell-mediated immune evasion. These findings provide mechanistic insight into CRC cell–macrophage crosstalk by integrating rigorous EVs characterization with functional validation in immune-relevant in vivo mouse models. Collectively, this work lays a mechanistic foundation for future investigations into EV-mediated immune regulation in cancer.

Keywords: Colorectal cancer (CRC), tumor microenvironment (TME), extracellular vesicles (EVs), tumor-associated macrophages (TAMs).

Oral-02

Development of arginine oleate-mediated drug delivery system

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Abstract

The present study deals with the synthesis of arginine oleate. The synthesized arginine oleate is characterized preliminary by surface tension and viscosity. Thin layer chromatography (TLC) confirmed purity of synthesized arginine oleate. The Fourier transform infrared spectroscopy (FTIR) established synthesis of arginine oleate. To have increased availability of drug, encapsulation of azithromycin (azi) with arginine oleate was done. The micelle formed by arginine oleate can encapsulate azithromycin. The antimicrobial activity of micelle with azi was tested on Gram-negative organisms by agar well diffusion method. The finding suggests azi-loaded micelle was effective on Gram-negative organisms.

Critical micelle concentration (CMC), a key physicochemical parameter for surfactant characterization and self-assembly behavior, was determined and calculated to be 40 mM. The findings indicate that arginine oleate is a promising surfactant for micellar drug delivery with improved antimicrobial performance.

Keywords: Arginine oleate, Surface tension, Viscosity, Micelle, CMC.

Oral-03

Honey environmental DNA and AI for global surveillance of vector-borne diseases and antimicrobial resistance

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Abstract

The accelerating convergence of climate change, biodiversity loss, urbanization, and antimicrobial misuse has intensified the global burden of vector-borne diseases and antimicrobial resistance (AMR), threatening human, animal, and environmental health. Conventional surveillance systems remain fragmented, labor-intensive, and spatially limited, constraining early-warning capacities in vulnerable regions. This review introduces an integrative, next-generation surveillance paradigm that leverages honey-derived environmental DNA (eDNA) and artificial intelligence (AI) to enable scalable, cost-effective, and ecosystem-wide health intelligence within the One Health framework. Honey functions as a natural biological sampler, encapsulating genetic signatures from vectors, pathogens, host species, and surrounding microbiomes across extensive foraging landscapes. We critically synthesize recent advances in metabarcoding, shotgun metagenomics, and biosensor-enabled sequencing platforms for extracting high-resolution disease and resistance signals from honey matrices. Furthermore, we examine the transformative role of deep learning, federated analytics, and explainable AI in automating pattern recognition, outbreak forecasting, and resistance gene tracking from complex multi-omic datasets. Integrating geospatial, climatic, and socio-ecological variables, this framework enables real-time risk mapping and predictive modeling at local-to-global scales. We highlight methodological challenges, ethical considerations, and data-governance requirements essential for clinical translation and policy integration. By positioning honey eDNA–AI surveillance as a unifying interface between ecology, epidemiology, and digital health, this review establishes a foundational blueprint for resilient, precision-driven global health monitoring systems capable of mitigating emerging infectious threats and advancing sustainable planetary health.

Keywords: Honey eDNA, Artificial Intelligence, One Health, Vector-borne diseases, Antimicrobial resistance, Digital epidemiology.

Oral-04

Holistic vector control methods for the Indian environment

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Abstract

India carries a significant burden of vector-borne diseases such as malaria, dengue, chikungunya, Japanese encephalitis, and lymphatic filariasis due to its tropical climate, monsoon-driven ecology, rapid urbanization, and diverse socioeconomic conditions. Conventional vector control strategies often rely heavily on chemical insecticides, which face growing challenges including insecticide resistance, environmental contamination, and community acceptance issues.

Therefore, a holistic, integrated approach tailored to India's ecological and sociocultural context is essential for sustainable vector management.

Holistic vector control emphasizes Integrated Vector Management (IVM), combining environmental, biological, chemical, technological, and community-based strategies. Environmental management plays a central role by reducing vector breeding habitats through improved water management, sanitation, waste disposal, and urban planning. Biological control methods such as larvivorous fish (e.g., *Gambusia* and *Poecilia*), bacterial larvicides (*Bacillus thuringiensis israelensis* and *Bacillus sphaericus*), and natural predators provide eco-friendly alternatives to chemical insecticides. Botanical repellents and plant-derived insecticides, including neem-based formulations, offer locally available and sustainable solutions.

Community participation and behavior change communication are critical components, promoting practices such as elimination of stagnant water, use of bed nets, and improved household hygiene. Advances in technology—including GIS mapping, remote sensing, and mobile-based surveillance—enhance monitoring and targeted interventions. Climate-informed planning further supports seasonal preparedness and risk forecasting in monsoon-prone regions. Policy integration under the One Health framework strengthens collaboration across public health, veterinary, environmental, and municipal sectors. While challenges remain in funding, infrastructure, and public awareness, holistic vector control offers a sustainable pathway to reduce disease transmission while minimizing ecological harm. Such integrated strategies are essential for achieving long-term vector control and improving public health resilience in the Indian environment.

Keywords: Integrated Vector Management (IVM), Vector-borne diseases, Biological control, Environmental management, Larvivorous fish, Neem-based insecticides, One Health, Sustainable public health.

Oral-05

Antimicrobial resistance in foodborne pathogens: Consequences of antibiotic use in livestock production

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Abstract

The widespread use of antibiotics in food animal production has accelerated the emergence of antimicrobial resistance (AMR) in zoonotic pathogens of critical importance to human health. Among these, *Campylobacter* and *Escherichia coli* represent major concerns due to their prevalence in livestock and their role in foodborne and extraintestinal infections. Antibiotic administration in poultry, cattle, and swine exerts selective pressure that fosters resistant strains, particularly fluoroquinolone- and macrolide-resistant *Campylobacter* and extended-spectrum beta-lactamase (ESBL)-producing *E. coli*. These resistant bacteria can be transmitted to humans through contaminated meat, direct contact, or environmental pathways, compromising the efficacy of frontline therapies for gastroenteritis, urinary tract infections, and bloodstream infections. The persistence and dissemination of resistance genes, often via plasmid-mediated transfer, further amplify the public health threat. Addressing this challenge requires a One Health approach that integrates prudent antibiotic stewardship in agriculture, enhanced surveillance, and the adoption of alternative strategies such as vaccination, improved biosecurity, and non-antibiotic growth promoters. Reducing antibiotic use in food animals is essential to safeguard the effectiveness of critical antimicrobials and mitigate the global burden of AMR.

Keywords: Antimicrobial resistance, *E. coli*, Antibiotic, Foodborne pathogens.

Oral-06

Ceftriaxone-induced anaphylactic shock in a term pregnant woman: A rare but life-threatening adverse drug reaction

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Abstract

Ceftriaxone is the most commonly prescribed third-generation cephalosporin antibiotic for obstetric patients. Although ceftriaxone is generally considered safe, immediate hypersensitivity reactions, including anaphylaxis, can occur. Anaphylaxis during pregnancy poses a serious threat to both maternal and fetal life due to rapid hemodynamic compromise.

A 28-year-old female, G4P3L2D1, who was at 38 weeks and 6 days of gestation, had been previously delivered by two lower-segment caesarean sections and was admitted for premature rupture of membranes. After receiving ceftriaxone intravenously as prophylaxis, she developed severe breathlessness, hypotension (Blood pressure 50–70 mm Hg), tachycardia (Heart rate 130–140 bpm), and hypoxemia within several minutes of administration. She had no history of asthma or heart disease. Ceftriaxone was stopped immediately. The patient was managed with high-flow oxygen, intravenous fluids, adrenaline, hydrocortisone, antihistamines, and noradrenaline infusion. After receiving adequate treatment, she was transferred to the intensive care unit for stabilization. The adverse drug reaction was assessed using the Naranjo probability scale, indicating a probable relationship between ceftriaxone and anaphylactic shock.

This case indicates that while ceftriaxone is a frequently prescribed antibiotic, it may lead to severe anaphylaxis, particularly in women who do not have a known allergy to ceftriaxone. Complete drug history, early recognition by vigilant monitoring after parenteral drug administration, are of the utmost importance. Reporting such serious adverse drug reactions is essential to enhance drug safety awareness in maternal healthcare and strengthen pharmacovigilance systems.

Keywords: Ceftriaxone, Anaphylaxis, Pregnancy, Adverse drug reaction.

Oral-07

Harnessing Next-Generation Molecular Diagnostics to combat antimicrobial resistance: A 2026 perspective

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Abstract

Antimicrobial resistance (AMR) continues to escalate as a critical global health emergency, with projections indicating millions of annual deaths by 2050 if effective interventions are not implemented. Conventional phenotypic culture-based antimicrobial susceptibility testing (AST), although considered the gold standard, is limited by prolonged turnaround times of 48–72 hours, contributing to empirical broad-spectrum antibiotic use and accelerating resistance development. This review highlights the ongoing "molecular shift" in diagnostics, focusing on CRISPR-Cas-based detection, real-time Nanopore sequencing, and artificial intelligence (AI)-integrated metagenomics. These next-generation platforms enable rapid, culture-independent identification of pathogens and their resistome within hours. The integration of such technologies into clinical workflows is essential for precision therapy, real-time surveillance, and effective antimicrobial stewardship in 2026 and beyond.

Keywords: Antimicrobial resistance (AMR), Antimicrobial susceptibility testing (AST), Artificial intelligence (AI).

Oral-08

Investigation of the antibiotic resistance of silver (Ag) nanoparticles synthesized from aqueous bulb extract of *Scilla hyacinthina* (Roxb.) Macbr.

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Abstract

Plant-mediated synthesis of nanomaterials has gained increasing attention due to its eco-friendly, sustainable, and cost-effective approach. In this study, silver nanoparticles (AgNPs) were synthesized using aqueous bulb extracts of *Scilla hyacinthina* as a bioreducing and stabilizing agent through an ultrasonic-assisted green synthesis method. Ultrasound-assisted extraction enhances the release of bioactive phytochemicals, thereby improving the reduction efficiency and stability of the synthesized nanoparticles compared to conventional methods. The antibacterial activity of the synthesized AgNPs and the aqueous bulb extract was evaluated against Gram-positive *Staphylococcus aureus* and Gram-negative *Escherichia coli* using minimum inhibitory concentration (MIC) and disc diffusion assays. The synthesized AgNPs demonstrated significant antibacterial activity, exhibiting a zone of inhibition of 20 mm against both *S. aureus* and *E. coli*. In contrast, the aqueous bulb extract showed comparatively lower inhibition zones of 15 mm and 17 mm against *S. aureus* and *E. coli*, respectively. These results indicate that AgNPs possess enhanced antimicrobial efficacy over the crude extract against both Gram-positive and Gram-negative bacterial strains. Previous phytochemical analyses of the aqueous bulb extract confirmed the presence of bioactive compounds such as phenols, flavonoids, saponins, glycosides, terpenoids, and steroids, which likely play a crucial role in the reduction, capping, and stabilization of AgNPs. Overall, this study highlights the effectiveness of ultrasonic-assisted green synthesis of silver nanoparticles using *Scilla hyacinthina* bulb extract and demonstrates their promising antibacterial potential for biomedical applications. Although preliminary characterization confirms nanoparticle formation, comprehensive chemical characterization of the synthesized AgNPs is essential for deeper understanding and future applications.

Keywords: Ultrasonic-assisted extraction, AgNPs synthesis, *Scilla hyacinthina*, Bulb extract, Antibacterial activity.

Oral-09

Emerging threats of antimicrobial resistance in vector-borne diseases: A global perspective

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Abstract

Vector-borne diseases (VBDs) remain a major global health concern, particularly in tropical and subtropical regions. In recent years, the emergence and spread of antimicrobial resistance (AMR) among pathogens associated with vector-borne infections have intensified the burden on healthcare systems. Resistance to antimalarial drugs, antibiotics used for rickettsial and bacterial infections, and antiparasitic agents threatens effective disease management and increases morbidity and mortality. This review examines the current global status of AMR in major vector-borne diseases, including malaria, dengue-associated secondary infections, leishmaniasis, chikungunya-related complications, and tick-borne bacterial diseases. The paper discusses the drivers of resistance such as antimicrobial misuse, environmental contamination, climate change, vector expansion, and inadequate surveillance. It also highlights molecular mechanisms of resistance, emerging epidemiological trends, and the need for integrated strategies under the One Health framework. Strengthening surveillance systems, improving antimicrobial stewardship, developing novel therapeutics, and implementing integrated vector management are critical to mitigate the dual burden of VBDs and AMR.

