SAVEETHA
INSTITUTE OF MEDICAL AND TECHNICAL SCIENCES
(Declared as Deemed to be University under Section 3 of UGC Act 1956)

Accredited by NAAC A++ GRADE

SCIMAGO-2026 RANK: 6 DENTISTRY

SIMATS DEEMED UNIVERSITY 25 WORLD RANK QS WORLD UNIVERSITY RANKINGS by subject QS UNIVERSITY RANKING OF DENTISTRY 2026

SUSTAINABLE DEVELOPMENT GOALS

nirf (By MHRD, Govt. of India) 1ST RANK Among All Private & Deemed Universities in India

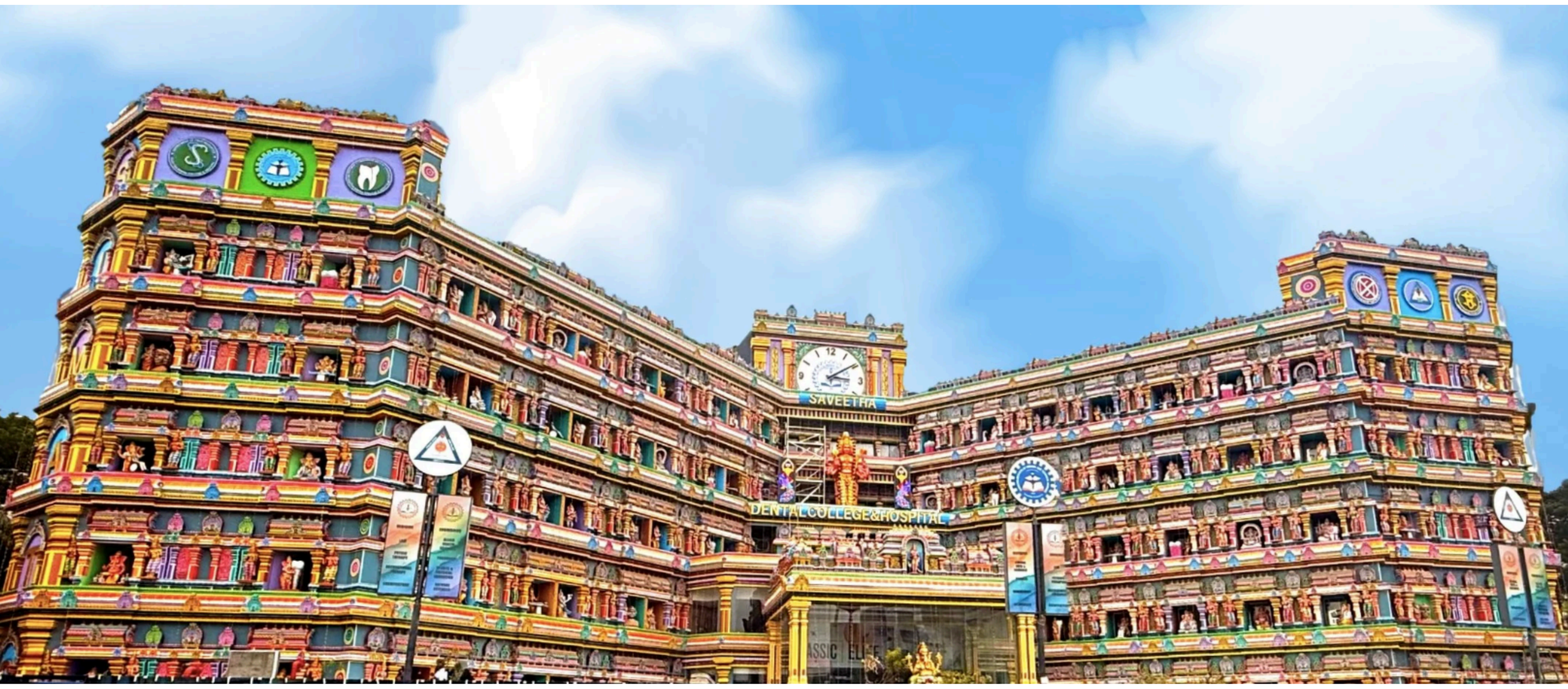
Department of Microbiology
[Centre for Infectious diseases]
In Association with
Antiviral Research Scociety (AVRS)

BIOINTELLIGENCE 2026
International Conference
on
Prediction, Prevention, & Management of Emerging Infectious Diseases

CONFERENCE PROCEEDINGS

ISBN Number : 978-93-5933-810-1

31st July & 1st August 2026



Our Sponsors

ARAVINDH HERBAL LABS (P) LTD RAJAPALAYAM
ARAVINDH HERBAL LABS
PRIVATE LIMITED RAJAPALAYAM

YAZHINI BIOTECH
YAZHINI BIOTECH LAB
Approved by MSME
5/616 Sai Durga Nagar, Padikasuvaidan Patti - 626154
Stivilliputtur Taluk, Virudhu Nagar District
Cell: 9384318275 | E-mail: selvaamin@gmail.com

edutravllr™
simplifying education

Gainz India Peripherals Pvt Ltd
Your trusted partner in IT solutions

pharmafabrikon

Synergy Scientific Services

PREFACE

It gives us immense pleasure and a profound sense of academic responsibility to present the official proceedings of ***BIOINTELLIGENCE 2026: International Conference on Prediction, Prevention, & Management of Emerging Infectious Diseases***. Hosted on July 31st and August 1st, 2026, this landmark event was organised by the Department of Microbiology (Centre for Infectious Diseases) at Saveetha Dental College and Hospital—a constituent institution of Saveetha Institute of Medical and Technical Sciences (SIMATS)—in association with the Antiviral Research Society (AVRS).

In an era characterised by rapid global connectivity, environmental changes, and evolving pathogen profiles, the threats posed by novel viral entities and emerging infectious diseases are unprecedented. Effective countermeasures demand a paradigm shift from reactive treatment strategies to proactive, intelligence-driven paradigms. **BIOINTELLIGENCE 2026** was envisioned precisely to bridge this gap by bringing together clinicians, microbiologists, computational biologists, epidemiologists, and researchers on a shared platform to address the critical pillars of infectious disease management: **Prediction, Prevention, and Management**.

The conference highlighted cutting-edge advances across a broad spectrum of sub-disciplines. Key discussions focused on predictive modelling that leverages artificial intelligence and computational biology to forecast outbreak trajectories and identify emerging viral threats before they cause widespread disruption. On the preventative front, speakers and contributors showcased innovative vaccine development, novel diagnostic tools, and robust public health strategies designed to intercept transmission pathways. Furthermore, sessions dedicated to disease management emphasised advanced therapeutic modalities, including natural compounds, novel antivirals, and integrative biomanufacturing approaches.

This proceedings volume (ISBN: 978-93-5933-810-1) compiles a curated selection of peer-reviewed research papers, insightful reviews, and abstracts presented during the two-day conference. Each contribution reflects the high standards of scientific rigour and original inquiry needed to advance our collective defence against microbial threats. Readers will

find actionable clinical insights, innovative laboratory methodology, and scalable public health approaches that offer valuable benchmarks for both current practice and future research agendas.

We extend our heartfelt gratitude to the management of Saveetha Dental College & Hospital and SIMATS for their continuous support and visionary leadership. Special appreciation goes to the Antiviral Research Society (AVRS) for their invaluable partnership in making this international conference a resounding success. We are deeply thankful to the organising committee, members of the technical review board, session chairs, distinguished keynote speakers, and delegate authors whose contributions form the foundation of this publication.

We also express our sincere appreciation to our esteemed sponsors—Aravindh Herbal Labs, Gainz India Peripherals, Edu Travllr, Yazhini Biotech Lab, Synergy Scientific Services and Pharmafabrikon—for their generosity and commitment to promoting biomedical science and education.

We hope this volume will serve as a vital resource, spark new interdisciplinary collaborations, and inspire continued academic excellence as we work together toward a safer, more resilient future against emerging infectious diseases.

Organizing Committee
Team Micro
BIOINTELLIGENCE 2026
Department of Microbiology (Centre for Infectious Diseases)
Saveetha Dental College & Hospital, SIMATS

I am delighted to welcome all esteemed delegates, keynote speakers, researchers, academicians, clinicians, industry experts, and students to the 7th MicroSummit – BioIntelligence 2026: International Conference on Prediction, Prevention, and Management of Emerging Infectious Diseases

The increasing complexity of emerging and re-emerging infectious diseases, coupled with the growing threat of antimicrobial resistance, demands innovative, interdisciplinary, and technology-driven solutions. The convergence of artificial intelligence, bioinformatics, genomics, digital epidemiology, and precision medicine is transforming the way we understand, predict, prevent, and manage infectious diseases. This conference aptly reflects these advancements by providing a dynamic platform for scientific exchange and collaborative innovation.

At Saveetha Institute of Medical and Technical Sciences (SIMATS), we are committed to fostering a culture of academic excellence, research innovation, and global partnerships that address pressing healthcare challenges. Through conferences such as BioIntelligence 2026, we continue to strengthen our vision of nurturing scientific inquiry and promoting translational research that benefits humanity. I commend the Department of Microbiology and the Centre for Infectious Diseases, Saveetha Dental College and Hospitals, for their exemplary efforts in organizing this prestigious international conference. My sincere appreciation also goes to the organizing committee, invited speakers, scientific reviewers, sponsors, and all participants whose valuable contributions have made this event a remarkable academic endeavor.

I am confident that the deliberations, discussions, and research presented in these proceedings will inspire future collaborations, stimulate innovative discoveries, and contribute significantly to global efforts in infectious disease research and public health. I extend my heartfelt best wishes for the grand success of BioIntelligence 2026 and trust that this conference will leave a lasting impact on the scientific community.

Dr. V. Deepak Nallasamy
Pro-Chancellor
Saveetha Institute of Medical and Technical Sciences (SIMATS)

It is a matter of great pride and satisfaction to welcome all participants to the 7th MicroSummit – BioIntelligence 2026: International Conference on Prediction, Prevention, and Management of Emerging Infectious Diseases.

Scientific progress has always been driven by collaboration, innovation, and the continuous pursuit of knowledge. As infectious diseases evolve alongside global environmental and societal changes, there is an urgent need to integrate emerging technologies such as artificial intelligence, machine learning, bioinformatics, and digital health into disease surveillance, prevention, diagnosis, and treatment.

This conference reflects the vision of Saveetha Institute of Medical and Technical Sciences to promote cutting-edge research, international collaboration, and academic excellence. Bringing together renowned scientists, clinicians, educators, industry leaders, and young researchers from across the globe will undoubtedly stimulate intellectual exchange and foster multidisciplinary partnerships that translate research into impactful healthcare solutions.

I commend the Department of Microbiology and the Centre for Infectious Diseases for conceptualizing this timely conference and providing an outstanding platform for scientific interaction. I also congratulate every contributor whose research forms part of these proceedings.

I extend my best wishes for a highly successful conference and trust that the discussions and discoveries emerging from this event will significantly contribute to the global fight against infectious diseases.

Dr. Ashwani Kumar
Vice-Chancellor
Saveetha Institute of Medical and Technical Sciences (SIMATS)

It gives me immense pleasure to extend my warm greetings to all the delegates, researchers, academicians, clinicians, industry experts, and students participating in the 7th MicroSummit – BioIntelligence 2026: International Conference on Prediction, Prevention, and Management of Emerging Infectious Diseases.