Keywords: Vector-borne diseases, Antimicrobial resistance, Malaria resistance, Leishmaniasis, One Health, Global health.

Oral-10

Epidemiological study of rapidly emerging uropathogens isolated from urinary catheters and its influential demographic factors responsible for contamination

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Abstract

Urinary tract infections (UTI) are very common in all the developed as well as developing countries in which the majority of infections are catheter associated. Catheter-associated urinary tract infection (CAUTI) is one of the major causes of hospital acquired infections. The aim of this study is to investigate influential demographic factors responsible for contamination associated with the rate of CAUTI, while taking into account type of urinary catheter used, the most common organisms found, patient diagnosis, age, gender, and comparison with other studies. During the study, 22 uropathogenic species were isolated from the different segments of urinary catheter samples of the patients collected from 12 different hospitals of Amravati city, Maharashtra. Gram-negative organisms were the most frequent isolates, with *Pseudomonas aeruginosa* (16.08%) being the most common followed by *Escherichia coli* (10%) and *Candida albicans* accounted for almost 11% of all the uropathogens. It was found that the majority of uropathogens were isolated from the section A (Catheter segment inside the bladder) and section E (Catheter segment connected to drainage tube) of the urinary catheter. The duration of the catheterization plays the major role in the contamination and further infection to continue. It was observed that the female catheterized patients are more prone to the contamination and infection as compared to male catheterized patient. The antibiotic sensitivity pattern indicates that MAR (Multiple Antibiotic Resistance) index was more than 0.2 for almost all the uropathogens tested concluding that there is antibiotic stress on uropathogens and rate of resistance increased rapidly. Also, it was found that there was a statistically significant association between the duration of catheterization, type of disease, age of patient and type of catheter with respect to gender.

Keywords: Catheter-associated urinary tract infection (CAUTI), Urinary tract infection (UTI), Uropathogen.

Oral-11

Antibiotic susceptibility pattern of Uropathogenic *Escherichia coli* isolated from urine Samples

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Abstract

Multidrug-resistant (MDR) *Escherichia coli* is a serious worldwide health problem, especially when it comes to UTIs. The current investigation focuses on the molecular identification of MDR isolates using 16S rRNA gene sequencing, the isolation of *E. coli* bacteria from urine samples, and their antibiotic susceptibility profile. A total of 10 *E. coli* isolates were isolated from urine samples obtained from individuals suspected of having UTIs and grown on selective media. These isolates were tested using the disc diffusion technique for antibiotic resistance to several classes of antibiotics. 16S rRNA gene sequencing was used to further identify and validate MDR *E. coli* strains exhibiting resistance to many drugs. MacConkey's agar plate was used to isolate the *E. coli* isolates for this study. The strain SUC-2 shown resistance to antibiotics from class β-lactam, cephalosporin, sulphonamide, quinolones, macrolides, glycopeptides, and polymyxin. The MDR isolate strain SUC-2 was identified as *Escherichia* coli and assigned Accession No. PP854586 to the GenBank database. These findings highlight the alarming prevalence of MDR *E. coli* in UTIs and emphasize the urgent need for continuous surveillance, rational antibiotic use, and development of alternative therapeutic strategies to combat antimicrobial resistance.

Keywords: *Escherichia coli*, Urinary tract infection, Multidrug-resistant, Antibiotics, 16S rRNA.

Oral-12

Evaluation of Triethylenemelamine as a potential inhibitor of Testosterone 17beta-dehydrogenase (NADP+) for targeted anticancer therapy

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Abstract

Bryonopsis laciniosa is a well-known spiritual plant as the seeds of it having the shape Shivling. The fruits of it appears berry type and having colored zigzag line on its outer covering. Immature fruits are green in color, while mature fruits appear shiny reds and gradually it will dry on the vines itself. This twine grows on fencing, plants and even on the ground surfaces. The dried seeds of it were taken and grinded with mixture and mortar pestle. The fine powder out of it were further subjected to methanolic extraction using soxhletion. The obtained crude extract after soxhletion was used for the isolation and characterization of secondary metabolites present in it using HR-LCMS. Large number bioactive compounds were recorded in this plant. This compound is also compare with the database library using their retention time and peaks. By using the library of the compounds, numerous group of bioactive compounds were revealed among them Triethylenemelamine were chosen for further investigation.

In this study, we found that Triethylenemelamine is having strong affinity towards Testosterone 17beta-dehydrogenase (NADP+). Direct exposure or conjugation of this compound with other standard molecule will enhance the rate of tumor reduction. This drug specifically targets Testosterone 17beta-dehydrogenase (NADP+) and blocks its activity.

Keywords: Testosterone 17beta-dehydrogenase (NADP+), Triethylenemelamine, *Bryonopsis laciniosa*.

Oral-13

DESIGN, SYNTHESIS AND SCREENING OF HETEROCYCLIC COMPOUNDS AGAINST MULTIDRUG RESISTANT BACTERIA

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Abstract:

The rapid emergence of multidrug-resistant (MDR) bacteria poses a significant threat to public health, necessitating the development of novel antimicrobial agents with improved efficacy. Heterocyclic compounds, particularly triazole derivatives, have gained attention due to their structural versatility and promising biological activities. The present study focuses on the synthesis, characterization, and evaluation of triazole-based compounds for antibacterial activity against MDR bacterial isolates obtained from different clinical samples collected across multiple districts. Triazole derivatives were synthesized using optimized chemical procedures to obtain stable compounds with good yield and purity. Structural characterization was carried out using standard analytical and spectroscopic techniques to confirm molecular structure and integrity. The antibacterial potential of the synthesized compounds was evaluated against clinically relevant MDR bacterial strains including Klebsiella pneumoniae, Bacillus subtilis, Pseudomonas spp., Staphylococcus aureus, and Escherichia coli. These isolates represented diverse infection sources and geographical variations, providing a broad evaluation of antibacterial efficacy.

Antibacterial screening was performed using established microbiological assays to assess inhibitory activity against both Gram-positive and Gram-negative organisms. Results demonstrated that the synthesized triazole compounds exhibited notable antibacterial activity against MDR pathogens, indicating their effectiveness against resistant bacterial strains. The presence of the triazole moiety contributes to enhanced interaction with microbial targets, supporting its importance as a pharmacophore in antimicrobial development. This work highlights the successful integration of synthetic chemistry and microbiological evaluation to identify triazole derivatives with significant antibacterial activity against MDR bacterial isolates.

Keywords: Triazole derivatives, Antibacterial activity, Multidrug-resistant (MDR) bacteria, Clinical isolates, Heterocyclic compounds, antimicrobial screening

POSTER PRESENTATION

Poster-01

An Increasingly Serious Risk to Public Health: Antimicrobial Resistance

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Abstract:

Acquired antimicrobial resistance (AMR) is a serious danger to global public health, antibiotics have played a major role in saving lives from infectious illnesses. Antibiotic abuse has led to the development of antimicrobial resistance (AMR), which is mainly transmitted by people both inside and outside of healthcare facilities. AMR is made worse by agricultural and healthcare factors, especially the use of antibiotics in cattle. High morbidity, mortality, and financial consequences result from the limited therapy options for diseases brought on by resistant bacteria. Monitoring antibiotic use, increasing access to reasonably priced medications, and enforcing laws are examples of urgent measures that are required. Collaborative worldwide action is necessary to prevent the approaching threat of a post antibiotic era. The mechanisms of microbial resistance and methods for addressing AMR are covered in this review.

Keywords: Antimicrobial resistance (AMR), Antibiotics.

Poster-02

Tackling vector-borne diseases amid climate shifts and global challenges

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Abstract

Diseases spread by vectors like mosquitoes, ticks, and flies pose a persistent danger worldwide, carrying agents such as *Plasmodium* for malaria, dengue virus, Zika, and West Nile. They strike millions each year, hitting hardest in warmer climates and overburdening health services and local economies.

Shifting weather patterns worsen the issue by broadening insect ranges, extending breeding periods, and boosting pathogen spread. Rapid city growth, global mobility, and growing resistance to bug sprays amplify epidemics, evident in dengue spikes across India and chikungunya waves in Africa. At-risk groups— including kids, expectant mothers, and those with weak immunity—suffer most, enduring symptoms from aches and fevers to life-threatening brain issues or fatality.

Winning the fight requires multifaceted tactics: robust monitoring for quick alerts, public awareness on safeguards like treated nets and repellents, and nature-based solutions such as microbial controls and site cleanups. Promising vaccines for dengue and malaria advance, alongside genetic tracking of insect adaptations. Leaders should embrace One Health frameworks, uniting efforts across people, wildlife, and ecosystems to prevent flare-ups.

Keywords: Vectors, *Plasmodium*, Chikungunya.

Poster-03

Antimicrobial surveillance of *Mycobacterium tuberculosis*: identification, impediments and improvements for disease management in *Betta splendens* (Regan)

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Abstract

Antimicrobial resistance (AMR) has become a major global health concern that affects aquatic ecosystems and ornamental fisheries in addition to human medicine. Non-tuberculous mycobacteria (NTM), namely *Mycobacterium marinum*, *M. fortuitum*, and *M. chelonae* are known to produce tuberculosis-like diseases in *Betta splendens*, a commonly traded ornamental fish. In addition to being persistent in aquatic settings, many diseases show both acquired and innate resistance to a variety of antimicrobial treatments. The current research focuses on disease transmission, diagnostic methods, and resistance patterns while highlighting AMR trends and surveillance views of mycobacterial infections in *Betta splendens*. Tuberculosis in *B. splendens* known as chronic wasting, granuloma formation, spinal deformities, and increased mortality, often leading to indiscriminate antimicrobial usage in ornamental aquaculture. This study emphasizes the need for systematic AMR surveillance in ornamental fish systems using integrated phenotypic, molecular, and AI-assisted image-based diagnostics for early detection and resistance profiling. Strengthening biosecurity, antimicrobial study, and exploring alternative therapeutic strategies such as plant-derived antimicrobials and nanomaterial-based interventions. Understanding AMR strategies in *B. splendens* not only improves fish health management, but also contributes to the zoonotic and environmental risks associated with aquatic tuberculosis.

Keywords: Antimicrobial resistance (AMR), Non-tuberculous mycobacteria (NTM), *Mycobacterium marinum*, *M. fortuitum*, *M. chelonae*, AI, Zoonotic, *Betta splenden*s.

Poster-04

Sustainable metal nanoparticles as emerging tools for antimicrobial resistance control: Implications for aquaculture and major carps

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Abstract

The extensive and usually unregulated use of antibiotics to treat illnesses makes aquaculture systems vulnerable to antimicrobial resistance (AMR). The increase in multidrug-resistant diseases in aquatic environments poses a threat to fish health, food security, and environmental sustainability, particularly for economically important species like big carps. Because of their broad-spectrum activity, eco-friendly manufacturing method, and lower risk of resistance development, sustainable metal nanoparticles have emerged as a suitable substitute antibacterial agent in this context. Sustainable synthesis methods that utilize biological resources can improve the environmental safety and biocompatibility of metal and metal oxide nanoparticles, including those based on iron, copper, zinc, and silver. These nanoparticles exhibit antibacterial properties through a number of mechanisms, including the generation of reactive oxygen species, the disintegration of bacterial membranes, the inactivation of proteins, and the degradation of genetic material. This study highlights recent advancements in antimicrobial mechanisms, the manufacturing of ecologically safe metal nanoparticles, and their potential use in aquaculture to reduce bacterial infections and stop the spread of AMR. Special focus is paid to their impacts on major carps, which are crucial to the synthesis and dispersion of freshwater aquaculture globally. The review also covers contemporary issues such bioaccumulation, regulatory limitations, nanoparticle toxicity, and extensive use in aquaculture settings. Prospects for the future that center on water treatment techniques, feed additives based on nanoparticles, and integration within a One Health framework are also examined. One effective strategy to enhance disease control and reduce antibiotic resistance in aquaculture systems is to use sustainable metal nanoparticles.