Emerging and re-emerging infectious diseases continue to pose significant challenges to global health, demanding innovative scientific solutions and strong interdisciplinary collaborations. This conference provides an excellent platform for exchanging knowledge, presenting pioneering research, and fostering collaborations that will contribute to the advancement of infectious disease research and healthcare.

The integration of artificial intelligence, bioinformatics, molecular diagnostics, and precision medicine into infectious disease management represents a transformative era in biomedical sciences. I am confident that the scientific deliberations, keynote lectures, workshops, and research presentations will inspire meaningful discussions and generate innovative ideas that benefit society.

I congratulate the Department of Microbiology, Centre for Infectious Diseases, Saveetha Dental College and Hospitals, for organizing this prestigious international conference. I also appreciate the efforts of the organizing committee, distinguished speakers, reviewers, and participants whose dedication has made this event possible.

I wish the conference great success and hope the proceedings serve as a valuable scientific resource for researchers across the world.

Dr. Sheeja S. Varghese
Registrar
Saveetha Institute of Medical and Technical Sciences (SIMATS)

It is my privilege to welcome all participants to the 7th MicroSummit – BioIntelligence 2026: International Conference on Prediction, Prevention, and Management of Emerging Infectious Diseases.

The rapid emergence of infectious diseases and antimicrobial resistance underscores the importance of scientific innovation, translational research, and multidisciplinary collaboration. The Department of Microbiology has consistently promoted excellence in research and education, and this conference reflects our commitment to addressing global healthcare challenges through evidence-based science and technological advancement.

The scientific program, encompassing keynote lectures, workshops, oral and poster presentations, provides an exceptional opportunity for researchers, clinicians, faculty members, and students to exchange ideas, establish collaborations, and explore emerging developments in microbiology, infectious diseases, artificial intelligence, genomics, and precision medicine.

I congratulate the organizing committee for their meticulous planning and dedication in bringing together eminent experts from academia, healthcare, research organizations, and industry. I also extend my appreciation to all authors whose valuable contributions have enriched these conference proceedings.

I wish every participant a rewarding academic experience and hope that the knowledge shared during this conference will inspire future discoveries that improve global health and patient care.

Dr. S. Aravind Kumar
Dean
Saveetha Dental College and Hospitals
Saveetha Institute of Medical and Technical Sciences (SIMATS)

7TH MICROSUMMIT - BIOINTELLIGENCE 2026

International Conference on Prediction, Prevention, and Management of Emerging Infectious Diseases

PROGRAMME SCHEDULE | 31st July 2026

08:00 AM - 09:00 AM	**Registration***
09:00 AM - 10:00 AM	**Scientific Session - Ph.D Scholars and PG (Session 1)**
10:00 AM - 10:30 AM	**Responsive Nanomedicine and Biofilm Models for Future Infection Control** Dr. Rohan Shah, Swinburne University of Technology, Australia
10:30 AM - 11:00 AM	**Inaugural Ceremony**
11:00 AM - 11:15 AM	**Tea Break**
11:15 AM - 12:00 PM	**Emerging Infectious Diseases: Insights from SARS-CoV-2 and Re-emerging Arboviral Threats** Dr. Chandramathi, Universiti Malaya, Malaysia
12:00 PM - 12:30 PM	**Gut Microbiota-Mediated Enhancement of Anti-Colon Cancer Effects by Encapsulated Exopolysacharides and Fermented Perilla Leaf Extracts** Dr. Vijayalakshmi Selvakumar, University of Rocheste, Newyork, USA
12:30 PM - 01:30 PM	**LUNCH BREAK**
01:30 PM - 02:00 PM	**Computational Drug Discovery Pipelines for Rapid Identification of Anti-Infective Agents: From Structure to Simulation** Dr. Harshit Kumar Soni, Government PG College, Madhya Pradesh
02:00 PM - 02:30 PM	**Epitope Mapping of HBV Polyproteins for Multi-epitope Vaccine Design: A Reverse Vaccinology Approach** Dr. M. Karthikeyan, Alagappa University, Karaikudi
02:30 PM - 04:00 PM	**Scientific Session - Faculty**

Registration* - All participants should attend both days of the conference to receive their certificates.

7TH MICROSUMMIT - BIOINTELLIGENCE 2026

International Conference on Prediction, Prevention, and Management of Emerging Infectious Diseases

PROGRAMME SCHEDULE | 1st August, 2026

08:30 AM - 09:30 AM	**Scientific Session - PG (Session 2)**
09:30 AM - 10:00 AM	**Decoding Bioactive Peptides from Azadirachta indica: An Integrated Experimental and Computational Pipeline for Antioxidant Discovery** Dr. Raman Pachaiappan, SRMIST, Kattankulathur
10:00 AM - 10:30 AM	**Ruling Biophysical Tools in Modern Drug Designing** Dr. K. Gunasekaran, University of Madras, Chennai
10:30 AM - 10:45 AM	**Tea Break**
10:45 AM - 11:30 AM	**Role of Artificial Intelligence in Drug Discovery and Development** Prof. Dr. A. K. Gnanchandran, Ex Pharmacists Supervisor MOH KSA, Professor & Principal, Pranav Institute of Pharmaceutical Sciences and Research , Gwalior
11:30 AM - 12:00 PM	**Systems Biology Approach to Genome-Scale Modeling of Methanogens for Renewable Methane Production** Dr. R. Prathiviraj, Rajagiri College of Social Sciences, Kochi
12:00 PM - 12:30 PM	**Role of Artificial Intelligence, Machine Learning & Deep Learning in Drug Design and Discovery** Dr. P. Selvam, Mahatma Gandhi college of pharmacy, Tenkasi
11:00 AM - 12:30 PM	**Scientific Session - UG**
12:30 PM - 01:30 PM	**LUNCH BREAK**
01:30 PM - 03:00PM	**Valedictory Function**

BIOINTELLIGENCE 2026

7TH MICROSUMMIT

BIOINTELLIGENCE 2026
International Conference
on
Prediction, Prevention, & Management of Emerging Infectious Diseases

SCIENTIFIC SESSIONS

31st of July & 1st of August 2026

CATEGORY: FACULTY

Name of the delegate	Name of the Institution	Title
Dr PHILIP RAJ ABRAHAM	ICMR-NATIONAL INSTITUTE OF NUTRITION (NIN)	Next-Generation Diagnostic Approaches for Dengue NS1 Antigen Detection
Dr. GOBIANAND KUPPANNAN	NOORUL ISLAM COLLEGE OF DENTAL SCIENCES	Nanoparticle–Peptide Conjugates for Antibacterial Therapy
Ms. SANGEETHA S	SAVEETHA DENTAL COLLEGE	Phytochemical Analysis of Swietenia Macrophylla for Its Bioactive Components through Gas Chromatographic Mass Spectrometry (GCMS)
Mrs. DHANYA. S	NOORUL ISLAM COLLEGE OF DENTAL SCIENCES	Prevalence and Antimicrobial Resistance Profiles of Multidrug-Resistant (MDR) *Pseudomonas aeruginosa*
Mrs. NEETHU. S. S.	NOORUL ISLAM COLLEGE OF DENTAL SCIENCES	Nanotechnology and Antimicrobial Peptides: A Promising Strategy to Combat Antibiotic Resistance
Dr. ANUSHA BALASINGH	ETHIRAJ COLLEGE FOR WOMEN	Smart and Sustainable Management of Medical and Pharmaceutical Waste through Microbial and AI-Based Interventions: A Review
Dr. PRIYADHARSHINI R	SAVEETHA DENTAL COLLEGE	Integrated Molecular and Bioinformatics Evaluation of Epithelial-Mesenchymal Transition-Associated Biomarkers in Head and Neck Squamous Cell Carcinoma: A Systematic Review and Experimental Validation
Ms. JENNIFER PRINC	MEENAKSHI ACADEMY OF HIGHER EDUCATION & RESEARCH	The Rising Menace of Carbapenem-Resistant *Klebsiella pneumoniae*: Co-dominance of blaNDM, blaKPC and blaOXA-48 with Emerging blaVIM and blaIMP in a Tertiary Care Hospital

BIOINTELLIGENCE 2026

CATEGORY: RESEARCH SCHOLARS

Name of the delegate	Name of the Institution	Title
AJITHA P	AKG CIHS	Phytochemical characterization, Antibiofilm and wound healing activity of ethanolic extract of *Simarouba glouca*
Mrs ANURANJINI C	AKG CIHS	Phytochemical-driven antibiofilm effects of *Ruellia tuberosa* L. against *Escherichia coli* and *Klebsiella pneumonia*
Ms. ANJANA V K	SIMATS	Phytochemical Profiling and In Vitro Evaluation of Groundnut Skin Polyphenols for Antidiabetic and Anti-inflammatory Activities
Mr.ARUN MT	NOORUL ISLAM CENTRE FOR HIGHER EDUCATION	Bacteriophage derived endolysin as potential therapeutic agent against multi-drug resistant *Klebsiella pneumoniae* infection
MS.SIVASREE M	NOORUL ISLAM CENTRE FOR HIGHER EDUCATION	Study on the network pharmacology and *Candida glabrata* biofilm inhibitory potentials of *Metapenaeus dobsoni* derived astaxanthin
Mrs.SUMATHY DEVARAJAN	MEENAKSHI AMMAL DENTAL COLLEGE	Salivary Biomarkers as a Prognostic Aid in Oral Potentially Malignant Disorders and Oral Squamous Cell Carcinoma: A Cross-Sectional Study
Mr.G.RAJA	VISTAS	Significance of Point-of-Care Diagnostics in Rapid Disease Diagnosis
Mr. P ANANTHA KRISHNAN	VISTAS	Computational Screening of Phytochemical–Chitosan Nano-Conjugates Against WHO-Priority Pathogens in Contaminated Freshwater Ecosystems
Ms. M. RITHISHA	VISTAS	Antimicrobial Potential of Endophytic Fungi Isolated from Marine Macroalgae of the Southeast Coast of India
Mr. ARUN MT	NOORUL ISLAM CENTRE FOR HIGHER EDUCATION	Isolation and Characterization of a Novel Lytic Bacteriophage Against *bla*TEM-Producing Multidrug-Resistant *Klebsiella pneumoniae* Clinical Isolates: Implications for Phage Therapy Against ESBL Pathogens