Keywords: Sustainable nanotechnology, Metal nanoparticles, Antimicrobial resistance, Aquaculture health management, Major carps.

Poster-05

Ethnomedicinal relevance and antimicrobial resistance-targeted arsenal of *Vachellia farnesiana*: A critical review

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Abstract

The escalating prevalence of antimicrobial resistance (AMR) constitutes a formidable threat to global public health, compelling the scientific community to investigate alternative and adjunctive therapeutic modalities derived from natural sources. *Vachellia farnesiana* (L.) Wight & Arn., a pharmacologically significant medicinal plant with extensive ethnomedicinal relevance, has emerged as a promising candidate in the search for novel antimicrobial interventions. The species is endowed with a diverse repertoire of bioactive phytoconstituents, including flavonoids, condensed and hydrolysable tannins, alkaloids, saponins, and phenolic acids, which collectively confer pronounced antimicrobial efficacy. Phytochemical extracts obtained from the bark, leaves, flowers, and pods of *V. farnesiana* have demonstrated substantial inhibitory activity against a broad spectrum of Gram-positive and Gram-negative bacterial strains, as well as pathogenic fungi, including organisms implicated in multidrug-resistant infections. The antimicrobial mechanisms underlying these effects are postulated to involve perturbation of microbial cell membrane integrity, inhibition of critical metabolic enzymes, suppression of nucleic acid biosynthesis, and interference with quorum sensing and biofilm formation. Within the contemporary framework of AMR, *V. farnesiana* represents a valuable reservoir of lead compounds with potential application as standalone antimicrobials or as resistance-modifying agents capable of potentiating conventional antibiotics. Nevertheless, rigorous pharmacodynamic, pharmacokinetic, toxicological, and clinical investigations are imperative to substantiate its efficacy and safety, and to facilitate its translational advancement into evidence-based antimicrobial therapeutics.

Keywords: *Vachellia farnesiana*, Antimicrobial efficacy, Antimicrobial Resistance (AMR).

Poster-06

The study of prevalence of bacterial wound infection-related antibiotics resistance pattern in Latur (M.S.), India

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Abstract

Wound infections remain a major clinical concern in hospital settings, often complicated by the emergence of multidrug-resistant (MDR) pathogens. Identification of the causative organisms and their distribution is essential for effective management and infection control. This study aimed to determine the prevalence and distribution of bacterial pathogens associated with wound infections among patients attending a tertiary care hospital in Maharashtra, India. A cross-sectional, hospital-based study was conducted at Vilasrao Deshmukh Government Medical College and Hospital (VDGMCH), Latur from January 2022 to December 2024. A total of 367 wound samples, including pus, swabs, and tissue specimens, were collected aseptically from clinically suspected cases of wound infection. Bacterial isolation and identification were performed following standard microbiological techniques, and results were interpreted according to CLSI (2023) guidelines. Out of 367 samples processed, 329 (89.64%) showed positive bacterial growth, whereas 38 samples (10.35%) did not yield any microbial growth despite appropriate culture conditions. These culture-negative samples were considered valid specimens but were excluded from subsequent bacteriological and antimicrobial resistance analysis.

Keywords: Wound infection, Bacterial isolates, *Escherichia coli*, *Staphylococcus aureus*, *Pseudomonas aeruginosa*, Gram-negative bacteria, Hospital-based study.

Poster-07

Studies on surgical site bacterial infection and related antimicrobial resistance pattern in Aurangabad

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Abstract

Surgical site infections (SSIs) are among the most common postoperative complications, significantly contributing to patient morbidity, prolonged hospital stays, and increased healthcare costs. The emergence of antibiotic-resistant bacteria has further complicated the management of these infections. A total number of 160 clinical samples were collected from patients with suspected SSIs admitted to various surgical wards of Hospital, Aurangabad. Samples were processed using standard microbiological techniques. Bacterial isolates were identified based on cultural, morphological, and biochemical characteristics. Antimicrobial susceptibility testing was performed using the Kirby-Bauer disk diffusion method as per CLSI guidelines. Among the isolates, Staphylococcus aureus was the predominant organism, followed by *Escherichia coli*, *Pseudomonas aeruginosa*, and *Klebsiella pneumoniae*. A significant proportion of *S. aureus* isolates were Methicillin-resistant (MRSA). Gram-negative isolates showed high resistance to β-lactam antibiotics but were more sensitive to carbapenems and aminoglycosides. The study highlights the predominance of multidrug-resistant bacteria in surgical site infections. Regular surveillance of antimicrobial resistance patterns and strict infection control measures are essential to reduce the incidence of SSIs and improve patient outcomes.

Keywords: Surgical site infection, Antimicrobial resistance, *Staphylococcus aureus*, MRSA, Whole genome.

Poster-08

“Freshwater Benthic Biodiversity and Vector Borne - Diseases."

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Abstract:

Freshwater environments, which include lentic and lotic water bodies such as lakes, reservoirs, rivers, streams, channels, and ponds, sustain a varied range of benthic biodiversity that is critical to maintaining ecological balance and managing aquatic food webs. Freshwater benthic ecosystems contain a diverse range of species from several taxonomic groups, including insects, molluscs, annelids, crustaceans, nematodes, and associated microbial groups that live in bottom sediments and submerged substrates.These benthic creatures play an important role in the breakdown of organic matter, the cycling of nutrients, the stability of sediments, and the transmission of energy between trophic levels. Freshwater ecosystems, which are regulated by the hydrological cycle, offer vital functions such water purification, flood attenuation, aquifer recharge, and habitat support for wetlands and aquatic species. Benthic communities connect environmental conditions throughout time and are sensitive indicators of changes in water and sediment quality because of their stationary character, relatively prolonged life cycles, and close interaction with sediments and the overlying water column.

Benthic community structure, diversity, and functional composition frequently change as a result of changes in freshwater habitats caused on by pollution, eutrophication, climate variability, and increasing anthropogenic disturbances. Since many disease vectors, including mosquitoes, depend on aquatic settings during their larval stages and are heavily impacted by habitat quality and biological interactions within benthic ecosystems, such ecological changes may have an indirect impact on the dynamics of vector-borne diseases. While polluted ecosystems with lower benthic biodiversity sometimes encourage vector proliferation and increased risk of disease transmission, healthy and diverse benthic organisms can naturally control vector populations through competition, predation, and habitat disruption. The present knowledge about the relationship between freshwater benthic biodiversity and vector-borne diseases is summarized in this review-based study, with a focus on how variations in water and sediment quality impact benthic communities and, in turn, vector ecology. The results highlight the significance of restoring and conserving freshwater benthic biodiversity as an ecosystem-based, sustainable strategy for lowering the risks of vector-borne diseases while continuously promoting ecological health and biodiversity conservation.

Keywords:

Freshwater ecosystems; Benthic biodiversity; Vector-borne diseases; Aquatic invertebrates; Water and sediment quality; Ecosystem-based management.

Poster-09

A Comprehensive Review of the Biology of Nile Tilapia (Oreochromis niloticus) and Importance in Aquaculture.

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Abstract:

Oreochromis niloticus, commonly known as Nile tilapia, is one of the most widely cultured freshwater fish species in the world due to its rapid growth, high adaptability, and economic significance. Native to Africa, this species has been extensively introduced to tropical and subtropical regions across Asia, Americas, and parts of the Middle East to support food security and aquaculture development. Nile tilapia thrives in a wide range of environmental conditions, tolerating variations in temperature, salinity, and dissolved oxygen, which makes it particularly suitable for diverse farming systems, including ponds, cages systems. Biologically, O. niloticus is characterized by fast growth rates, early sexual maturity, and efficient feed conversion, allowing it to perform well on low-cost, plant-based diets. These traits contribute to its popularity among small-scale and commercial farmers alike. The species is primarily omnivorous, feeding on phytoplankton, algae, detritus, and small invertebrates. Nile tilapia exhibits strong reproductive capacity through mouthbrooding behaviour, enhancing larval survival in natural and cultured environments. Despite its benefits, the widespread introduction of O. niloticus has raised ecological concerns. In non-native habitats, it may compete with indigenous fish species for food and breeding sites, potentially altering ecosystem dynamics. As a result, responsible management practices and controlled breeding programs are essential to balance production goals with environmental sustainability. Overall, Oreochromis niloticus plays a critical role in global aquaculture, contributing significantly to protein supply, rural livelihoods, and economic growth. Tilapia reaches sexual maturity early (about 5–6 months) in warm conditions, parental care where the female carries fertilized eggs and fry in her mouth for protection. Spawning is temperature-dependent, typically starting when water reaches around 24 °C. Rapid growth and high fecundity (egg production) are key life-history traits supporting population expansion and aquaculture viability. Nile tilapia can also filter feed, using mucus to trap suspended particles. Nile tilapia has a deep-bodied shape typical of cichlids. It exhibits high plasticity in morphology in response to environmental conditions.

Physiologically, Nile tilapia is tolerant of a wide range of temperature (approx. 11–42 °C) and can survive in both freshwater and moderately brackish water. It possesses adaptive osmoregulation, enabling survival across varying salinity levels. Nile tilapia is one of the most extensively cultured fish species worldwide and is often called as “aquatic chicken” due to its importance in food systems. It ranks among the top aquaculture species globally, providing affordable protein and supporting nutritional security, especially in developing countries. Tilapia aquaculture was producing over 4–5 million tonnes annually.

Keywords: Nile tilapia, aquaculture, freshwater fish, economic significance, high adaptability

Poster-10

From Data to Defence: AI in Vector-Borne Disease Prevention

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Abstract:

Vector-borne diseases (VBDs) such as malaria, dengue, chikungunya, Zika, yellow fever, and Lyme disease remain among the most persistent global public-health threats, accounting for millions of infections and hundreds of thousands of deaths annually. Their transmission is strongly influenced by climate variability, land-use change, population mobility, urbanization, and socio-economic disparities, making prediction and control highly complex. Conventional surveillance systems often rely on delayed reporting, limited field sampling, and fragmented datasets, which restrict timely outbreak response. In recent years, Artificial Intelligence (AI) has emerged as a powerful interdisciplinary approach capable of transforming vast, multi-source data into predictive intelligence and targeted prevention strategies.

AI-driven machine learning and deep learning models enable integration of diverse datasets including meteorological variables, satellite remote sensing imagery, geographic information systems (GIS), entomological surveillance records, human mobility patterns, and social media signals. By identifying hidden patterns and nonlinear relationships, these models can forecast vector population dynamics, map high-risk transmission zones, and generate early warning systems with fine spatial and temporal resolution. Predictive analytics supports proactive interventions by enabling health agencies to anticipate outbreaks weeks or months in advance. Computer vision technologies further enhance vector surveillance through automated identification and counting of mosquitoes, ticks, and other vectors using smartphone-based imaging and smart traps. Natural language processing (NLP) enables real-time monitoring of digital health data, online search trends, and community reporting to detect early disease signals. AI also supports precision public-health strategies by optimizing insecticide deployment, habitat management, and resource allocation based on risk prioritization.

Moreover, AI-powered mobile health platforms, chatbots, and participatory surveillance apps facilitate community engagement, rapid symptom reporting, and public awareness. However, the effective implementation of AI faces challenges related to data scarcity, interoperability,

ethical governance, privacy protection, algorithmic bias, and infrastructure inequality in low-resource regions.

Overall, AI is revolutionizing the shift from reactive response to predictive prevention, transforming raw data into actionable defense against vector-borne diseases and strengthening global health security.

Keywords:

Artificial Intelligence (AI); Vector-borne diseases; Disease prediction; Machine learning; Deep learning; Climate change; Remote sensing; GIS; Early warning systems; Mosquito surveillance; Digital epidemiology; Public health analytics; Precision vector control; Predictive modeling; One Health.