BIOINTELLIGENCE 2026

CATEGORY: POSTGRADUATE STUDENTS

Name of the delegate	Name of the Institution	Title
S.SUVASHINI MATHIVANAN, JANANI V, B. DANAPOORNIMA	BHAKTAVATSALAM MEMORIAL COLLEGE FOR WOMEN	Targeting NF-κB Signaling to Combat Antimicrobial Resistance: A Molecular Approach
Ms. HARINI B	VISTAS	Production of eco-friendly antifungal liquid hand wash by using plant extract
Mr. SAMJABARAJ R	DG VAISHNAV COLLEGE	Studies on the Virulence and Biofilm Inhibitory Potentials of 3-Formylchromone Against Acinetobacter baumannii
Ms. RESHMA.B	ETHIRAJ COLLEGE FOR WOMEN	Antibacterial properties of Rhodococcus rhodochrous assisted silicon dioxide nanoparticles synthesized by sol gel method
Ms. SHINEY JENITA Y M	VISTAS	Isolation and characterization of endophytic bacteria from Ocimum sanctum (Tulsi) and Murraya koenigii (Curry leaves) for their antimicrobial potential against foodborne pathogens
Ms. DHANYASRI Y	ETHIRAJ COLLEGE FOR WOMEN	CRISPR-Cas Systems as Dual-Purpose Tools Against AMR in WHO Priority Pathogens: Bridging Rapid Resistance Diagnostics and Emerging Gene - Editing Therapeutics
Ms. FATHIMA MUNAVAR AHAMED BASHEER	SAVEETHA DENTAL COLLEGE	In Silico Design and Evaluation of a Multi-Epitope Vaccine Against Bluetongue Virus
Ms SHOBANA SHREE P	DG VAISHNAV COLLEGE	Comparative Bioinformatic Profiling of Human microRNAs Targeting Nipah and Hendra Virus Genomes
Ms. REVATHY.M	SAVEETHA DENTAL COLLEGE	Bioelectricity generation from banana and tomato waste using microbial fuel cell

BIOINTELLIGENCE 2026

CATEGORY: POSTGRADUATE STUDENTS

Name of the delegate	Name of the Institution	Title
Ms. DIVYADHARSHINI S	ETHIRAJ COLLEGE FOR WOMEN	From Reactive to Predictive: Integrating Artificial Intelligence and One Health Frameworks for Zoonotic Disease Surveillance in India
Ms. R.RAMYA	DG VAISHNAV COLLEGE	Pro Wheat: A Functional Probiotic Drink with Antimicrobial Potential
Ms. S. PRIYADHARSHINI	VISTAS	Exploring the Antimicrobial and Wound-Healing Potential of Mimosa pudica
MS.YUVASREE.D.S	DG VAISHNAV COLLEGE	Efficient adsorptive removal of heavy metals using sugarcane bagasse ash and chitosan composite biosorbent
Ms. SRI DEVI M	MMM COLLEGE OF HEALTH SCIENCE	Digital Epidemiology: AI and social media for disease outbreak prediction
Mr. S. MUKESH	DG VAISHNAV COLLEGE	Isolation and characterization of antimicrobial compound from soil derived Streptomyces and its application
Ms. POOJA S	SAVEETHA DENTAL COLLEGE	HLA-optimized multi-epitope vaccine design against nipah, marburg, lassa, ebola, and crimean-congo hemorrhagic fever viruses
Ms.BHAVATHAARANI U	ETHIRAJ COLLEGE FOR WOMEN	Metabolomic and Bioinformatic Insights into Chia Seed–Fortified Synbiotic Yoghurt: A Dietary Intervention for Preventing Emerging Infectious Diseases
Dr. RANJANA N.I	SAVEETHA DENTAL COLLEGE	Comparative Evaluation of Citrus reticulata-mediated Carbon Dots and Chitosan Nanoparticles as Potential Nanoparticles for Salivary α-Amylase-Based Forensic Biosensing

BIOINTELLIGENCE 2026

CATEGORY: UNDERGRADUATE STUDENTS

Name of the delegate	Name of the Institution	Title
Ms. HRUDHAYA K	VISTAS	Precision Medicine in Infectious Disease Management: Integrating Biomarkers and Artificial Intelligence for Personalized Therapeutics
Mr. S. MOHAN RAJ	VISTAS	AI-Assisted Drug and Vaccine Discovery Targeting the E1 and E2 Envelope Proteins of Chikungunya Virus
Ms. PRIYADARSHINI H, Ms SHRAVANI B	MMM COLLEGE OF ALLIED HEALTH SCIENCE	Deep learning in medical imaging for infectious disease diagnosis
Mr. JOSHIN	ALAGAPPA COLLEGE OF TECHNOLOGY	Artificial Intelligence in Infectious Disease Prediction: Advancing Public Health Surveillance
Mr. A R ADARSH	VISTAS	Artificial Intelligence in the Prediction, Early Detection, and Management of Tuberculosis
Ms. DHARSHINI G, Ms. B.R ADITHYA	MMM COLLEGE OF ALLIED HEALTH SCIENCE	CRISPR-Driven Antimicrobial Technologies for Combating Multidrug-Resistant Pathogens
Mr. K. RAJMOHAN	VISTAS	Malaria Prediction, Prevention, and Diagnosis: A Comparative Review of Conventional and AI-Based Methods
Mr. S.NISHAL	VISTAS	AI-Integrated Salivary Biomarker Analysis for Early Detection and Prevention of Periodontitis

Role of Artificial Intelligence in Drug Discovery and Development

Prof. Dr A. K. GNANCHANDRAN
Ex-Pharmacist Supervisor, MOH KSA
Professor & Principal, Pranav Institute of Pharmaceutical Sciences and Research, Gwalior.
Email ID: appiakrishnan@gmail.com

Abstract

Artificial intelligence (AI) has emerged as a transformative technology in drug discovery and development by accelerating research, improving decision-making, and reducing the time and cost associated with bringing new therapeutics to market. Conventional drug development is a lengthy, expensive, and high-risk process, often requiring more than a decade and billions of dollars to successfully develop a single drug. AI integrates machine learning, deep learning, natural language processing, computer vision, and predictive analytics to analyse vast biomedical datasets, identify novel drug targets, predict molecular interactions, optimize lead compounds, and support clinical decision-making. AI-driven platforms facilitate virtual screening of millions of chemical compounds, quantitative structure–activity relationship (QSAR) modelling, de novo drug design, drug repurposing, and prediction of pharmacokinetic and toxicological properties, thereby enhancing the efficiency and success rate of drug discovery. During preclinical and clinical development, AI assists in biomarker identification, patient stratification, clinical trial optimization, real-time monitoring, and personalized medicine by integrating genomic, proteomic, and clinical data. The application of AI has been particularly valuable in the rapid identification of therapeutic candidates for emerging diseases, including COVID-19, demonstrating its potential to address urgent global health challenges. Despite these advances, several challenges remain, including limited availability of high-quality datasets, algorithm transparency, data privacy, regulatory acceptance, model interpretability, and ethical considerations. Addressing these limitations through robust validation frameworks, standardised data-sharing practices, interdisciplinary collaboration, and regulatory guidance will be essential for broader clinical adoption. Overall, AI is revolutionising pharmaceutical research by enabling faster, more precise, and cost-effective drug discovery and development, paving the way toward precision medicine, innovative therapeutic strategies, and improved healthcare outcomes for diverse patient populations worldwide.

Keywords: Artificial intelligence, COVID-19, Drug discovery, QSAR

Emerging Infectious Diseases: Insights from SARS-CoV-2 and Re-emerging Arboviral Threats

CHANDRAMATHI SAMUDI[1*], GEISHAMINI[1], AMNI ADILAH[1]
Department of Medical Microbiology, Faculty of Medicine, Universiti Malaya, Kuala Lumpur, Malaysia.
Email: chandramathi@um.edu.my

Abstract

The emergence of SARS-CoV-2 and the continued burden of arboviral diseases such as dengue and Zika underscore the evolving challenges posed by RNA viruses to global health. While the COVID-19 pandemic transformed approaches to infectious disease surveillance, diagnostics, vaccine development, and pandemic preparedness, dengue remains a major public health concern due to its increasing incidence, complex immunopathogenesis, and limited therapeutic options. Although large-scale Zika outbreaks have declined, its epidemic potential, devastating congenital complications, and the absence of licensed vaccines or specific antiviral therapies continue to warrant sustained vigilance and preparedness. This talk will highlight key lessons learned from the COVID-19 pandemic and discuss how these can strengthen the prediction, prevention, and management of re-emerging arboviral diseases. Emphasis will be placed on viral evolution, genomic surveillance, host immune responses, biomarkers of disease severity, and advances in vaccine development. Recent research on SARS-CoV-2 genomic diversity and emerging variants, together with ongoing studies investigating endothelial dysfunction, metabolic comorbidities, and immune-mediated vascular leakage in dengue infection, will also be presented. By integrating insights from molecular biology, immunology, genomics, and translational research, this talk will demonstrate how multidisciplinary approaches can enhance preparedness for future outbreaks. Drawing on lessons from SARS-CoV-2 while addressing the ongoing burden of dengue and the future epidemic potential of Zika, it will provide a forward-looking perspective on strengthening global strategies for the prediction, prevention, and management of emerging infectious diseases.

Keywords: SARS-CoV-2, prediction, prevention, management

Epitope Mapping of HBV Proteins For Multi-Epitope Vaccine Design: A Reverse Vaccinology Approach

Dr. KARTHIKEYAN MUTHUSAMY
Professor, Department of Bioinformatics, Alagappa University, Karaikudi, Tamil Nadu, India
Research Officer, Tamil Nadu State Council for Higher Education (TANSCHE), Chennai, Tamil Nadu, India
Email ID: karthikeyanm@alagappauniversity.ac.in

Abstract

The hepatitis B virus (HBV) continues to be a major global public health concern, and its considerable genetic diversity contributes to differences in the course of the disease and the effectiveness of treatment. In this study, we employed a reverse vaccinology approach to identify potential multi-epitope vaccine candidates targeting eight major HBV genotypes (A–H), using a comprehensive in silico pipeline. Protein sequences (n = 111,128) representing HBe, HBx, HBc, Pol, LHBs, MHBs, and SHBs were retrieved from HBVdb, a curated database that excludes recombinant and low-quality entries. Genotypes I and J were not considered, as genotype I is a complex recombinant of multiple genotypes, and genotype J remains putative with only one known isolate. Redundancy in the protein dataset was minimized using CD-HIT at an 80% identity threshold, resulting in 21 representative proteins. Homology filtering against the human proteome (BLASTp, E-value ≤ 0.005) eliminated one human-homologous protein. The remaining 20 proteins were screened for antigenicity (AntigenPro, VaxiJen v2.0) and solubility (SolPro), leading to the selection of nine highly antigenic and soluble proteins for downstream epitope prediction. Using NetMHCpan 4.1, NetMHCIIpan 4.1 (IEDB MHC-II EL mode with full HLA reference set), and ABCPred, we predicted Cytotoxic T Lymphocyte (CTL), Helper T Lymphocyte (HTL), and B-cell epitopes, respectively. Post-filtering based on antigenicity, allergenicity, immunogenicity, toxicity, and IFN-γ induction, a total of 134 epitopes were shortlisted: 50 CTL, 40 HTL, and 44 B-cell epitopes. Combined population coverage of CTL and HTL epitopes reached 99.92% globally and 99.95% for the Indian population, indicating broad immunological relevance. This study provides a robust foundation for the design of a universal HBV vaccine. Further work including vaccine construct assembly, structural modelling, and molecular dynamics simulations is necessary to validate these findings structurally and dynamically and advance toward preclinical development.

Keywords: Hepatitis B virus, epitopes, in silico, molecular dynamics

Responsive Nanomedicine and Biofilm Models for Future Infection Control

ROHAN M. SHAH[1,2]

[1] Department of Chemistry and Biotechnology, Swinburne University of Technology, Hawthorn, Melbourne, Australia

[2] Iverson Health Innovation Research Institute, Swinburne University of Technology, Hawthorn, Melbourne, Australia

Email ID: rshah@swin.edu.au

Abstract

The growing threat of antimicrobial resistance and persistent infections demands innovative therapeutic strategies that move beyond conventional antimicrobial approaches. Advances in nanomedicine and biointerface engineering are creating new opportunities to develop responsive systems capable of delivering therapeutic agents with greater precision, efficacy, and safety. This plenary lecture will present recent advances in the design of targeted nanoparticles, antimicrobial nanovesicles, and engineered biointerfaces for infection control applications. Drawing on examples from biomaterials, nanomedicine, and translational bioengineering, the presentation will highlight how surface-driven design principles can be harnessed to improve interactions between therapeutic systems, host tissues, and microbial communities. These approaches enable the development of next-generation technologies for combating infection, reducing treatment burden, and improving clinical outcomes. The lecture will also briefly discuss the role of biologically relevant biofilm models as platforms for evaluating emerging antimicrobial technologies and understanding their performance within complex infection environments. By integrating responsive material design with clinically relevant testing approaches, new pathways are emerging for the prevention, diagnosis, and treatment of infectious diseases. These advances illustrate how responsive nanomedicine can help address some of the most pressing challenges in infection control, offering opportunities for more targeted, effective, and sustainable healthcare solutions in the era of antimicrobial resistance.

Keywords: Antimicrobial resistance, infection, antimicrobial nanovesicles, bioengineering

Gut Microbiota-Mediated Enhancement of Anti-Colon Cancer Effects by Encapsulated Exopolysaccharides and Fermented Perilla Leaf Extracts

VIJAYALAKSHMI SELVAKUMAR
Department of Immunology & Microbiology,
University of Rochester, Rochester, New York, USA
Email ID: Vijayalakshmi_Selvakumar@URMC.Rochester.edu

Abstract

Colorectal cancer (CRC) imposes a substantial global health challenge due to its high rates of morbidity and mortality, highlighting the urgent need for new and innovative treatments. This study investigates the enhanced anti-colon cancer effects of encapsulated exopolysaccharides (ECM) derived from *Limosilactobacillus reuteri* and fermented *Perilla* leaf extracts (FPLE) utilizing *Lactobacillus fermentum* (562), with a focus on their impact on gut microbiota modulation. SEM analysis revealed that EPS particles had varying sizes and shapes, while FPLE demonstrated an increased polyphenol content, enhancing its anti-colon and anti-inflammatory activities. FTIR spectra confirmed the successful encapsulation of polyphenols onto Exopolysaccharides (EPS), and particle size analysis indicated effective encapsulation and stability. The encapsulation efficiency was 77.79%, with significant release profiles observed under simulated gastrointestinal conditions, particularly in the colonic phase, suggesting targeted release. In laboratory experiments, ECM was found to decrease the viability of CaCo2 cells and lower the release of pro-inflammatory cytokines in RAW 264.7 cells. In animal studies, ECM treatment improved symptoms of colitis induced by AOM/DSS and influenced the balance of gut microbiota, promoting beneficial bacteria while reducing pathogens linked to cancer risk. This study utilized an early-stage, acute colitis-associated CRC mouse model to assess therapeutic effects. The focus of this study is to explore the synergistic anti-colon cancer potential of encapsulated EPS and FPLE through modulation of gut microbiota.

Keywords: Colorectal cancer (CRC); Exopolysaccharides; *Perilla* leaf extract; *Limosilactobacillus reuteri; Lactobacillus fermentum;* gut microbiota

From Prediction to Preparedness: A Translational Intelligence Framework for Emerging Infectious Diseases

HARSHIT KUMAR SONI
HOD, Department of Biotechnology, Government PG College, Satna
Email ID: hksoni2003@gmail.com

Abstract

Emerging infectious diseases evolve faster than conventional biomedical response systems. The COVID-19 pandemic responsible, for more than seven million confirmed deaths and an estimated $8–16 trillion in global economic losses, exposed with catastrophic clarity the structural inadequacy of reactive drug and vaccine development pipelines. A fundamentally different preparedness architecture is required: one that integrates predictive surveillance, systems biology, multi-omics intelligence, structural biology, artificial intelligence, and adaptive clinical translation into a continuously learning biological ecosystem that operates before, during, and after outbreak emergence. This review introduces and develops the Translational Intelligence Framework (TIF), an integrated preparedness ecosystem comprising six mutually reinforcing pillars: (I) genomic and ecological predictive surveillance; (II) host-pathogen network biology and interactomics; (III) multi-omics intelligence integrating genomic, transcriptomic, proteomic, metabolomic, and single-cell spatial data; (IV) structural biology and computational chemistry enabled by AlphaFold2/3, cryo-EM, and protein language models; (V) AI-driven vaccine and therapeutic design including generative molecular diffusion models; and (VI) adaptive clinical translation incorporating platform trial designs and precision endotype stratification.

We demonstrate that computational intelligence is not one technology among many but the integrating infrastructure through which biological knowledge generated at any stage of the preparedness continuum flows automatically to every other stage, enabling the system to improve with every pathogen it encounters. Drawing on landmark studies including the SARS-CoV-2 host-pathogen interactome (Gordon et al., Nature, 2020), the AlphaFold revolution (Jumper et al., Nature, 2021), the clinical validation of nirmatrelvir (Owen et al., Science, 2021; Hammond et al., NEJM, 2022), the AI- guided repurposing of baricitinib (Stebbing et al., EMBO Mol Med, 2020; Kalil et al., NEJM, 2021), and the AI discovery of halicin and abaucin (Stokes et al., Cell, 2020; Wong et al., Nature Chemical Biology,

2023), we establish that the TIF has already delivered clinically transformative therapeutics. A novel conceptual isomorphism between computational oncology and computational infectiology — demonstrating direct transferability of driver gene analysis, tumor microenvironment modeling, synthetic lethality, and resistance evolution frameworks — is developed as a strategic cross-disciplinary resource. Critical evaluation of computational limitations, including mechanistic analysis of the hydroxychloroquine and ivermectin failures, provides the epistemic grounding for responsible framework deployment. Future directions encompassing genomic foundation models (Evo2), next-generation protein design (RFdiffusion, ProteinMPNN, Chai-1, Boltz-1), autonomous laboratories, digital twins, and precision infectious disease endotyping define the scientific agenda through which the continuously learning preparedness ecosystem will reach its full realisation.

Keywords: Translational Intelligence Framework; emerging infectious diseases; computational drug discovery; host-pathogen interactomics; network pharmacology; AlphaFold; artificial intelligence; pandemic preparedness; multi-omics integration; host-directed therapeutics; structural vaccinology; antimicrobial resistance

Implementation of Artificial Intelligence in Systems Biology for Advanced Biomethanation Technologies

RADHAMANALAN GUHANRAJ[1], RAGOTHAMAN PRATHIVIRAJ[2*]
Department of Microbiology, Saveetha Dental College, Chennai, Tamil Nadu, India
Division of Bioinformatics and Systems Biology, Department of Biosciences, Rajagiri College of Social Sciences, (Autonomous), Rajagiri P.O., Kalamassery, Kochi-683104, India
Email ID: prathiviraj@rajagiri.edu

Abstract

Artificial Intelligence (AI), a new paradigm, is changing the face of systems biology and is now able to accurately predict, reconstruct, and optimize microbial metabolism for sustainable biomethanation. In this work, we propose an integrated approach that integrates genome annotation, genome-scale metabolic reconstruction, constraint-based modeling and machine learning to enhance the production of methane from carbon dioxide. High-quality Genome interpretation tools such as AI-assisted annotation tools (DeepEC, DRAM, Prokka, ESM2) and automated metabolic network reconstruction tools (ModelSEED, CarveMe, KBase) are available. Flux balance analysis, flux variability analysis, and parsimonious FBA are employed to analyze these genome-scale metabolic models to infer metabolic behavior. Metabolic engineering targets, bottleneck reactions, flux distributions, and methane yield and growth rate are predicted using machine learning algorithms such as Random Forests, XGBoost, and Graph Neural Networks. AI-driven optimization and synthetic pathway design through CRISPR-based methods combined with experimental validation and digital twin modelling create a powerful toolset for the efficient construction of microbial cell factories for carbon dioxide bioconversion into renewable methane that will aid future carbon-neutral bioenergy technologies. Moreover, AI-driven metabolic engineering, synthetic pathways design, experimental validation, and digital twin modelling all represent a complete AI toolbox for designing efficient microbial cell factories that convert carbon dioxide to renewable methane, helping to achieve sustainable biomethanation and future carbon-neutral bioenergy technologies.

Keywords: Artificial Intelligence; DeepEC; Metabolic model; Systems biology; Biomethanation

Decoding Bioactive Peptides from *Azadirachta indica:* An Integrated Experimental and Computational Pipeline for Antioxidant Discovery

Dr. PACHAIAPPAN RAMAN

Department of Biotechnology, School of Bioengineering, Faculty of Engineering and Technology, SRM Institute of Science and Technology, Kattankulathur - 603 203, Tamil Nadu, India

Abstract

Azadirachta indica (neem) occupies a prominent place in the Indian traditional system of medicine because of its antiviral, antimicrobial, insecticidal, and antiparasitic properties. While neem phytochemicals such as azadirachtin and nimbin have been extensively investigated, its peptide repertoire remains largely unexplored despite its considerable therapeutic potential.

In this study, peptide-rich fractions were isolated from neem shoot apex, flowers, and defatted seed meal using membrane-based ultrafiltration. Peptide profiling by reverse-phase HPLC coupled with MALDI-TOF mass spectrometry identified several biologically significant peptides and proteins, including antifungal proteins (AFP1–AFP3), defensins, agglutinins, cyclotides, cytokinin dehydrogenase, 14-3-3 proteins involved in growth regulation, and peptides with reported anticancer potential. The antioxidant capacity of the peptide-rich fractions was comprehensively evaluated using DPPH, ABTS, nitric oxide scavenging (NOS), and ferric reducing antioxidant power (FRAP) assays. The fractions exhibited strong free radical scavenging and reducing activities, indicating their ability to restore cellular redox homeostasis, mitigate reactive oxygen species (ROS)-induced lipid peroxidation, and attenuate hepatic inflammation. The exceptional stability of cysteine-rich peptides, particularly cyclotides and defensins, further supports their potential as hepatoprotective biomolecules.

To expand the repertoire of candidate bioactive peptides, an integrated computational workflow was developed. Peptide mass fingerprinting generated a diverse peptide library, which was further enriched through ***in silico*** proteolytic digestion using a parallel peptide-cutter strategy. Both experimentally identified peptides and computationally generated fragments underwent redundancy filtering, physicochemical characterization, bioactivity prediction, toxicity and allergenicity assessment using ToxinPred and AllerTOP, functional annotation against PubChem and ChEMBL, and integrated scoring through an automated peptide analysis pipeline.