Poster-11

The Rapid CRAB Vigilance Kit: Precision Screening for Carbapenem-Resistant *Acinetobacter baumannii*

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Abstract

Carbapenem-resistant *Acinetobacter baumannii* is a major cause of morbidity and mortality in intensive care units, with *Acinetobacter baumannii* emerging as one of the most prevalent and highly drug-resistant pathogens. The organism's ability to survive in hospital environments and rapidly acquire resistance, particularly carbapenem-hydrolysing oxacillinases, severely limits therapeutic options and delays effective treatment. Conventional culture-based identification and antimicrobial susceptibility testing are time-consuming, often leading to inappropriate empirical therapy. This study aimed at detection of the *bla*OXA-51 gene for the rapid identification of *Acinetobacter baumannii* and its AMR gene *bla*OXA-23 directly from clinical samples in Amravati, Maharashtra, India. DNA extraction was done by the automated nucleic acid extractor, followed by the amplification of the desired gene by using the PCR method, and the amplified PCR product was subjected to agarose gel electrophoresis for the detection of the *bla*OXA gene. A total of 664 different clinical samples were processed. The *bla*OXA-51 gene was detected in 43 (6.47%) clinical isolates, confirming the isolates to be *Acinetobacter baumannii*. Out of 43 confirmed isolates of *Acinetobacter baumannii*, the prevalence of *bla*OXA-23 was found to be 83.7% (n=36). Rapid detection can be achieved using direct molecular assays on respiratory samples and multiplex PCR targeting resistance genes. These approaches significantly reduce turnaround time, support timely targeted therapy, improve antimicrobial stewardship, and help prevent further dissemination of multidrug-resistant strains. Rapid detection of CRAB is therefore critical for improving clinical outcomes and infection control in critical care settings.

Keywords: CRAB, *Acinetobacter baumannii*, *bla*OXA genes

Poster-12

Antimicrobial Resistance in Carbapenem-Resistant *Klebsiella pneumoniae*: Challenges and Treatment Approaches

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ABSTRACT

Background: Carbapenem-resistant *Klebsiella pneumoniae* (CRKP) is a significant nosocomial pathogen associated with high morbidity and mortality, particularly among mechanically ventilated intensive care unit (ICU) patients. Limited therapeutic options necessitate exploration of effective antibiotic combinations against multidrug-resistant strains.

Objectives: This study aimed to isolate and characterize CRKP from ventilated ICU patients and to evaluate the in vitro synergistic activity of selected antibiotic combinations against these resistant isolates.

Methods: Four *K. pneumoniae* isolates were recovered from endotracheal tube samples of ventilated ICU patients. Bacterial identification and antimicrobial susceptibility testing were performed according to Clinical and Laboratory Standards Institute (CLSI) guidelines. Carbapenemase production was confirmed using the Modified Hodge Test and Carba NP assay. Molecular detection of the carbapenemase gene *bla*OXA-48 was carried out by polymerase chain reaction (PCR). Synergistic interactions of colistin–doxycycline, colistin–levofloxacin, and doxycycline–levofloxacin were assessed using the checkerboard assay.

Results: All isolates exhibited multidrug resistance and tested positive for carbapenemase production, with universal detection of the *bla*OXA-48 gene. Combination therapy demonstrated enhanced antibacterial activity compared to monotherapy. Among the tested combinations, colistin–doxycycline showed the most pronounced synergistic effect, resulting in a significant reduction in minimum inhibitory concentrations (MICs) across all isolates.

Conclusion: The findings underscore the growing threat posed by CRKP in ICU settings and highlight the potential of colistin-based combination therapy, particularly colistin-doxycycline, as an effective treatment strategy against CRKP infections.

Keywords: CRKP, Colistin, Doxycycline, Combination therapy, Antimicrobial resistance

Poster-13

Order Diptera as Vectors of Human Diseases: Ecological and Public Health Perspectives

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Abstract

The order Diptera, commonly known as true flies, includes some of the most important vectors of human and animal diseases. This group comprises mosquitoes, sand flies, black flies, tsetse flies, and house flies, many of which play a critical role in the transmission of vector-borne diseases. Dipteran vectors are responsible for spreading major diseases such as malaria, dengue, chikungunya, Zika, filariasis, leishmaniasis, trypanosomiasis, and Japanese encephalitis, particularly in tropical and subtropical regions. Their distribution and abundance are strongly influenced by ecological factors such as climate, availability of breeding habitats, host presence, and human activities. Rapid urbanization, climate change, and inadequate water management have significantly enhanced breeding opportunities for dipteran vectors, increasing disease risk. Understanding the ecology, life cycle, and behavior of dipteran insects is essential for effective vector control and disease management. Recent advances in integrated vector management emphasize environmental control, biological agents, and reduced reliance on chemical insecticides to minimize resistance and ecological damage. This abstract highlights the significance of Diptera in the epidemiology of vector-borne diseases and underscores the need for interdisciplinary approaches combining entomology, ecology, and public health. Strengthening knowledge on dipteran diversity and vector biology will support sustainable strategies for disease prevention and improved public health outcomes.

Keywords: Diptera**,** Vector-borne diseases**,** Mosquitoes**,** Disease transmission**,** Public health.

Poster-14

Sustainable Extraction and HPTLC Profiling of *Abrus precatorius* L. under One Health

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Abstract

Antimicrobial resistance (AMR) poses a critical challenge across human, veterinary, and environmental health sectors, necessitating sustainable research strategies aligned with the One Health framework. The present study established a green extraction and analytical standardization protocol for *Abrus precatorius* L. leaves. Microwave-Assisted Extraction (MAE) was employed to enhance extraction efficiency while reducing solvent consumption and processing time, supporting environmentally responsible methodology. Preliminary phytochemical screening of the hydroalcoholic extract confirmed the presence of phenolics, flavonoids, tannins, alkaloids, and saponins, phytoconstituent classes widely associated with antimicrobial mechanisms. High-Performance Thin-Layer Chromatography (HPTLC) profiling generated distinct chromatographic fingerprints with reproducible Rf values and densitometric peaks, ensuring batch-to-batch consistency and quality control. The integration of sustainable extraction with chromatographic standardization provides a robust analytical foundation for future antimicrobial validation studies. This integrative approach supports responsible phytopharmaceutical development and contributes to AMR mitigation strategies under the One Health paradigm.

Keywords

Abrus precatorius L., Microwave-Assisted Extraction, HPTLC fingerprinting, Antimicrobial resistance, One Health.

Poster-15

India's population: its present and future

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Abstract:

India has become world's most populated country and has been affecting many nature made ecosystems. Both biotic and abiotic factors are being affected in India. The government has been making many commissions to feed the ever increasing population. Because of this dramatic increase the habitat encroachment of humans to the jungles is happening and demand of water is also increasing. With this increase water is being available only to humans and wild animals are dying because of lack of water. Although there is such huge impact there are no measures to keep water level maintained. However there are no measures being taken to control it. If it is not controlled in time, it is going to explode one day. In the present study we have found how adversely the abiotic factors of the ecosystem are being exploited and a dire need of sustainable habitat for wild life with reduction of human population.

Keywords: Ecosystem, biotic and abiotic factors, sustainable habitat, human population.

Poster-16

Ecological Impact of Pest Species and Emerging Strategies for Sustainable Vector Control

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Abstract

Vector-borne diseases remain a serious public health challenge, particularly in tropical and subtropical regions where environmental conditions favor rapid vector multiplication. Effective disease prevention depends on a sound understanding of pest ecology and habitat dynamics. The present study examines the ecological role of major insect vectors and evaluates how urbanization, environmental disturbance, and climate variability influence their population structure and transmission potential. Special emphasis is placed on mosquito genera Anopheles, Aedes, and Culex, focusing on their breeding habitats, life cycle patterns, and adaptive responses to human-modified environments.

The association between vector density and disease prevalence is analyzed, indicating that increased vector abundance contributes directly to higher transmission of malaria, dengue, and filariasis. The study further evaluates sustainable control strategies within the framework of Integrated Pest Management. Approaches such as biological control, environmental sanitation, habitat modification, community awareness, and selective use of insecticides are discussed as practical alternatives to excessive chemical dependence and resistance development.

The findings emphasize that long-term vector control requires an ecologically balanced and interdisciplinary approach. Adoption of the One Health concept, integrating human, animal, and environmental health, provides a sustainable pathway for reducing disease burden while preserving biodiversity and ecosystem stability.

Keywords: Vector ecology, Integrated Pest Management, One Health, Disease transmission, Sustainable control

Poster-17

Candida auris: An Emerging Superbug in Healthcare Settings with Multidrug Resistance and Urgent Infection Control Needs

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Abstract

Since its emergence over the last decade, *Candida auris* has transitioned from a localized medical curiosity to a global "superbug" threat. This resilient fungal pathogen is uniquely dangerous due to its high level of multidrug resistance, environmental tenacity, and ability to trigger severe invasive infections. Unlike many of its counterparts in the *Candida genus*, *C. auris* frequently resists all three primary classes of antifungal medications—azoles, echinocandins, and polyenes—with some strains exhibiting near-total pan-resistance.

The pathogen's "superbug" status is reinforced by its unusual ecological behavior. It persists on human skin and healthcare surfaces for weeks, fueling difficult-to-contain outbreaks in clinical settings. This challenge is exacerbated by the fact that traditional laboratory methods often misidentify the species, leading to delayed treatment and unintentional spread. Research into its genome reveals that *C. auris* employs sophisticated defense mechanisms, including target-site mutations, the upregulation of efflux pumps, and the formation of robust biofilms that shield it from both drugs and the host's immune system. With mortality rates for invasive cases reaching alarming levels among the critically ill, the global medical community must prioritize a multifaceted response. This includes the adoption of rapid molecular diagnostics, rigorous hygiene protocols, and the pursuit of next-generation antifungals. This review analyzes the biological traits and clinical hurdles that define *C. auris* as a primary fungal threat in modern medicine.

Keywords: *Candida auris,* Multidrug Resistance, Fungal Superbug, Nosocomial Outbreaks, Antifungal Stewardship, Clinical Mycology.

Poster-18

Mechanistic and Fermentation Engineering Analysis of Arthrobacter crystallopoietes PJC-S08 for Enhanced Phosphate Bioavailability under Alkaline Conditions.

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Abstract

Phosphorus immobilization in alkaline soils restricts crop productivity due to precipitation of applied phosphates as insoluble calcium–magnesium complexes. This study characterizes Arthrobacter crystallopoietes PJC-S08, an alkaliphilic actinobacterium isolated from Lonar Lake (pH 9.5–10.5), for its phosphorus-mobilizing and plant growth-promoting potential. The strain exhibited dual phosphate mobilization through organic acid production and extracellular alkaline phosphatase (ALP) activity regulated by the Pho regulon. Optimized fermentation conditions (pH 9.0, 25 °C, 5 days) yielded 88.66 U mL^{-1} ALP in a 2 L bioreactor, with stable performance during 20 L scale-up. Oxygen transfer rate and volumetric mass transfer coefficient (kLa) analyses confirmed efficient aeration and scalability.

Additionally, PJC-S08 produced indole-3-acetic acid (up to 154.47 µg mL^{-1} with tryptophan supplementation) and cytokinins (67.8 µg mL^{-1}). Pot trials in Triticum aestivum, Zea mays, and Sorghum vulgare showed significant improvements in shoot growth, root length, and biomass under alkaline conditions.These findings highlight the strain's potential as a scalable bioinoculant for sustainable phosphorus management in alkaline agroecosystems.

Keywords: Arthrobacter crystallopoietes, Alkaline phosphatase, Phosphate mobilization, Bioreactor scale-up, kLa, Alkaliphilic actinobacteria, Alkaline soils.

Poster-19

Antimicrobial resistance in vector-borne disease in Gondia – a threat

Mahesh Akolkar

Abstract

Vector-borne diseases (VBDs), such as malaria and dengue, account for >17% of infectious diseases, causing >700,000 deaths annually. Antimicrobial resistance (AMR) is rendering treatments for these diseases, particularly bacterial and parasitic ones, less effective, while insecticide resistance simultaneously reduces vector control. The combination of climate change, urbanization, and rapid evolution of resistance makes managing these diseases increasingly difficult. In India, Gondia is highlighted as a high-risk area for malaria, often mentioned alongside Gadchiroli and Chandrapur districts in Maharashtra for high malaria incidence, particularly in rural and tribal areas. Studies analyzing data from 2016-2017 showed that both Plasmodium vivax (47.17%) and Plasmodium falciparum (42.61% to 56.41%) are present, with P. falciparum contributing to mortality risks. While malaria is the primary concern, other vector-borne diseases such as dengue, chikungunya, Japanese encephalitis (JE), and scrub typhus are also reported in the wider central Indian region (including neighboring districts and state-level data). Now a days, antimicrobial resistance is a serious issue in malaria positive patients. Anti-malarial drug resistance is one of the major problems for malaria control and elimination programme. First information of chloroquine resistant P. falciparum was reported from Assam in 1973 within India and resistance gradually spread to other states covering almost entire country. Emergence of sulfadoxine-pyrimethamine (SP) resistance was also reported in Karbi-Anglong, district of Assam in 1979. SP resistance was again reported in 1992 from Changlang district of Arunachal Pradesh, a state of north-east India. Later artemisinin-based combination therapy (ACT), using artesunate plus sulfadoxine-pyrimethamine (AS + SP), was introduced as the second-line drug in 2005, in case of chloroquine treatment failures. In 2007, AS + SP was selected as the first-line treatment in areas with identified resistance. In 2010, this treatment became the first-line treatment throughout India [9]. Later, due to reports of resistance to partner drug SP in North Eastern States, Co-formulated tablet of artemether-lumefantrine (AL) was introduced by programme for the treatment of P. falciparum cases.

Key words: Malaria, antimicrobial resistance, chloroquine, sulfadoxine pyramethamine, artemether lumefantrine

Poster-20

In Vitro Evaluation of the Antibacterial and Antifungal Efficacy of Actinomycetes Derived from Undisturbed Forest Rhizosphere

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Abstract

Despite the historical success of soil-derived antibiotics, the rapid emergence of multi-drug resistant (MDR) pathogens has outpaced the discovery of new antimicrobial agents. Standard environments have been over-explored, leading to the frequent 're-discovery' of known compounds. Forest soils, characterized by complex organic matter and unique microbial competitions, represent an underexplored 'hotspot' for actinomycetes. There is a critical need to isolate and characterize these specific strains to identify novel secondary metabolites capable of inhibiting resistant clinical pathogens.Actinomycetes are renowned for their ability to produce bioactive secondary metabolites. This study focuses on forest soil, a niche environment, to discover strains with potent antimicrobial properties.Soil samples were collected from Painganga forest area. Actinomycetes were isolated using actinomycetes Isoaltion agar ,Starch Casein Agar etc and identified based on morphological characteristics. The antimicrobial activity of the isolates was tested against a panel of Gram-positive and Gram-negative bacteria and pathogenic fungus using the agar Well Diffusion technique. A total of 30 isolates were obtained. Of these, 3 showed most significant inhibitory activityagainst bacteria. Notably, isolate CSI20 &CSI 24 exhibited a broad-spectrum zone of inhibition against fungus and bacteria.

Keywords: Actinomycetes, antimicrobial, MDR. Agar well diffusion.

Poster-21

Distribution of various Integron classes in uropathogenic *Klebsiella pneumoniae* isolates form tertiary health care hospitals of Amravati.

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Abstract

Urinary tract infections (UTIs) are one of the most common and widely distributed bacterial infection globally, caused by *Klebsiella pneumoniae* recognized as one of the major uropathogens after *Escherichia coli*. This increase in antimicrobial resistance has been associated with the presence of integrons.

Integrons are genetic element well known for their role in the dissemination of antibiotics. Resistance in Gram-negative bacterial pathogens. This study was aimed to determine the prevalence of class 1 integron and class 2 integron in clinical isolates of *K. pneumoniae* obtained from urinary tract infections at tertiary health care hospitals in Amravati, and to evaluate the antibiotic resistance profile. Isolated samples were identified using Vitek-2, proceeding with antibiotic susceptibility testing and PCR Based identification. Our study revealed that Integrons and specifically class 1 Integrons are the key promoters of antibiotic resistance among *K. pneumoniae*. A total of 168 isolates were studies and analysed by PCR for presence of Integrons (Class I, II and III), revealed that Clas I were 53%, Class II (19%) and Class III (6%). Class I Integron had highest antibiotic resistance.

Keywords: *Klebsiella pneumoniae*, Integron classes, Uropathogen, antibiotic resistance

Poster-22

Low-Frequency Electromagnetic Field Exposure Triggers Oxidative Imbalance and Genomic Instability in *Drosophila Nasuta* Implications for Vector Biology and Translational Disease Research

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Abstract

Environmental electromagnetic fields (EMFs), generated by expanding power infrastructures and electronic devices, represent an emerging but underexplored ecological stressor influencing insect physiology. Understanding how such environmental factors modulate oxidative balance and genomic stability is critical for vector biology and infectious disease dynamics. The present study investigates the impact of 50 Hz low-frequency electromagnetic field (LF-EMF) exposure on behavioural, biochemical, and molecular parameters in *Drosophila nasuta*, a well-established genetic model organism. Adult flies were exposed to controlled LF-EMF conditions, and subsequent analyses were performed to evaluate locomotor behavior, oxidative stress markers, protein content, antioxidant enzyme activity, and genomic DNA integrity. EMF exposure resulted in significant behavioural alterations, elevated oxidative stress responses, reduced total protein levels, and detectable DNA damage compared to controls ($p < 0.05$). These findings suggest that electromagnetic stress disrupts redox homeostasis and compromises molecular integrity. Oxidative imbalance and genomic instability are key determinants of vector competence, pathogen survival, and antimicrobial resistance development. By establishing a mechanistic link between environmental EMF exposure and molecular damage pathways, this study provides translational insights into how anthropogenic stressors may influence vector adaptability and resistance mechanisms. Furthermore, the observed DNA alterations highlight the importance of integrating molecular diagnostic approaches to monitor environmental stress-induced genomic perturbations.

Collectively, this work underscores the relevance of environmental electromagnetic exposure as a potential modifier of insect physiology, with broader implications for vector-borne disease dynamics, antimicrobial resistance evolution, and translational vector control strategies.

Keywords: Low-frequency electromagnetic field (LF-EMF), *Drosophila nasuta*, oxidative stress, genomic instability, vector biology, antimicrobial resistance, molecular diagnostics, translational research.

Poster-23

Whole Genome Sequencing of AMR Pathogens Isolated from Deoni cattle

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Abstract

Antimicrobial resistance (AMR) is a global threat to both human and animal health, driven by the emergence and dissemination of resistant bacterial pathogens. Indigenous cattle breeds such as Deoni cattle play a vital role in rural dairy production in India, yet there is limited genomic-level information on the AMR profiles of pathogens associated with them. This study aims to characterize the whole genome sequences of antimicrobial-resistant bacterial isolates obtained from clinical and subclinical infections, faecal samples, and farm environments of Deoni cattle. A total of *Escherichia coli, Staphylococcus aureus,* and *Salmonella* spp. isolates exhibiting phenotypic resistance to commonly used antibiotics will be subjected to whole genome sequencing (WGS) using next-generation sequencing platforms. Genomic data will be analyzed to identify resistance determinants, mobile genetic elements (plasmids, transposons), virulence factors, and potential clonality of isolates. Comparative genomic analyses will be performed to detect genetic signatures of resistance and to map resistome profiles across isolates from different sources. The study will further explore correlations between antimicrobial usage patterns on farms and the distribution of AMR genes. Findings from this research will provide crucial insights into the molecular mechanisms driving AMR in indigenous cattle pathogens, inform antibiotic stewardship practices in livestock production, and contribute to the development of targeted interventions under the One Health framework. The generated genomic database will serve as a valuable resource for future surveillance and mitigation strategies against AMR in animal health.

Keywords: Antimicrobial resistance, Whole genome sequencing, Deoni cattle, Multidrug resistance, Bacterial genomics, One Health.

Poster-24

Nanobiotechnology-based eco-friendly vector control strategies: A sustainable alternative to chemical insecticides

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Abstract

Vector-borne diseases (VBDs), including malaria, dengue, chikungunya, Zika virus infection, and lymphatic filariasis, remain significant public health concerns worldwide, particularly in tropical and subtropical regions. Conventional vector control methods largely depend on synthetic chemical insecticides; however, their extensive use has resulted in environmental pollution, ecological disruption, insecticide resistance, and potential health risks to humans and non-target organisms. In recent years, nanobiotechnology has emerged as a sustainable and eco-friendly alternative, offering innovative tools for targeted and efficient vector control.

This paper reviews the development and application of nanobiotechnology-based strategies, including green synthesis of nanoparticles using biological resources, nano-larvicides, nano-repellents, nano-emulsions, and smart nano-delivery systems. It examines their mechanisms of action, effectiveness, environmental compatibility, and potential integration into integrated vector management programs. The study also discusses how nano-enabled interventions can help mitigate insecticide resistance and contribute to sustainable disease prevention within a One Health framework.

Additionally, key challenges such as biosafety evaluation, large-scale production, regulatory approval, and public acceptance are critically analyzed. Overall, nanobiotechnology-based vector control approaches present a promising, environmentally responsible alternative to chemical insecticides and hold substantial potential to strengthen global efforts to reduce vector-borne disease burden.

Keywords: Vector-borne diseases (VBDs), Nanobiotechnology.

Poster-25

In Vitro Antibacterial and Antifungal Activities of Selected Plants of Myrtaceae using Agar Well Diffusion Assay

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Abstract

The emergence of antimicrobial resistance has intensified the search for alternative therapeutic agents from plant sources. The present study evaluated the in vitro antibacterial and antifungal potential of methanolic solvent extracts of selected Myrtceae plant samples against clinically and agriculturally important microbial strains. For these study leaves, stem and fruits plants parts used. Antimicrobial screening was performed using the agar well diffusion method. The test organisms included Gram-positive bacteria (*Bacillus subtilis* NCLM-2063 and *Staphylococcus aureus* NCLM-2098), Gram-negative bacteria (*Escherichia coli* NCLM-2112 and *Pseudomonas syringae* p.v. pisi NCLM-2204), and plant pathogenic fungi (*Aspergillus flavus*, *Penicillium chrysogenum*, *Helminthosporium gramineum*, and *Mucor plumbeus*).

Methanolic extracts were tested at concentrations of 30, 60, and 120 µg/mL. Tetracycline and fluconazole were used as standard antibacterial and antifungal agents, respectively. The results demonstrated concentration-dependent antimicrobial activity across most extracts. Among the tested samples, ERL and CRS extracts exhibited comparatively higher antibacterial activity, particularly against *Pseudomonas syringae* and *Bacillus subtilis*, showing zones of inhibition up to 20 mm and 19 mm, respectively, at 120 µg/mL. Moderate inhibition was also observed against *Escherichia coli* and *Staphylococcus aureus*. In antifungal assays, notable inhibitory effects were recorded against *Penicillium chrysogenum* and *Aspergillus flavus*, where certain extracts produced zones of inhibition ranging from 14 to 19 mm at higher concentrations. The ERL extract demonstrated strong antifungal activity against *Helminthosporium gramineum* (up to 16 mm), while CRS and PGF extracts showed moderate to significant inhibition against multiple fungal strains. As expected, standard drugs exhibited higher zones of inhibition (28–36 mm), confirming assay validity.

Overall, the findings indicate that selected plant extracts possess broad-spectrum antimicrobial properties, with activity increasing proportionally to concentration. These results support the potential of medicinal plant-derived extracts as promising candidates for the development of alternative antimicrobial agents. Further phytochemical characterization and minimum inhibitory concentration (MIC) studies are recommended to identify active constituents and validate their therapeutic efficacy.

Keywords: Antibacterial, Antifungal activity, Myrtaceae etc.

Poster-26

Diversity and Evolution of Fish-Associated Bacteria Carrying Antimicrobial Resistance Genes

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Abstract

Antimicrobial resistance (AMR) is becoming one of the most serious threats to global health, and aquatic environments such as rivers, lakes, and coastal waters play an important role in its spread. When antibiotics enter water systems through sources like wastewater discharge, agricultural runoff, aquaculture, and pollution, they create pressure that allows resistant bacteria to survive and multiply. Over time, these resistant bacteria and the genes that make them resistant can spread through the environment. Fish are especially important in this context. Because they live in constant contact with water, sediments, and diverse microbial communities, they can accumulate and carry antimicrobial-resistant bacteria in their bodies. This makes fish not only potential reservoirs (organisms that harbor resistant bacteria) but also useful indicators of the overall health of aquatic ecosystems. By studying bacteria associated with fish, we can better understand how resistance develops and spreads in freshwater and coastal systems. In this study, bacteria will be collected from fish tissues, gut contents, and from the surrounding water and sediments. These samples will first undergo laboratory testing to determine which antibiotics the bacteria can resist. After that, molecular and genomic methods will be used to look more closely at their genetic makeup. Techniques such as polymerase chain reaction (PCR) and whole genome sequencing will help identify specific antimicrobial resistance genes, mobile genetic elements (such as plasmids that allow genes to move between bacteria), and virulence factors that may increase their ability to cause disease. To understand how these resistance genes evolve and spread, phylogenetic and comparative genomic analyses will be performed. These analyses will allow researchers to trace relationships between bacterial strains and identify possible transmission pathways of resistance genes across environments and species. In addition, environmental factors such as water quality, pollution levels, and aquaculture practices will be evaluated to determine how human activities influence the emergence and dissemination of AMR in aquatic ecosystems. The results of this research will help clarify the ecological and evolutionary processes that drive antimicrobial resistance in aquatic systems. Importantly, the findings will support evidence-based management strategies within the One Health framework promoted by the World Health Organization, which recognizes the interconnected health of humans, animals, and the environment. Ultimately, this study will contribute to biodiversity conservation, sustainable fisheries management, and the protection of public health by improving our understanding of how antimicrobial resistance circulates in aquatic ecosystems.