The ***in silico*** digestion strategy substantially increased peptide diversity and significantly expanded the pool of safe, bioactive candidates. Functional annotation revealed peptides with promising antioxidant, hepatoprotective, immunomodulatory, and regenerative properties. Collectively, these findings establish neem-derived peptides as a previously underutilized reservoir of therapeutic molecules with considerable potential for combating oxidative hepatic injury and promoting tissue repair. The identified peptide candidates provide a strong foundation for future mechanistic investigations and ***in vitro*** and ***in vivo*** validation toward the development of peptide-based detoxification and regenerative therapeutics.

Keywords: Neem, Meristem, CLE peptide, Ultrafiltration, Shoot apex

Ruling Biophysical Tools in Modern Drug Designing

Dr. K. GUNASEKARAN
CAS IN Crystallography and Biophysics, University of Madras,
Guindy Campus, Chennai – 600025
Email ID: gunaunom@gmail.com, gunabiophy@unom.ac.in.

Abstract

The modern-day drug discovery process is Structure-driven. In every such effort, 3D structures of the protein target and drug-like compounds, along with their intermolecular interactions, are exploited to design effective drugs. X-ray crystallography is the ultimate tool for determining protein 3D structures, thereby elucidating the mechanism of action of these biomolecules. Though biochemical assays play a vital role, biophysical tools such as ITC and SPR could explain the nature of proteins in solution state and the mode and stability of binding as well. In our lab, structural analysis of lectins revealed a new mode of sialic acid binding that we could confirm using ITC, which ruled out the classical assumption that mannose binding and sialic acid binding are the same mode. The crystal structure of a plant chitinase could be determined, through which the presence and conformation of an intact chitinase domain is established. When treated with a protease inhibitor, though inhibition could be achieved in the live parasite, longer treatment could enable the mosquito parasite to overcome such protease inhibition. From crystal soaking experiment, a new paradigm that lectins could not only bind carbohydrates but any molecule with vicinal diol could be realized, verified and documented. Formation of non-covalent enzyme-product complex during inhibitor treatment could be evidenced with filarial parasite protease.

Keywords: Drugs, Enzyme, Protein, Microbes

Recent Advances in AI /ML/DS in Drug Design and Discovery

Dr. P. Selvam
Antiviral Research Society AVRS Srivilliputtur

Abstract

AI is intelligence created by machines, similar to the brain; machine learning is training machines for intelligent functions; and Data science is the collection of data, networks, or a galaxy of data storage. In this presentation use of AI ML and DS used in design and development of Antiviral agent-anti HIV drug discovery large data base of molecule selected from Zinc and Pub Chem data base and performed for docking with HIV integrase pharmacokinetic and toxicity studied with AI methods also specific binding with HIV Integrase - LEDGF interaction studied by using machine learning process to refine lead molecule isatins derivatives. From the above research study, compound SPIII 5H was optimised as a potential anti HIV drug with inhibition of HIV integrase-LEDGF as a novel target for HIV drug discovery.

Keywords: Drug design, Drug discovery, HIV

Next-Generation Diagnostic Approaches for Dengue NS1 Antigen Detection

Dr. PHILIP RAJ ABRAHAM

Scientist – D, Pathology and Microbiology Division, ICMR-National Institute of Nutrition, Hyderabad

Email ID: philipicmrningmail.com

Abstract

Dengue is a major mosquito-borne viral disease, causing an estimated 400 million infections annually, with nearly 70% of cases occurring in Asia. Early diagnosis is essential for timely clinical management and effective disease surveillance. The dengue virus non-structural protein 1 (NS1), a highly conserved 48-kDa glycoprotein secreted during the early stages of infection, serves as an important biomarker for early dengue diagnosis. Our research was focused on developing and evaluating innovative platforms for NS1 antigen detection. Initially, commercially available NS1 antigen ELISA kits, including Dengue NS1 Ag Microlisa, DENV Detect™ NS1 ELISA, and Merilisa i Dengue NS1 Antigen, were evaluated for detecting recombinant NS1 antigen spiked into *Aedes aegypti* mosquito homogenates, demonstrating their applicability for vector surveillance (Abraham et al., 2021, 2022, 2024). To overcome the limitations of monoclonal antibody-based assays, we purified polyclonal antibodies generated against dengue NS1 antigen from individuals who recovered from the dengue infection and developed in-house immunoassays using Human Polyclonal Antibodies against Dengue (HPAD) and also developed the Rabbit Polyclonal Antibodies against Dengue (RPAD) assay for sensitive NS1 antigen detection (Abraham et al., 2025 and 2026). We further explored Aptamers, which are most commonly known as synthetic antibodies and developed an Aptamer-Linked Immobilized Sorbent Assay (ALISA) for NS1 detection in mosquito pools. In addition, an Enzyme-Linked Lectin Assay (ELLA) employing plant lectins was developed and evaluated for sensitivity across dengue virus serotypes and specificity against NS1 antigens of other flaviviruses. These studies demonstrate the potential of antibody, aptamer, and lectin-based platforms as innovative, reliable alternatives to conventional dengue NS1 antigen assays. These next-generation diagnostic approaches for Dengue NS1 antigen detection could significantly improve early dengue diagnosis, mosquito surveillance, and public health preparedness in dengue-endemic regions.

Keywords: Biomarker, Dengue, ELISA, Diagnosis

Nanoparticle–Peptide Conjugates for Antibacterial Therapy

Dr. GOBIANAND KUPPANNAN

Reader, Department of Microbiology, Noorul Islam College of Dental Sciences, NIMS Medicity, Thiruvananthapuram – 695123. Kerala

Email ID: rajgobi@gmail.com

Abstract

Marine invertebrates were explored as sources of antimicrobial peptides (AMPs) with activity against ESKAPE pathogens. Crude extracts from crab (*Portunus sanguinolentus*), octopus (*Octopus indicus*), mussel (*Perna viridis*), and squid (*Loligo duvauceli*) exhibited inhibition zones ranging from 8.33–15.33 mm, with squid extracts showing the broadest activity and highest AMP recovery. Purified squid fractions revealed Fraction-3 as the most potent, with a minimum inhibitory concentration of 30 µg/ml. Green synthesis of silver nanoparticles (AgNPs) was confirmed by UV-Vis (412 nm peak), DLS (~51.3 nm), FT-IR (hydroxyl and carboxylate groups), SEM, and TEM analyses. Conjugation with AMPs produced AgNP-AMP complexes of larger, irregular morphology (66.53–84.24 nm). These conjugates demonstrated enhanced antibacterial activity (12.66–24.33 mm) against all ESKAPE pathogens, comparable to ciprofloxacin, and showed high biocompatibility in L929 fibroblast assays (>99% viability at 10 µg). From 83 wound swabs, predominant isolates included *Staphylococcus aureus* and *Escherichia coli*. Wound dressing materials coated with AgNP-AMP conjugates exhibited strong antibacterial activity (30.33–33.66 mm zones) and supported fibroblast adhesion, confirming biocompatibility. Loligo duvauceli AMP–AgNP conjugates and coated wound dressings demonstrated potent activity against MDR ESKAPE pathogens and promoted wound healing, highlighting their potential as novel therapeutic agents.

Keywords: Marine invertebrate AMPs, AgNP–AMP conjugates, ESKAPE pathogens, *Loligo duvauceli*, Multidrug resistance (MDR)

Phytochemical Analysis of Swietenia Macrophylla for Its Bioactive Components through Gas Chromatographic Mass Spectrometry (GCMS)

Ms. S. SANGEETHA

Assistant Professor, Department of Anatomy, Saveetha Dental College and Hospitals, Saveetha Institute of Medical and Technical Sciences, Chennai

Email ID: sangeethas.sdc@saveetha.com

Abstract

Swietenia macrophylla King is an endangered species of plant in the Meliaceae family and a medicinally important plant indigenous to tropical and subtropical regions of the world. *S. macrophylla* has been widely used in Asia and many other countries to treat various ailments based on its antimicrobial, anti-inflammatory, antioxidant effects, antimutagenic, anticancer, antitumour, antidiabetic and also in cardiovascular diseases. The seeds are used traditionally to treat wounds, hypertension, diabetes, malaria, cardiovascular diseases and to relieve pain. However the bioactive components of this seed are not yet established completely. In the present study, the ethanol extract of this seed was subjected to phytochemical qualitative analysis through Gas Chromatographic Mass Spectrometry (GCMS) and the bioactive components were identified.The analysis revealed the presence of flavonoid, tannins, alkaloid, glycosides, terpenoids, steroids and carbohydrates.The detection of these bioactive constituents in the plant extract may provide scientific validation for its diverse pharmacological activities and therapeutic potential.

Keywords: Bioactive compound, Plants, Therapeutic

Prevalence and Antimicrobial Resistance Profiles of Multidrug-Resistant (MDR) *Pseudomonas aeruginosa*

DHANYA. S*

Senior Lecturer, Department of Microbiology, Noorul Islam College of Dental Sciences, NIMS Medicity, Thiruvananthapuram – 695123. Kerala

Email ID: dhansidh@gmail.com

Abstract

Pseudomonas aeruginosa remains a leading cause of severe nosocomial (hospital-acquired) infections, including ventilator-associated pneumonia and catheter-associated urinary tract infections. The global rise of multidrug-resistant (MDR) and extensively drug-resistant (XDR) strains severely limits definitive therapeutic options, drastically increasing patient morbidity and healthcare costs. This study aimed to determine the prevalence, antibiotic resistance profiles, and phenotypic detection of beta-lactamase production among P. aeruginosa clinical isolates recovered from a tertiary care hospital. A total of 120 clinical specimens (pus, sputum, urine, blood) were processed. *P. aeruginosa* was identified by culture, Gram stain, biochemical tests, and pigment production on cetrimide agar. Antimicrobial susceptibility was assessed using Kirby-Bauer disk diffusion per clinical guidelines. Isolates resistant to ≥1 drug in ≥3 classes were defined as MDR. ESBL and MBL production were detected phenotypically using combined disk tests. Out of 45 *P. aeruginosa* isolates, 37.8% were MDR. Highest resistance was to ceftazidime (64.4%) and ciprofloxacin (55.6%), while amikacin and piperacillin-tazobactam were most effective. ESBL was detected in 22.2% and MBL in 13.3% of isolates. MDR *P. aeruginosa* with co-resistance to key drugs underscores the urgent need for routine surveillance, strict infection control, and strong antibiotic stewardship.

Keywords: *Pseudomonas aeruginosa,* ESBL, MBL, Carbapenems

Nanotechnology and Antimicrobial Peptides: A Promising Strategy to Combat Antibiotic Resistance

NEETHU. S. S

Senior Lecturer, Department of Pharmacology, Noorul Islam College of Dental Sciences, NIIMS Medicity, Athiyanoor, Neyyatinkara, Thiruvananthapuram, Kerala – 695123.

Email ID: neethusathiadas07@gmail.com

Abstract

The rapid escalation of multidrug-resistant (MDR) bacterial pathogens poses a catastrophic threat to global healthcare, rendering conventional antibiotics increasingly ineffective. To prevent a post-antibiotic era, novel therapeutic paradigms are urgently required. Antimicrobial peptides (AMPs) have emerged as highly promising candidates due to their broad-spectrum activity and low propensity for inducing resistance, primarily mediated by physical membrane disruption. However, the clinical translation of native AMPs is severely bottlenecked by systematic limitations, including poor metabolic stability, high cytotoxicity, and rapid systemic clearance. Nanotechnology offers a transformative strategy to overcome these hurdles. By engineering advanced nanocarriers—such as liposomes, polymeric nanoparticles, solid lipid nanoparticles, and metallic nanostructures —AMPs can be effectively shielded from proteolytic degradation, ensuring targeted delivery and sustained release at infection sites. Furthermore, the synergistic integration of AMPs with inherently antimicrobial nanomaterials (e.g., silver or gold nanoparticles) has demonstrated augmented bactericidal efficacy, successfully disrupted recalcitrant biofilms and lowering individual therapeutic doses. This review/study highlights the recent advancements in AMP-nanoparticle formulation strategies, elucidates their dual mechanisms of action against resistant strains, and discusses the current translational challenges, emphasizing nanomaterial toxicity and regulatory hurdles, that must be addressed to unlock the full potential of this next-generation antimicrobial platform.

Keywords: Antimicrobial Peptides, Nanotechnology, Antibiotic Resistance, Nanocarriers, Biofilms, Synergistic Therapeutics

Smart and Sustainable Management of Medical and Pharmaceutical Waste through Microbial and AI-Based Interventions: A Review

Dr. ANUSHA BALASINGH

Associate Professor Department of Microbiology, Ethiraj college for Women, Chennai, Tamil Nadu, India

Email ID: anushabalasingh@ethirajcollege.edu.in

Abstract

The rapid expansion of healthcare systems and pharmaceutical industries has led to a significant increase in biomedical and pharmaceutical waste, posing severe environmental and public health risks. Conventional waste treatment methods such as incineration and landfilling often result in secondary pollution, including toxic emissions and persistent chemical residues. Hence sustainable and innovative approaches integrating microbial biotechnology and artificial intelligence (AI) have emerged as promising alternatives. Microbial waste management utilizes bacteria, fungi, and algae capable of degrading complex pharmaceutical compounds, antibiotics, and hazardous organic materials through processes such as bioremediation, biodegradation, and biosorption. Specific microbial strains, including *Pseudomonas spp.*, *Bacillus spp.*, and white-rot fungi, have demonstrated efficiency in breaking down active pharmaceutical ingredients, reducing toxicity, and restoring environmental quality. Additionally, microbial consortia and genetically engineered microorganisms enhance degradation efficiency and adaptability to diverse waste streams. Parallelly, AI-driven technologies play a transformative role in optimizing waste management systems. Machine learning algorithms, computer vision, and IoT-enabled smart systems facilitate real-time waste segregation, classification, and monitoring. AI models can predict waste generation patterns, identify hazardous components, and optimize treatment pathways, thereby improving operational efficiency and regulatory compliance. Integration of AI with robotics enables automated sorting of biomedical waste, minimizing human exposure to infectious materials. The convergence of microbial biotechnology and AI offers a holistic, eco-friendly, and cost-effective framework for managing medical and pharmaceutical waste.

Keywords: Biomedical waste management, Pharmaceutical waste, Microbial bioremediation Biodegradation Artificial intelligence (AI), Machine learning

Integrated Molecular and Bioinformatics Evaluation of Epithelial-Mesenchymal Transition-Associated Biomarkers in Head and Neck Squamous Cell Carcinoma: A Systematic Review and Experimental Validation

Dr. R. PRIYADHARSHINI
Reader, Department of General Pathology, Saveetha Dental College and Hospitals
SIMATS, Chennai
Email ID: priyadharshinir.sdc@saveetha.com

Abstract
Head and neck squamous cell carcinoma (HNSCC) is an aggressive malignancy characterized by tumour heterogeneity, local invasion, lymph node metastasis, and poor survival. Although conventional clinicopathological staging remains the standard for disease assessment, it inadequately reflects the underlying molecular alterations that drive tumour progression. This study combined a systematic review with molecular validation and bioinformatics analyses to evaluate epithelial–mesenchymal transition (EMT)-associated biomarkers and their potential diagnostic and prognostic significance in HNSCC. A systematic review was conducted following the PRISMA 2020 guidelines using PubMed, Scopus, and Web of Science databases to identify studies investigating EMT-associated biomarkers in HNSCC. Methodological quality was assessed using the QUIN tool. In parallel, thirty-four paired HNSCC and adjacent non-tumour tissue samples were analysed for mRNA expression using quantitative real-time PCR. Integrated bioinformatics analyses were performed using TCGA datasets through UALCAN and cBioPortal to evaluate gene expression, genomic alterations, clinicopathological associations, and survival outcomes. Protein–protein interaction networks were analysed using STRING, while candidate regulatory microRNAs were identified using miRDB. The systematic review demonstrated consistent dysregulation of EMT-associated biomarkers, with altered expression strongly associated with tumour invasion, lymph node metastasis, recurrence, and poor clinical outcome. Molecular validation confirmed significant overexpression of the investigated biomarkers in HNSCC tissues compared with adjacent normal tissues despite relatively infrequent genomic alterations. Increased expression correlated with advanced tumour stage and histological grade. Protein interaction analysis identified interconnected signalling networks regulating epithelial–mesenchymal transition, extracellular matrix remodelling, and metastatic pathways, while microRNA analysis revealed several potential post-transcriptional regulators. Survival analysis demonstrated variable prognostic significance across the investigated biomarkers. The integration of systematic review evidence with molecular and bioinformatics analyses provides comprehensive evidence that EMT-associated biomarkers contribute substantially to HNSCC progression. Combined biomarker assessment offers greater potential for prognostic stratification than individual markers and may facilitate the development of precision-based diagnostic and therapeutic strategies. Further multicentre validation is required before clinical implementation.

Keywords: Head and Neck Squamous Cell Carcinoma (HNSCC), Epithelial–Mesenchymal Transition (EMT), Molecular Biomarkers, Bioinformatics Analysis, Prognostic Biomarker

The Rising Menace of Carbapenem-Resistant *Klebsiella pneumoniae*: Co-dominance of blaNDM, blaKPC and blaOXA-48 with Emerging blaVIM and blaIMP in a Tertiary Care Hospital

JENNIFER PRINCY R[1,2], JAIDEEP MAHENDRA[3]

[1,2]Assistant Professor, Department of Microbiology, Meenakshi Ammal Dental College and Hospital, Chennai, Tamilnadu, India.

E mail: jenniferprincy@gmail.com

[3]Professor, Department of Microbiology, Meenakshi Ammal Dental College and Hospital, Chennai, Tamilnadu, India

E mail ID: jaideep_m_23@yahoo.co.in

Abstract

Increase in the prevalence of Carbapenem-resistant *Klebsiella pneumoniae* (CR-Kp) has become a serious cause of concern in healthcare settings, due to limited treatment options and high mortality rates. This study aimed to determine the prevalence, phenotypic resistance patterns, and molecular characteristics of CR-Kp isolates. A total of 150 *Klebsiella pneumoniae* isolates from various samples were subjected to antibiotic susceptibility testing. Phenotypic detection of carbapenemase production was performed using the modified carbapenem inactivation method (mCIM), and eCIM. Genotypic analysis using Real Time PCR was performed on 53 representative CR-Kp isolates to detect *bla*^{NDM}, *bla*^{KPC}, *bla*$^{OXA-48}$, *bla*^{IMP}, and *bla*^{VIM} genes. Out of 150 *K. pneumoniae* isolates, 53 (35.33%) were carbapenem-resistant based on Kirby-Bauer disc diffusion method. Phenotypic methods detected carbapenemase activity in 34% using mCIM and 29.33% using eCIM of *K. pneumoniae* isolates. Genotypic testing revealed *bla*$^{OXA-48}$ in 69.51%, *bla*^{NDM} in 60.3% and *bla*^{KPC} in 66.04% of the tested isolates, with *bla*^{VIM} detected in 18.87% and *bla*^{IMP} genes in 3.33% of isolates. CR-Kp isolates exhibited high resistance to fluoroquinolones, cephalosporins, and aminoglycosides. The high prevalence of *bla*^{NDM}, *bla*$^{OXA-48}$, bla^{KPC} mediated carbapenem resistance in *K. pneumoniae* highlights genetic diversity of carbapenem resistance mechanisms circulating in the study setting. The significant occurrence of rarely reported *bla*^{IMP} and *bla*^{VIM}, in addition to the commonly reported *bla*^{NDM} and blaOXA-48, indicates the emergence and dissemination of multiple carbapenemase determinants among clinical isolates. Routine molecular surveillance and robust infection control measures are urgently needed to curb the spread of CR-Kp in clinical outcomes.

Keywords: Carbapenem resistant, *Klebsiella pneumoniae*, Disc Diffusion method, Phenotypic analysis, Real Time PCR, Molecular surveillance.

Phytochemical characterization, Antibiofilm and wound healing activity of ethanolic extract of *Simarouba glouca*

[1]AJITHA P, [2]Dr R V GEETHA

[1]Department of Medical Microbiology, AKG Co-Operative Institute of Health Sciences (AKG CIHS), Mavilayi, Kannur

[2]Professor, Department of Microbiology, Saveetha Dental College & Hospital, SIMATS

Email ID: ajitharajithkumar@gmail.com

Abstract

Simarouba glauca is a medicinal plant rich in phytochemicals that has been traditionally used for the treatment of various infectious and inflammatory disorders. Chronic wound infections are frequently associated with microbial biofilm formation, which enhances antimicrobial resistance and delays the wound-healing process. This presentation explores the role of phytochemical constituents of the ethanolic extract of Simarouba glauca and evaluate its antibiofilm and wound-healing activities using in vitro assays. The ethanolic extract of Simarouba glauca was subjected to preliminary phytochemical screening using standard qualitative methods to identify major secondary metabolites. Antibiofilm activity was evaluated against selected bacterial pathogens using a crystal violet microtiter plate assay, and the percentage inhibition of biofilm formation was determined spectrophotometrically. Preliminary phytochemical analysis revealed the presence of several bioactive constituents, including alkaloids, flavonoids, phenolic compounds, tannins, terpenoids, saponins, steroids, and glycosides. The ethanolic extract demonstrated significant inhibition of bacterial biofilm formation, indicating its ability to interfere with microbial adhesion and biofilm development. In the scratch wound healing assay, treatment with the extract enhanced cell migration and accelerated wound closure compared with the untreated control, suggesting improved cellular proliferation and tissue repair. Overall, these findings suggest that the extract has potential as a natural therapeutic agent for the management of biofilm-associated wound infections.