Keywords Antimicrobial resistance, Fish diversity, AMR genes, Aquatic ecosystems, Health fish

Poster-27

Emerging Biofloc Technology to Rearing of *Catla catla* for Enhanced Growth, Disease Management and Immunological Improvement

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Abstract

Biofloc Technology (BFT) has emerged as a sustainable and eco-friendly aquaculture practice that enhances fish productivity through in situ microbial biomass production and efficient nutrient recycling. The present study focuses on the application of Biofloc Technology in the indoor rearing of *Catla catla* (Indian Major Carp), a commercially important freshwater species widely cultured across India. Indoor Biofloc systems offer advantages such as reduced water exchange, improved feed conversion efficiency, enhanced growth performance, and better biosecurity under controlled environmental conditions. The primary objective of this study was to evaluate the effectiveness of Biofloc application in enhancing the growth and production performance of *Catla catla*. Growth parameters such as weight gain, specific growth rate (SGR), feed conversion ratio (FCR), and survival rate were assessed and compared with conventional rearing systems. Additionally, the study aimed to investigate the impact of Biofloc on fish health by analyzing disease incidence and key immunological parameters, including total leukocyte count, lysozyme activity, and serum protein levels. Another significant objective was to identify and study common bacterial pathogens responsible for fish diseases in carp culture systems, including species of *Aeromonas*, *Pseudomonas*, and *Vibrio*, and to evaluate how Biofloc microbial communities contribute to disease resistance and immune stimulation. The microbial consortium present in Biofloc systems is known to improve gut health and enhance innate immunity, thereby reducing dependence on antibiotics.

The findings highlight that Biofloc Technology not only improves production efficiency of *Catla catla* under indoor conditions but also strengthens fish health management through natural immunostimulation and pathogen suppression. Thus, BFT represents a promising, sustainable approach for intensive carp aquaculture with enhanced productivity and reduced environmental impact.

Keywords: Biofloc Technology, *Catla catla*, aquaculture.

Poster-28

Evaluation of Herbal Therapeutic Potential of *Acacia leucophloea* Plant Through Phytochemical and Antimicrobial Studies.

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Abstract

The increasing emergence of antimicrobial resistance necessitates the exploration of plant-derived bioactive compounds as alternative therapeutic agents. The present study aimed to evaluate the herbal therapeutic potential of *Acacia leucophloea plant* through phytochemical screening and in vitro antimicrobial assessment. Dried plant material was extracted using aqueous, methanolic, and ethanolic solvents by Soxhlet extraction. Preliminary qualitative phytochemical analysis revealed the presence of alkaloids, flavonoids, tannins, phenolics, saponins, terpenoids, and glycosides. Quantitative estimation showed total phenolic content ranges from 0.010 gm/L to 0.149 gm/L extract and total flavonoid content ranges from 0.0062 mg/ml to 0.098 mg/ml extract in the petroleum ether, chloroform, ethanol and water fraction.

In case of antimicrobial activity, the total MIC count of *Candida albicance* were calculated as 3.07mg/ml, 1.85mg/ml, 7.35mg/ml and 1.4mg/ml, and the total MIC count of *E-coli* were calculated as 3.075mg/ml, 0.74mg/ml, 14.5mg/ml and 5.65mg/ml of concentrations in pet. Ether, chloroform, ethanol and water extract of *Acacia leucophloea plant* leaf respectively.

Keywords: *Acacia leucophloea*, Flavnoids, Phenolic content, MIC.

Poster-29

Unani concept of healthy ageing and age-related Mizaj changes: A review

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Abstract

Ageing is a universal, continuous process that results in gradual functional decline. Unani Medicine views ageing through the lens of *Mizāj* (Temperament), *Ṭabī‘at* (vital energy), and the balance of *Arkān*, *Akhlāṭ*, *A‘ḍā’*, *Arwāḥ*, and *Quwā.* Classical scholars such as Ibn Sīnā, Zakariyā Rāzī, and Jurjānī describe predictable age-related alterations in intrinsic heat, moisture, and humoral balance that affect physical, mental, and emotional well-being in old age. Integrating these traditional concepts with contemporary geriatric principles may help promote healthy ageing and prevent degenerative disorders.

The objective of this review is to integrate modern public health perspectives with Unani theoretical foundations to explore ageing comprehensively, highlighting the relevance of both systems in promoting health and well-being in the elderly population.

A systematic literature review was conducted using major databases, including PubMed, Scopus, Google Scholar, ResearchGate, ScienceOpen, and SpringerLink, along with resources from the Central Library of the National Institute of Unani Medicine, Bengaluru. Eligible sources included peer-reviewed articles, conference proceedings, theses, dissertations, refereed books, and abstracts. Keywords used in the search included *Healthy Ageing*, *Mizāj*, *Ruṭūbat-e-Gharīziyya*, *Ḥarārat Gharīziyya*, and *Asbāb-i-Sitta Ḍarūriyya*.

Classical Unani texts describe ageing as a natural outcome of diminishing *Ḥarārat Gharīziyya* (innate heat) and *Ruṭūbat Gharīziyya* (innate moisture), leading to a shift in temperament toward *Bārid Yābis* (cold and dry) in old age. These physiological changes lead to functional decline and increased susceptibility to chronic, neurological, musculoskeletal, and metabolic disorders. The Unani concept of *Asbāb-i-Sitta Ḍarūriyya*, including air, food and drink, physical activity, mental activity, sleep–wake balance, and elimination, provides a comprehensive preventive framework that parallels modern public health recommendations.

Therapies such as *‘Ilāj bi’l Tadbīr* (regimental therapy), *‘Ilāj bi’l Ghidhā’*(dietotherapy), and *‘Ilāj bid Dawā* (pharmacotherapy) are highlighted for their roles in conserving innate heat and moisture, correcting humoral imbalance, and enhancing functional well-being in elderly individuals.

Unani medicine provides a strong, comprehensive, and preventative approach for good ageing, with many parallels with modern geriatric principles. The Unani system, which addresses age-related temperament and humoral changes through lifestyle modification and therapeutic interventions, has significant implications for current integrative healthcare systems aiming to promote healthy ageing.

Keywords: Unani medicine, Healthy ageing, *Mizāj*, *Ruṭūbat Gharīziyya*, *Ḥarārat Gharīziyya*, *Asbāb*-*i*-*Sitta Ḍarūriyya*, Humoral Theory, Geriatric health.

Poster-30

Role of Sri Lankan "Kolakenda" (Gruel) as *Ghidhā' Dawā'ī* (dietary drug) in the management of non-communicable diseases: A scientific review

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Abstract

"Kolakenda" is a traditional Sri Lankan herbal gruel made of cereals, mainly raw rice, coconut milk, ginger, garlic, and the fresh juice of medicinally valued green leaves, which is commonly consumed as a breakfast. These herbal gruels are rich in both nutritional and nutraceutical values. According to the Unani System of Medicine, *Ghidhā' Dawā'ī* is a substance that is primarily used as a diet but produces some pharmacological actions. However, there is a lack of scientific literature regarding its role in the prevention and management of Non-Communicable Diseases (NCDs) and promotion of overall health. "This review aims to explore the available literature regarding the role of Sri Lankan "Kolakenda" as *Ghidhā' Dawā'ī* in the prevention of NCDs and promotion of overall health. All the available information was compiled from electronic databases such as Google Scholar, PubMed, Medline, Scopus, and classical books. The literature search revealed that *Murraya koenigi spreng*, *Cassia auriculata*, *Asparagus racemosus*, *Cardiospermum microcarpum*, *Abrus precatorius*, *Zingiber officinale*, *Eclipta prostrata*, and *Allium sativum*, etc, are the herbs that are generally used for the preparation of "Kolakenda". As a result, "Kolakenda" is considered a rich source of nutritional and nutraceutical properties as it contains various macro and micro nutrients and phytoconstituents such as phenols, flavonoids, alkaloids, tannins, that are associated with significant antioxidant, antihyperglycemic, lipid-lowering, antihypertensive, hepatoprotective, and cardioprotective properties. Considering the richness of nutritional as well as nutraceutical values of Sri Lankan “Kolakenda”, it can be complemented as a *Ghidhā’ Dawā’ī* in the prevention of Non-Communicable Diseases (NCDs) and promotion of overall health

Key words: *Ghidhā’ Dawā’ī*, Kolakenda, Nutraceuticals, Nutrition.

Poster-31

"HR-LCMS-Based Metabolite Profiling and *In Silico* Evaluation of *Canthium coromandelicum* (Burm F.) Leaf Extract Targeting Antimicrobial Resistance, Viral Protease and EGFR-Mediated Cancer Pathway"

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Abstract

The increase in antimicrobial resistance (AMR) is a critical global issue alongside the viral infections and cancer highlights the need for bioactive molecules. Medicinal plants offer valuable source for such bioactive compounds and alternatives to traditional antibiotics. In this study, we analyzed the leaf extract of *Canthium coromandelicum* using High-Resolution Liquid Chromatography and Mass Spectrometry (HR-LCMS) to identify bioactive phytochemicals with possible therapeutic uses.

Important flavonoid derivatives, such as quercetin 3-rhamnoside-7-glucoside, luteolin 4′-O-glucoside, Myricitrin, and Genistein analogues, were predicted through PASS analysis to have antibacterial, enzyme-inhibiting, and anti-proliferative effects. Molecular docking was performed for the confirmation of bioactivity against target clinical proteins.

For antiviral activity, we docked the SARS-CoV-2 3C-like protease (PDB: 7P35) and the reference inhibitor substance Rupintrivir (−7.9 kcal/mol) and Dimepiperate from the leaves of *C. coromandelicum* (−5.4 kcal/mol). This indicated favorable binding of the phytochemical. In addition, for assessing anticancer activity, we performed molecular docking studies against the tyrosine kinase domain of epidermal growth factor receptor (PDB: 1M17) with Erlotinib (−7.1 kcal/mol) and Nigakilactone B (−7.8 kcal/mol), showing better binding for the natural compound. Further docking of flavonoid derivatives revealed strong interactions with enzymes linked to bacterial resistance, such as β-lactamase and DNA gyrase.

These findings suggest that *C. coromandelicum* is a promising source of multi-target bioactive compounds with potential activity against antimicrobial resistance (AMR) mechanisms, viral protease activity, and EGFR-related to cancer progressions. The combination of HR-LCMS profiling, PASS prediction, and structure-based molecular docking provides efficient way for speeding up the discovery of natural products-based drug discovery.

Keywords: Antimicrobial resistance (AMR), EGFR signaling, Anticancer, Antiviral, *Canthium coromandelicum*, HR-LCMS, Molecular docking.

Poster-32

Mosquito larvicidal activity of *Cassia tora* (L) leaves extract

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Abstract

Cassia tora L. (Family: *Fabaceae*) is an important medicinal plant widely distributed in tropical regions. It contains bioactive compounds such as anthraquinones, flavonoids, alkaloids, and phenolics, which are responsible for its antimicrobial, anti-inflammatory, and insecticidal activities. Traditional systems of medicine recognize its therapeutic value, particularly in treating skin disorders, antimicrobial and anticancer activities. The present study aimed to evaluate the larvicidal potential of *C. tora* leaf extract against third and fourth instar larvae of *Anopheles stephensi*, a major vector of malaria. Fresh leaves were collected from the S.R.T.M. University campus, shade-dried, powdered, and subjected to aqueous extraction to obtain a crude extract rich in secondary metabolites. Different concentrations of the extract were tested under laboratory conditions, and larval mortality was recorded after 24 hours, with experiments conducted in replicates to ensure reliability. The crude extract demonstrated significant larvicidal activity, causing 60–70% mortality within 24 hours in a concentration-dependent manner. This confirms that the bioactive anthraquinones and other phytochemicals in *C. tora* contribute to its larvicidal efficacy. These findings suggest that *C. tora* leaf extract is a promising eco-friendly botanical agent for integrated management of *An. stephensi* populations, offering a biodegradable alternative to chemical larvicides.

Keywords: *Cassia tora*, *Anopheles stephensi*, Larvicidal activity, Phytochemicals.

Poster-33

Insecticide resistance as a major threat in vector-borne disease control

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Abstract

Most dangerous human diseases are transmitted by insect vectors. The use of insecticides plays a major role in the prevention and control of these infectious diseases. However, the widespread and excessive use of insecticides has led to the development of insecticide resistance in various disease vectors, posing a serious public health challenge. Generally, four classes of chemical insecticides are used to control vector-borne diseases: organochlorines, organophosphates, carbamates, and pyrethroids. To date, four types of resistance mechanisms against these chemical insecticides have been identified: metabolic resistance, target-site resistance, penetration resistance, and behavioural resistance. Metabolic resistance involves the sequestration and detoxification of insecticides through the overproduction of specific enzyme groups, such as carboxylesterases, glutathione-S-transferases, and cytochrome P450-dependent monooxygenases. Target-site resistance is achieved through point mutations in the genetic sequence of the target site. Since most insecticides are neurotoxic, their primary targets are acetylcholinesterase, γ-aminobutyric acid (GABA) receptors, and sodium channels. Consequently, a mutation in any of these three target sites leads to resistance within a vector for a particular insecticide. Thus, the study of insecticide resistance in various vectors helps in the understanding for which insecticide the vector is already resistant and for which insecticide the vector is still not resistant. This helps in controlling the disease vector easily. This type of study should be done for all the vectors at particular time, which interval helps in the prevention and control of various vector-borne diseases and very helpful in the public health monitoring.

Keywords: Insecticide, Vector-borne disease, Resistance, Insect.

Poster-34

Novel compound from *Alstonia* targets L-asparaginase

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Abstract

The *Alstonia scholaris* is common ornamental plants observed more common on footpath and landscapes. The birds rarely nest on this plant as it is supposed to be toxic in nature. The insect *Pyropsylla tuberculata* infests to this plant on leaves, pods and sometimes on stems also. The infections are non-pathogenic and seasonal. In the seasonal blooming, flowers of the plants secretes strong insect-repellent odour. The plants bear numerous compounds having potential therapeutic applications. Among them pelargonic acid [SMILES: CCCCCCCCC(=O)O] can be used as the novel anti-cancerous compound. This compound screened using the online tools (way2drug) and further its affinity and binding were confirmed by running docking analysis. The pelargonic acid nine carbon containing saturated fatty acid. In this investigation, we found that the pelargonic acid strongly binds to L-aspiraginase and inactivates it. L-aspiraginase is important enzymes with respect to survival of the tumour cells. L-aspiraginase makes availability of L-aspiragine as one the essential nutrient for the tumour cell survival. Pelargonic acid is having strong affinity towards this enzyme L-aspiraginase with binding energy -3.689 kcal/mol, makes it non-functional. The inactivation of this enzyme results in the reduction in the development of tumour.

Keywords: Aspiraginase, Cancer, Pelargonic acid, docking.

Poster-35

Evaluation of a fluorinated chalcone derivative as Janus kinase inhibitor for targeted anticancer therapeutics

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Abstract

Alstonia scholaris is the ornamental tree observed commonly in the gardens and landscapes. The full-matured leaves of it, were taken and shade dried. Dried leaves were grinded with the help of mixture and mortar and pestle to make fine powder. Using this dry powder crude extract were isolated using methanol as the main solvent soxhletion. This crude extract was further characterized through the HR-LCMS. The plant bears numerous compounds having therapeutic potential. Among them one of the compounds, Chalcone showed significant potential by blocking Janus kinase. This enzyme is responsible for the survival of tumour cells. The chalcone is usually fluorinated having structure as (E)-1-(4-fluorophenyl)-3-(4-hydroxyphenyl) prop-2-en-1-one. This compound is screened for anti-cancer potential using online tools i.e. way2drug. This molecule shows strong affinity toward Janus kinase and has strong potential to inhibit it. The signaling was done by the Janus kinase is necessary for the tumor development. Inactivation of this enzyme helps in reduction of tumour growth.

Keywords: Alstonia, Chalcone, Janus kinase, Anticancer.

Poster-36

Multi-drug resistant *Pseudomonas aeruginosa* strain from clinical setting

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Abstract

The *Pseudomonas aeruginosa* causes severe diseases including pneumonia, urinary tract infection, and sepsis. It is frequently associated with infected individual and clinical setting area of Hospital. The management and treatment of infectious diseases require effective antimicrobial therapy using commonly available drugs such as antibacterial from class β-lactam, aminoglycosides and quinolones. The inherent and acquired ability of antibiotic resistance among the *P. aeruginosa* strains, the use of antibiotic therapy leads to failure. Therefore, the effective antimicrobial selection is important the selection of effective antibiotics is achieved through the determination of antibacterial sensitivity/resistance pattern of *P. aeruginosa*. The sensitivity pattern of *P. aeruginosa* PA5 against 40 antibiotics were determine using Kirby–Bauer disc diffusion method. Active culture of the *P. aeruginosa* PA5 strain was prepared and adjusted to 0.5 MacFarland. The bacterial strain was previously identified using morphological, biochemical and 16S rRNA sequencing. The 100 µl active culture of *P. aeruginosa* was spreaded on Mueller–Hinton Agar (MHA) plates and the selective antibiotic disc were placed accordingly and plates were incubated at 37°C for 24 hours, after incubation the plates were observed for zones of inhibition. The selected antibiotics in form of disc showed inhibition of *P. aeruginosa* growth on MHA plates, the zone of inhibition ranges from 23 to 44 mm, among the 40 antibiotics used. Similarly, *P. aeruginosa* strains showed resistant to 25 antibiotics from class viz. β-lactams, cephalosporins, carbapenems, glycopeptides, and lincosamides. The infection caused by *P. aeruginosa* strain can be treated by using antibiotics, which have shown zone of inhibition on MHA plates; however, remaining other antibiotics cannot be used in monotherapy. It can be use only as one of other antibiotics in combination therapy for treating infection.

Keywords: *Pseudomonas aeruginosa*, antibiotic resistance, Kirby-Bauer, 16S rRNA sequencing.

Poster-37

Transforming patterns of vector-borne illnesses following the COVID-19 outbreak in India

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Abstract

Though the extraordinary spread of coronavirus disease 2019 (COVID-19) and its extensive repercussions are evident in various sectors, the effects on vector-borne diseases (VBDs) remain inadequately comprehended. Consequently, the temporal patterns of significant VBDs like malaria, dengue, chikungunya, Japanese encephalitis, and kala-azar in India were examined prior to and following the COVID-19 outbreak. Information on annually documented VBD incidents, including malaria, dengue, chikungunya, Japanese encephalitis, and kala-azar, in India from 2014 to 2024 was gathered and displayed on a bar chart using Microsoft Excel. Distinct trend lines were created for each VBD before and after 2020, and the R^2 value was computed. The Pearson correlation coefficient (r value) for every trend was determined through Microsoft Excel to assess the trend's strength for each VBD before and after 2020. The trendline for each VBD, encompassing malaria, dengue, chikungunya, Japanese encephalitis, and kala-azar, exhibited varied patterns before and after 2020. The trend's r value revealed that the COVID-19 pandemic has changed the declining trend of malaria into a significantly increasing trend. Other trends impacted by the pandemic included Japanese encephalitis, dengue, chikungunya, and kala-azar.
This research highlights the distinct effect of the COVID-19 pandemic on the trends of VBDs, which range from subtle alterations to a complete reversal of the trends.

Keywords: COVID-19, Pandemic, Trend, Vector, Disease.

Poster-38

Integrated management of Potato Leaf Roll Virus under the threat of insecticide resistance in *Myzus persicae*

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Abstract

Potato leaf roll virus (PLRV) is one of the most common viral disease of potato causing major yield and quality loss. This virus is transmitted through the green peach aphid (*Myzus persicae*) making vector control central to the disease management. Effective management of PLRV is largely dependent on controlling its vector but due to continuous and excessive use of synthetic pesticides there has been emergence of resistant strains of aphids. Resistance has been reported against major chemical groups including pyrethroids, organophosphates, carbamates and neonicotinoids. The resistance in aphids is developed due to genetic mutation such as kdr and MACE as well as enhanced metabolic detoxification, where elevated esterase activity helps insect to neutralize insecticide. However, chemical efficacy is significantly reduced due to emergence of such resistance mechanism leading to sustained virus transmission and increasing selection pressure in agro-ecosystem. In such conditions, relying completely on chemical control could not be sustainable. Therefore, including the integrated management strategies such as using disease/virus-free tubers, vector surveillance, insecticide rotation based on the mode of action, using biological antimicrobials, conserving natural enemies, cultural practices, and resistance monitoring are necessary for suppressing vector population and interrupting PLRV transmission. By combining the multiple integrated management strategies reduce the dependence on single insecticide and reduces the risk of development of resistance in *M. persicae* and strengthens the control of PLRV.

Keywords: *Myzuz persicae*, Insecticide resistance, Integrated management strategies.

Poster-39

Isolation and characterization of halophilic exopolysaccharide-producing bacteria isolated from salt pan

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Abstract

Halophilic bacteria inhabiting hypersaline environments represent a promising yet underexplored source of industrially valuable biopolymers, particularly exopolysaccharides (EPS). This study focuses on the isolation and characterization of EPS-producing halophilic bacteria from salt pans. Samples were collected from Goa salt pan sediments, enriched and cultured on selective media containing high NaCl concentrations to enrich for halophiles. Distinct colonies exhibiting mucoid morphology were screened for EPS production.

The selected isolates were characterized based on the morphological, physiological, and biochemical properties. Molecular identification was carried out through 16S rRNA gene sequencing, revealing the presence of halophilic bacterial genera commonly associated with extreme saline habitats. The isolates demonstrated optimal growth at high salt concentrations, confirming their halophilic nature. EPS was extracted using alcohol precipitation methods and further characterized for yield, carbohydrate content, and physicochemical properties.

Overall, this study highlights the ecological importance of salt pan halophiles and their promise as sustainable sources of novel EPS with unique structural and functional attributes.

Keywords – Halophiles, Salt pan, Exopolysaccharides (EPS).

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Poster-40

Morpho-taxonomic description of *Procamallanus intestinalis* sp. nov. (Nematoda: Camallanidae) from the intestine of *Mastacembelus armatus* in Nanded, India

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Abstract

A new camallanid nematode, *Procamallanus intestinalis sp.* nov., is described from the intestine of the freshwater fish *Mastacembelus armatus* collected from the Nanded district of Maharashtra, India, between February 2011 and January 2013. Specimens preserved in 10% glycerine alcohol and mounted in glycerine jelly were examined for detailed morphological and morphometric characterization. The species is distinguished by a slender, semi-transparent body with a truncated head, cylindrical buccal capsule, bifurcated oesophagus, and clear sexual dimorphism. Males are smaller, bearing unequal spicules, eight pairs of caudal papillae, and a well-developed cloaca, whereas females are larger, with a post-equatorial vulva, distended uterine tubes, and oval eggs. Although superficially resembling *Procamallanus hyderabadensis* in several key traits, *P. intestinalis* differs in caudal papillae count, specific organ measurements, and host association. These findings enhance understanding of helminth diversity in Indian freshwater ecosystems and emphasize the taxonomic value of subtle morphological variations in nematode systematics.

Keywords: *Procamallanus intestinalis*, *Mastacembelus armatus*, Nematode taxonomy, Freshwater fish parasitology, Helminthology, Species differentiation, Indian freshwater ecosystems.