Keywords: Phytochemical, Antibiofilm, Therapeutic

Phytochemical-driven antibiofilm effects of *Ruellia tuberosa* L. against *Escherichia coli* and *Klebsiella pneumonia*

ANURANJINI CHARACKAL[1], ARUN BASKARAPILLAI[2], GEETHA ROYAPURAM VEERARAGAVAN[3]

[1]Department of Medical Microbiology, AKG Co-Operative Institute of Health Sciences (AKG CIHS), Mavilayi, Kannur, Kerala 670622, India;
[2]Department of Biotechnology and Microbiology, Janakiammal Campus, Kannur University, Kannur, Kerala 670002, India;
[3]Department of Microbiology, Centre for Infectious Diseases, Saveetha Dental College and Hospitals, Saveetha Institute of Medical and Technical Sciences (SIMATS), Saveetha University (Deemed to be University), Chennai, Tamil Nadu 600077, India
Email ID: anuranjinic@gmail.com

Abstract

Multidrug-resistant Gram-negative pathogens, including *Escherichia coli* (E. coli) and *Klebsiella pneumoniae* (K. pneumoniae) represent major clinical concerns due to their potent biofilm-forming ability and associated virulence traits that contribute to persistent infections and antibiotic failure. Bacterial biofilms consist of organized populations of microorganisms embedded within a self-produced extracel-lular polymeric matrix (EPS), enabling surface attachment and conferring substantial resistance to antimicrobial agents and host immune defense. Among these pathogens, Gram-negative bacteria characterized by their lipopolysaccharide rich outer membrane and intrinsic resistance mechanisms are particularly challenging. Notably, *Escherichia coli* (E. coli) and *Klebsiella pneumoniae* (K. pneumoniae) are key Gram-negative species commonly associated with infections of the urinary tract, respiratory system, bloodstream and indwelling medical devices, particularly among hospitalized or immunocompromised individuals. In response to the growing limitations of conventional antibiotics against biofilm-associated infections, the present study evaluated the antibiofilm potential of the ethanolic leaf extract of Ruellia tuberosa L. (R. tuberosa L.) using in vitro assays. The extract demonstrated antibacterial activity at the minimum inhibitory concentration (MIC) level and effectively inhibited biofilm formation at sub-MIC concen-trations, achieving 55% inhibition in E. coli at 10 mg/ml and 67.81% inhibition in *K. pneumoniae* at 20 mg/ml, without significantly affecting planktonic growth.

Keywords: Antimicrobial agents, Biofilm, Drug resistance, Phytochemical

Phytochemical Profiling and In Vitro Evaluation of Groundnut Skin Polyphenols for Antidiabetic and Anti-inflammatory Activities

ANJANA V. K[1], Dr. R. V. GEETHA[2]

Research scholar, Saveetha Institute of Medical and Technical Sciences (SIMATS), Saveetha University (Deemed to be University), Chennai, Tamil Nadu 600077, India

Professor, Department of Microbiology, Saveetha Institute of Medical and Technical Sciences (SIMATS), Saveetha University (Deemed to be University), Chennai, Tamil Nadu 600077, India

Email ID: anjanasajith2@gmail.com

Abstract

Medicinal plants are valuable sources of bioactive phytochemicals with potential therapeutic applications against inflammation and diabetes mellitus. Phytochemicals has been reported to exhibit anti-inflammatory and antidiabetic properties by inhibiting protein denaturation and carbohydrate-hydrolysing enzymes. This study investigated the phytochemical composition and the in vitro anti-inflammatory and antidiabetic activities of the plant extract. The extract demonstrated significant concentration-dependent anti-inflammatory and antidiabetic activities in vitro. These findings indicate that the extract is a promising natural source of anti-inflammatory and antidiabetic agents, warranting further phytochemical characterization and in vivo investigations to validate its therapeutic potential.

Keywords: Medicinal plants, Antiinflammatory, Antidiabetic

Bacteriophage derived endolysin as potential therapeutic agent against multi-drug resistant *Klebsiella pneumoniae* infection

ARUN M T[1], ANEESH NAIR[1,2*]

[1]Department of Allied Health Sciences, Noorul Islam Centre for Higher Education, Kanniyakumari, Tamil Nadu, India,- 629180

[2]NIMS Centre for Genomic Medicine, NIMS Medicity, Thiruvananthapuram, Kerala, India,- 695123

Email ID: arundasmt0@gmail.com

Abstract

The increasing prevalence of multidrug-resistant (MDR) *Klebsiella pneumoniae* poses a significant challenge to the treatment of chronic infections, particularly diabetic foot ulcers, due to its extensive antimicrobial resistance and strong biofilm-forming ability. The present study aimed to evaluate the antibiofilm potential of bacteriophage-derived endolysin and develop a hydrogel-based delivery system against MDR *K. pneumoniae* clinical isolates. A total of 20 clinical isolates of *K. pneumoniae* were collected and subjected to antimicrobial susceptibility testing using the VITEK automated system. Biofilm-forming capacity was assessed using the microtiter plate crystal violet assay. Lytic bacteriophages targeting MDR *K. pneumoniae* were isolated from hospital septic tank samples, followed by endolysin extraction and characterization using SDS-PAGE. Finally, phage- and endolysin-incorporated hydrogels were developed and tested for their sustained antibacterial efficacy. The antimicrobial susceptibility profile revealed extensive resistance to beta-lactams and carbapenems, confirming the multidrug-resistant nature of the isolates, while colistin and tigecycline retained effectiveness. All isolates demonstrated biofilm-forming ability, with strain-specific variations in intensity. A lytic bacteriophage exhibiting a high titre of was successfully isolated. Endolysin treatment significantly disrupted biofilms, particularly in strong biofilm-producing strains. Additionally, both phage- and endolysin-loaded hydrogels demonstrated effective antibacterial activity and sustained bacteriolytic potential against MDR *K. pneumoniae* up to day 14. In conclusion, bacteriophage-derived endolysin incorporated into hydrogel formulations exhibits promising antibacterial and antibiofilm activity against MDR *K. pneumoniae*. This approach may serve as a potential alternative therapeutic strategy for managing chronic biofilm-associated infections, particularly diabetic foot ulcers.

Keywords: *Klebsiella pneumoniae,* Multidrug Resistance (MDR), Bacteriophage Endolysin, Biofilm Disruption, Hydrogel Delivery System

Study on the network pharmacology and *Candida glabrata* biofilm inhibitory potentials of *Metapenaeus dobsoni* derived astaxanthin

SIVASREE M[1], ANEESH NAIR[1*], GOPIKA S GOPAN[2]

[1]Department of Allied Health Sciences, Noorul Islam Centre for Higher Education, Kanyakumari, Tamil Nadu

[2]Department of Post Graduate Zoology, Nesamony Memorial Christian College

Email ID: draneeshnair@gmail.com

Abstract

Candida glabrata is an emerging opportunistic fungal pathogen recognized for its intrinsic resistance to multiple antifungal agents and its remarkable ability to form resilient biofilms, which contribute to persistent and recurrent infections. The search for novel, naturally derived antifungal compounds has gained significant attention as an alternative strategy to overcome biofilm-associated drug resistance. In the present study, astaxanthin isolated from the marine shrimp *Metapenaeus dobsoni* was investigated for its antibiofilm potential against *C. glabrata* using an integrated network pharmacology approach and in vitro biofilm assays. Network pharmacology was employed to identify potential molecular targets and signaling pathways associated with astaxanthin-mediated antifungal activity. Protein protein interaction analysis, pathway enrichment, and molecular docking were performed to predict key therapeutic targets involved in biofilm formation, adhesion, stress response, and virulence. The computational findings were complemented by experimental evaluation of biofilm inhibition using the crystal violet assay. The results demonstrated that astaxanthin significantly reduced *C. glabrata* biofilm biomass in a concentration-dependent manner. Network analysis identified several biofilm-associated proteins and pathways potentially regulated by astaxanthin, suggesting its ability to interfere with fungal adhesion, extracellular matrix production, oxidative stress responses, and metabolic adaptation. Molecular docking further supported the strong binding affinity of astaxanthin toward selected biofilm-related target proteins, indicating a plausible mechanism underlying its antibiofilm activity. The integration of computational predictions with biological validation highlights the therapeutic promise of *M. dobsoni*-derived astaxanthin as a natural antibiofilm agent. This study provides valuable insights into the molecular mechanisms of astaxanthin against *C. glabrata* biofilms and supports its further development as a complementary antifungal candidate for managing biofilm-associated candidiasis.

Keywords: Candida glabrata, Astaxanthin, Metapenaeus dobsoni, Network pharmacology, Biofilm inhibition, Molecular docking, Marine bioactive compounds, Antibiofilm.

Salivary Biomarkers as a Prognostic Aid in Oral Potentially Malignant Disorders and Oral Squamous Cell Carcinoma: A Cross-Sectional Study

SUMATHY DEVARAJAN

Meenakshi Academy of Higher Education and Research, Chennai, India

Email ID: gsivaden@yahoo.com

Oral potentially malignant disorders (OPMDs) are precursor lesions with varying risks of malignant transformation into oral squamous cell carcinoma (OSCC). Salivary biomarkers offer a non-invasive approach for early diagnosis and prognostic assessment. This study evaluated the expression of IL-6, IL-8, Survivin, S100A7, ERBB2, and CD44 in saliva to determine their prognostic significance in OPMDs and OSCC. In this cross-sectional study, unstimulated saliva samples were collected from patients with OPMDs and histopathologically confirmed OSCC. Biomarker levels were quantified using enzyme-linked immunosorbent assay (ELISA) and compared between the groups using appropriate statistical analyses. Differential expression of IL-6, IL-8, Survivin, S100A7, ERBB2, and CD44 was observed between OPMDs and OSCC, indicating progressive molecular alterations associated with oral carcinogenesis. The combined biomarker profile demonstrated potential in distinguishing premalignant lesions from malignant disease. Salivary IL-6, IL-8, Survivin, S100A7, ERBB2, and CD44 show promise as non-invasive prognostic biomarkers for risk assessment and disease progression in OPMDs and OSCC. Further validation in larger cohorts is warranted.

Keywords: OSCC, OPMD, ELISA, Prognostic, Biomarkers

Computational Screening of Phytochemical–Chitosan Nano-Conjugates Against WHO-Priority Pathogens in Contaminated Freshwater Ecosystems

P. ANANTHAKRISHNAN[1], G.GAYATHRI[1*], A.K.KATHIRESHAN[1] AND RITHISHA M[1]

Department of Microbiology, School of Life Sciences, Vels Institute of Science, Technology and Advanced Studies (VISTAS)

Email: gayathrig.sls@vistas.ac.in

Abstract

Urban freshwater lakes, including those in rapidly growing cities like Chennai, act as important environmental reservoirs for antibiotic-resistant bacteria, driven largely by anthropogenic pollution and wastewater inputs. In this computational study, we synthesized published data on bacterial communities from Chennai lake water, with emphasis on two high-priority WHO pathogens: carbapenem-resistant Pseudomonas aeruginosa and methicillin-resistant Staphylococcus aureus. Resistance gene profiles were characterized through literature mining and visualized using Python libraries (Pandas, Matplotlib, Seaborn), highlighting dominant mechanisms including efflux pumps, enzymatic inactivation, and target-site alterations. Blind molecular docking simulations (CB-Dock2) assessed the binding potential of key phytochemicals isolated from Caesalpinia sappan—brazilin, brazilein, sappanchalcone, caesalpinin, and cholic acid—both alone and conjugated with chitosan nanoparticles, targeting the aminoglycoside-modifying enzyme Aac(6′)-Ib (PDB ID: 2QIR). Results demonstrated that chitosan conjugation markedly improved binding affinities for all tested ligands, with the most pronounced enhancements observed for brazilein (from −9.1 to −14.8 kcal/mol) and cholic acid (from −9.3 to −14.7 kcal/mol). These in silico findings indicate that C. sappan-derived compounds, particularly when combined with chitosan, may offer promising natural scaffolds for inhibiting resistance enzymes in contaminated aquatic systems. The work underscores the value of computational approaches in exploring sustainable bioremediation options while emphasizing the essential need for subsequent experimental confirmation, including in vitro assays and molecular dynamics simulations, to combat antimicrobial resistance in polluted freshwater environments.