Poster-41

Study of vocalization of birds for identification, associated behavior, and Database development

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Abstract: Birds are significant indicators of a healthy ecosystem and occupy almost all available habitats. They are present at every tropic level from primary consumers to tertiary consumers. Birds communicate with each other by producing sounds. This bird's vocalization is associated with different behaviors, which makes it a useful tool for monitoring populations and measuring biodiversity, but the importance of vocalizations in ecosystem conservation. Birds have a special organ for the vocalization. The songbirds both male and female use vocalizations to deliver specific information to the receiver. The bird vocalization is classified into calls and songs. Calls have a large functionality and 10 different call categories such as alarm, flight, feeding, etc. A spectrogram is a visualization of sounds and can be used to visualize the frequencies over time. The point–count method is one of the most popular techniques for surveying birds based on vocalization. Autonomous recording units (ARUs) are a new technology for the study and monitoring of animal's vocalizations. A review paper presents the review of the vocalization of birds for identification, associated behavior, and database development at the international and national levels.

Keywords: Bird vocalization, Bird identification, Bird acoustic, Vocal behavior of birds.

Poster-42

Microbiome-derived therapeutics: Integrative metagenomic and computational approaches for Next-Generation Drug Discovery

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Abstract

The growing serious threat of antimicrobial resistance among the pathogens and the diminishing productivity of conventional drug discovery approaches are gathering the attention towards urgent need for alternative therapeutic strategies. The human microbiome, comprising diverse and metabolically dynamic microbial communities, represents a major unexplored source of bioactive molecules with possible therapeutic applications. Recent advances in high-throughput sequencing and computational biology now allow systematic exploration of this resource for drug discovery.

In the present investigation, the attempts were made regarding outline an integrative workflow that combines metagenomic data mining with computational drug design to identify promising microbiome-originated therapeutic candidates. Metagenomic datasets are studied to explore the secondary metabolite producing biosynthetic gene clusters. Functional annotation and pathway reconstruction are assigned to infer the structural as well as biochemical features of predicted metabolites. With the help of structure-based virtual screening and molecular docking, these candidate molecules are subsequently evaluated through against clinically significant protein targets. To evaluate drug-likeness, safety, and potential multi-target effects, computational ADMET (Adsorption, Distribution, Metabolism, Excretion and Toxicity) profiling and network-based analyses are further incorporated.

Apart from traditional screening techniques, this multidisciplinary approach is offering an affordable and targeted substitute for providing the rational prioritization of microbiome-derived compounds for experimental validation. The approach underscores the potential of microbiome-based drug discovery protocol in advancing precision therapeutics and shaping the future of translational biomedical research and innovations.

Keywords: Microbiome, Metagenomics, Computational drug design, Biosynthetic gene clusters, Antimicrobial resistance.

Poster-43

Antimicrobial resistance: Effects, difficulties, and potential future developments

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Abstract

Antimicrobial resistance, commonly known as AMR, stands as a pressing global health concern fueled by the improper use and excessive prescription of antibiotics across various domains, resulting in the rise of resistant microbes. The origins of AMR trace back to the advent of penicillin, alongside the emergence of pathogens resistant to multiple drugs, presenting serious difficulties for healthcare systems on a global scale. The irresponsible usage of antibiotics in both human and animal health, including agricultural applications, facilitates the transmission of resistance genes, leading to what is referred to as a "Silent Pandemic" that may overshadow other mortality factors by the year 2050. AMR impacts both people and animals, with drug-resistant pathogens complicating the treatment of infections. Numerous mechanisms, including enzyme alteration and biofilm creation, allow microorganisms to endure the effects of antibiotics. The absence of effective antibiotic treatments endangers regular medical practices and could potentially result in millions of deaths each year if not addressed properly. The financial repercussions of AMR are considerable, with estimated losses amounting to trillions of dollars alongside heavy economic strains on healthcare systems and agricultural sectors. Artificial intelligence is being examined as a means to tackle AMR by enhancing diagnostic measures and treatment plans, although issues regarding data integrity and biases in algorithms need to be addressed. For an effective response to AMR, a One Health strategy is vital, taking into account human, animal, and environmental dimensions. This approach involves bolstering surveillance systems, endorsing stewardship initiatives, and channeling resources into the research and development of new antimicrobial alternatives. Raising public awareness, fostering education, and promoting international cooperation are critical steps in the fight against AMR and in safeguarding the effectiveness of antibiotics for upcoming generations.

Keywords: Antibiotics ,Resistance to antibiotics ,Management ,Artificial intelligence ,Bacteria resistant to multiple drugs ,Strategies for prevention ,Other treatment options ,One Health strategy etc.

Poster-44

Influence of Summer Hydrochemistry on Heavy Metal Levels in Sindaphana River

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Abstract

Bioaccumulation studies not only reveal the degree of environmental contamination but also help identify dominant exposure pathways and potential sources of pollution, the study reveals the concentration and bioaccumulation of heavy metals in water and selected fish tissues from the Sindaphana River, Maharashtra, during the summer season. Fish tissues, including liver, gill, and muscle, were analysed for Mercury (Hg), Arsenic (As), Lead (Pb), Cadmium (Cd), and Nickel (Ni) using inductively coupled plasma mass spectroscopy (ICPMS). Comparison with WHO/FAO permissible limits observed that Mercury levels in fish tissues (0.0005–0.02 mg/kg) were well below the safe limit of 0.5 mg/kg, while Arsenic (0.02–0.12 mg/kg) slightly exceeded the permissible limit in a few samples. Lead (0.27–2.3 mg/kg) and Nickel (1.0–6.4 mg/kg) concentrations in fish tissues were consistently above safe limits, indicating severe contamination. Cadmium levels were mostly within limits but exceeded 0.05 mg/kg in some tissues. Water samples also showed elevated concentrations of Arsenic (0.0606 mg/L), Lead (0.572 mg/L), and Nickel (1.31 mg/L), exceeding WHO drinking water standards. Tissue-specific accumulation followed the trend Liver > Gill > Muscle, with the liver exhibiting the highest metal concentrations. The results indicate significant contamination of the Sindaphana River with toxic heavy metals, posing potential health risks to local communities upon regular consumption of fish. The study provides baseline data for environmental monitoring and highlights the need for mitigation strategies to protect aquatic ecosystems and human health.

Keywords: Sindaphana River, Heavy metals, Bioaccumulation, Fish tissue, Lead, Nickel, Arsenic, Mercury, Cadmium, Water quality

Poster-45

Comparison of different spectral ranges of UV-LED lighting for outdoor mosquito trapping in forested area in Thailand

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Abstract

Mosquito surveillance is critical for actively tracking the location and monitoring population levels and the threat of mosquito-borne disease. Although light-emitting diodes (LEDs) light traps have grown in popularity, there is still a limited understanding of the application of light wavelengths for trapping nocturnally active wild mosquitoes in forest ecotypes. This study evaluated the performance of different UV wavelengths in trapping mosquito populations in a forested mountainous area in Nakhon Ratchasima province, Thailand. Traps with different UV wavelengths were deployed in 6 locations, following a 6 × 6 Latin square replicated 6 times over a total of 36 nights. Light traps were operated between 18:00 and 06:00 h from October 2022 to August 2023. Mosquitoes were separately collected from individual traps every 4 h at 22.00, 2.00, and 6.00 h. Mosquitoes were killed by placing in a freezer (− 20 °C) for at least 30 min and then were morphologically identified using illustrated keys for adult females. Traps fitted with the LED 365 wavelength light source were the most effective in capturing 790 (23.66%) of the total mosquitoes collected, followed by the UV fluorescent 632 (18.93%), with the other 4 LED wavelengths collecting between 16.89% (LED 385) and 12.64% (LED 375) of the mosquitoes. *Culex* was the most common genus, representing 56.00% of total mosquito abundance. LED 365 and LED 385 were comparable to the UV fluorescent traps (the standard reference). Optimal trapping times were during 18:00–22:00 h. Compared to the other wavelengths, LED 365 was significantly more effective at capturing *Coquillettidia* and *Culex* mosquitoes than the UV-based traps.

Keywords: mosquito, light-emitting diode, light trap, UV fluorescent lighting, wavelength

Poster-46

ON A NEW MARATHWADIAN FOREST GALL MIDGE SPECIES (DIPTERA: CECIDOMYIIDAE)

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Abstract

A new species *lasioptera garugai* infesting garuga pinnata roxb. (Family : Burseraceae), a forest tree from Aundha, Kandhar forest, dist. Hingoli and Nanded is described here. A survey of plant gall and gall midge flies from Aundha, Kandhar forest, dist. Hingoli and Nanded. A new leaf gall on *Garuga pinnata Roxb.* is recorded. Two gall midges, *lasiopetra garugai* and *Garugodiplosis braviplpi* were bred from this leaf gall. The first one is believed to be a gall former and second one an inquilines. Presently 12 species of *lasioptera* are known from the Oriental region. Lasiopteran midge flies heavily gall members of cucurbitaceae and different grasses.

Keywords: *Dipteral,Cecidomyiidae, Lasioptera, Garugai.*

Poster-47

Optimizing Soil Pre-Treatment Strategies for *Streptomyces* Isolation And Antibacterial Screening

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Abstract

The soil ecosystem hosts a diverse community of microorganisms capable of producing biologically active secondary metabolites, including therapeutically valuable antimicrobials. This research focused on microbial isolates from rhizospheric soil, with particular attention to actinomycetes and their biosynthetic potential. To selectively enrich actinomycetes, soil samples underwent a range of physical, chemical, and combined physicochemical pre-treatments designed to suppress fast-growing bacteria and fungi. Among the strategies tested, chemical treatment with Chloramine-T and the combined approach of heat drying followed by Chloramine-T proved most effective in isolating actinomycetes from compost soil, significantly reducing non-target microbial growth. The recovered isolates were screened using the cross-streak method to evaluate antibacterial activity against clinically important pathogens. Preliminary characterization based on morphological, cultural, and biochemical traits identified the active isolates as belonging to *Streptomyces* species, highlighting their potential for antibiotic production. By integrating ecological exploration with applied microbiological techniques, this study contributes to ongoing global efforts in antibiotic discovery and innovation.

Keywords: Soil microorganisms, Actinomycetes, Pre-treatment, Antibacterial screening, Antimicrobial compounds.

Poster 48

From Nature to Innovation: Candiguard Herbal Soap and Gel

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Abstract

Fungal infections have emerged as a significant global health concern, particularly with the increasing population of immunocompromised individuals and the rising incidence of antifungal drug resistance. Among human fungal pathogens, Candida albicans is one of the most prevalent opportunistic fungi, capable of causing infections that range from superficial mucocutaneous lesions to severe, life-threatening invasive diseases. Its pathogenic potential is attributed to a variety of virulence factors, including morphological switching, biofilm formation, secretion of hydrolytic enzymes, toxin production, and the ability to adapt to hostile host environments. Invasive fungal infections are associated with high morbidity and mortality, and their management is further complicated by delayed diagnosis and limited therapeutic options. This review provides a comprehensive overview of fungal pathogens with special emphasis on Candida albicans, its pathogenic mechanisms, clinical manifestations, and the growing problem of antifungal resistance. The limitations of conventional antifungal drugs, particularly the emergence of resistance to azoles and echinocandins, highlight the urgent need for alternative therapeutic strategies. In this context, medicinal plants such as Ocimum sanctum (Tulsi), Allium sativum (garlic), Cinnamomum verum (cinnamon), Cymbopogon citratus (lemongrass), and Tridax procumbens are discussed for their antifungal potential against Candida albicans. These plants contain diverse bioactive compounds that inhibit fungal growth, disrupt cell membranes, and reduce virulence by interfering with biofilm formation and hyphal development.

Overall, the review emphasises the importance of integrating knowledge of fungal pathogenesis, host susceptibility, and resistance mechanisms to improve prevention and treatment strategies. The exploration of plant-derived antifungal agents offers promising avenues for developing safer, cost-effective, and effective alternatives or adjuncts to existing antifungal therapies in the management of candidal infections.

Keywords: Candida albicans, antifungal, medicinal plants

Hands-on training programme on RT-PCR

Biotechnology Day Inauguration

Training Programme on Molecular Docking

Swami Ramanand Teerth Marathwada University, Nanded

Start-ups were felicitated at the hands of Hon’ble Shri Chandrakant Dada Patil and Hon’ble Vice-Chancellor Dr. Manohar Chaskar.

National Seminar on Extremophiles for Biotechnological and Commercial Applications