Keywords: Chennai lake water, antibiotic resistance, Pseudomonas, Staphylococcus, bioremediation, molecular docking, phytochemicals, chitosan nanoparticles

Antimicrobial Potential of Endophytic Fungi Isolated from Marine Macroalgae of the Southeast Coast of India

RITHISHA. M[1], G. GAYATHRI[1]*, P. KEERTHANA[1], A.K. KATHIRESHAN[1]

Department of Microbiology, School of Life Sciences, Vels Institute of Science, Technology and Advanced Studies (VISTAS)

Email ID: gayathrig.sls@vistas.ac.in

Abstract

Marine fungal endophytes are an important repository of novel bioactive compounds and secondary metabolites which could be potential drug targets. Among all the marine organisms, macro algae (seaweeds) is the paramount sources of fungal endophytes. Endophytic fungi have a strong mutualistic association with their host by secreting bioactive compounds that aids the host in stress resistance and tolerance. The present study aims at isolation of endophytic fungi from two seaweeds and to observe the antimicrobial activity of the fungal extracts. In this study, two seaweeds *Haloplegma* and *Halymenia* were collected from Mandapam coast, Ramnad district, Tamil Nadu, India. The endophytic fungi were isolated from the seaweed samples following standard procedure and the pure culture of the isolates were characterized based on the spore morphology. The crude extracts of the fungal isolates were extracted using hexane and screened for its anti-microbial activity through well diffusion assay. A total of four fungal endophytes from isolated from the two seaweeds. They were morphologically identified as *Alternaria sp., Mucor sp., Cladosporium sp., and Aspergillus sp*. The fungal extracts at varying concentration ranging from 100 µg-1000µg showed varying degrees of antimicrobial activity against four different pathogens viz., *Penicillium sp., Aspergillus flavus, Escherichia coli*, and *Staphylococcus aureus*. The Minimum inhibitory concentrations (MICs) were determined, that ranged from 0.1-1 mg of fungal extracts against the test pathogens. Our study is the first report to isolate endophytic fungi from *Haloplegma duperreyyi* seaweed. Our observations suggest that these fungal endophytes could be promising sources for metabolites with anti-microbial potential. Nonetheless, further detailed studies on other bioactive potentials of these fungal extracts would pave way for discovery of new antibiotics for a wide spectrum of infections.

Keywords: Endophytic fungi, Macro algae, Secondary metabolites, Anti-microbial activity, Pathogens.

Isolation and Characterization of a Novel Lytic Bacteriophage Against *bla*TEM-Producing Multidrug-Resistant *Klebsiella pneumoniae* Clinical Isolates: Implications for Phage Therapy Against ESBL Pathogens

ARUN M T[1], ANEESH NAIR[1,2*]

[1]Department of Allied Health Sciences, Noorul Islam Centre for Higher Education, Kanniyakumari, Tamil Nadu, India,- 629180

[2]NIMS Centre for Genomic Medicine, NIMS Medicity, Thiruvananthapuram, Kerala, India,- 695123

Email ID: arundasmt0@gmail.com

Abstract

Antimicrobial resistance (AMR) poses a global health threat concern in association with disease management, particularly among extended-spectrum -lactamase (ESBL)-producing Gram-negative *klebsiella pneumoniae*. This study details the isolation, characterization, and *in vitro* screening of a novel lytic bacteriophage isolated from hospital septic tank targeting multidrug-resistant (MDR) *Klebsiella pneumoniae* expressing the blaTEM resistance gene. Morphological examination via Transmission Electron Microscopy and Scanning Electron Microscopy revealed structural characteristics consistent with the order *Caudovirales*, demonstrating an icosahedral capsid head and a distinct, uncontracted tail machinery. Stability assays indicated that the phage retains complete structural integrity and lytic performance across a physiological temperature range of 4°C to 50°C and are stable at pH of 7.0 to 9.0; structural denaturation and complete inactivation were observed below pH 4.0. Automated phenotypic profiling via VITEK® 2 confirmed that 100% of the tested clinical isolates exhibited resistance profiles encompassing third-generation cephalosporins, -lactamase inhibitor combinations, and fluoroquinolones, with 68.89% demonstrating carbapenem co-resistance. Polymerase Chain Reaction (PCR) amplification validated the presence of the blaTEM marker within the target clinical isolates. Host range characterization showed specific lytic against 45% (9/20) of verified clinical *K. pneumoniae* strains alongside target cross-genus activity against *Escherichia coli* and *Pseudomonas aeruginosa*. Time-kill assays validated a robust, dose-dependent bactericidal response, where higher multiplicities of infection (MOI = 10 and 100) eliminated planktonic host loads within 5 hours. These insights indicate that the isolated lytic phage possesses significant potential as an alternative bio-control agent to mitigate ESBL-producing nosocomial pathogens like *klebsiella pneumoniae.*

Keywords: Bacteriophage therapy; *Klebsiella pneumoniae*; multidrug resistance; ESBL; bla_{TEM}; hospital wastewater; lytic bacteriophage.

Significance of Point-of-Care Diagnostics in Rapid Disease Diagnosis

G. RAJA[1], B. USHARANI [1], R. SENTHIL[2]

[1] Department of Biochemistry, School of Life Sciences, VISTAS, Chennai – 600117, Tamil Nadu, India

[2] Department of Bioinformatics, School of Life Sciences, VISTAS, Chennai – 600117, Tamil Nadu, India

Email ID: raniushab1@gmail.com

Abstract

Point of care testing (POCT) represents a transformation approach in clinical diagnostics, enabling rapid and accurate testing at or near the patient's location. Rapid and accurate diagnosis of pathogens is crucial to the timely treatment of patients. The conventional methods for detecting pathogens are usually performed in well-equipped clinical laboratories that rely on sophisticated equipment and well-trained personal. By eliminating the need for sample transport to centralized laboratories, POCT significantly reduces turnaround time (TAT), facilitating timely clinical decision-making and improving patient outcomes. Advances in multidisciplinary technologies, shifts in health management models and awareness of disease prevention have considerably driven the development of the POCT market. Technological advancements, such as miniaturization, microfluidics and biosensors, have driven the development of portable, user-friendly, and highly accurate POCT devices. Many portable low-cost and rapid POCT devices have been designed to promote health management, control disease spread and improve patient prognosis. These devices are utilized across diverse healthcare settings, including hospitals, outpatient clinics and non-clinical environments like homes and airports. POCT offers numerous advantages, including enhanced patient satisfaction, reduced treatment delay and to prevent unnecessary interventions. It is particularly for specific patient populations such as neonates, those prone to blood loss, due to minimal sample requirements. This study explores the methodology, benefits and limitations of POCT, emphasizing its clinical significance in improving healthcare delivery by leveraging the expertise of inter professional team and POCT can be effectively integrated into patients care, leading to improve clinical and economic outcomes.

Keywords: POCT, Clinical Diagnosis, Biosensors, Portable Diagnostic Devices, Rapid Analysis

Precision Medicine in Infectious Disease Management: Integrating Biomarkers and Artificial Intelligence for Personalized Therapeutics

HRUDHAYA.K, DR. K. SUDHARSAN*

Assistant Professor, Dept of Microbiology, Vels institute of Science technology & Advanced Studies (VISTAS),

Email ID: ksudharsan.sls@vistas.ac.in

Abstract

The increasing prevalence of antimicrobial resistance (AMR), emerging infectious diseases, and inter-individual variability in treatment response necessitate a paradigm shift from conventional empirical therapy to precision medicine. Precision medicine integrates genomic, transcriptomic, proteomic, metabolomic, and microbiome data with advanced computational tools to deliver personalized diagnostic and therapeutic strategies. Recent advances in next-generation sequencing, host-pathogen genomic profiling, and biomarker discovery have enabled rapid identification of pathogens and prediction of disease progression, facilitating timely and targeted interventions. Artificial intelligence (AI) and machine learning algorithms further enhance clinical decision-making by analyzing complex biological datasets to optimize antimicrobial selection, predict treatment outcomes, and reduce inappropriate antibiotic use. Additionally, pharmacogenomics allows individualized drug dosing, minimizing adverse drug reactions while improving therapeutic efficacy. Precision medicine also supports the development of personalized vaccines, immunotherapies, and microbiome-based interventions for infectious disease prevention and management. Despite its tremendous potential, challenges such as high implementation costs, limited genomic infrastructure, ethical concerns, data privacy, and disparities in healthcare access remain significant barriers to widespread clinical adoption. Future integration of multi-omics technologies with AI-driven clinical platforms and real-time digital health systems is expected to transform infectious disease diagnosis, surveillance, and treatment. This review highlights recent advances, current challenges, and future prospects of precision medicine in infectious disease management, emphasizing its potential to improve patient outcomes, combat antimicrobial resistance, and advance personalized healthcare.

Keywords: Precision Medicine, Infectious Diseases, Artificial Intelligence, Biomarkers, Antimicrobial Resistance, Pharmacogenomics, Personalized Medicine, Multi-omics.

AI-Assisted Drug and Vaccine Discovery Targeting the E1 and E2 Envelope Proteins of Chikungunya Virus

MOHAN RAJ S[1], SAI RAMESH A[1]

[1]Department of Bioengineering, Vels Institute of Science, Technology and Advanced Studies, Chennai 600117, India

Email ID: sairamesh.se@vistas.ac.in

Abstract

Chikungunya virus (CHIKV) is a re-emerging mosquito-borne alphavirus that continues to pose a major public health challenge in tropical and subtropical regions. Following transmission by infected Aedes aegypti or Aedes albopictus mosquitoes. But still there is no specific vaccines or antiviral drugs for chikungunya virus (CHIKV) because the virus is an RNA virus that mutate over time. It relies on human cell machinery, So drug then block viral replication can also damage health cells. Finding safe antiviral target is difficult. Research have identified several viral proteins that one potential drug target including (nsP1, nsP2, nsP3,nsP4 and envelope proteins E1and E2 viral protein). In this review The virus uses envelope protein E1 and E2 to attach and enter into the human cell. Without these proteins, the virus cannot enter the cell. Our idea if we can block the E1 and E2 proteins, the virus may be prevented from entering human cells. If the virus cannot enter the cell its RNA cannot replicate and new virus particles cannot be produce then human immune system can able to deafet the RNA virus. The role of Artificial intelligence (AI) can analyse the structure of E1 and E2 proteins, perform molecular docking, vitual screening,and immunoinformatics to identify molecules antibodies, or vaccines target that could block these protein more quickly then tradiational methods. AI (artificial intelligence) is not the treament itsef , but itcan speed up the discovery of new antiviral drugs and improval vaccines . So we lookforward to expose different vaccines and presepective to effective treatment.

Keywords: Chikungunya virus (CHIKV), Artificial Intelligence (AI), Envelope glycoproteins E1 and E2, Antiviral drug discovery, Molecular docking, Virtual screening, Immunoinformatics, Vaccine development, Host cell entry, Alphavirus.

Deep learning in medical imaging for infectious disease diagnosis

[1]SHRAVANI B, [2]PRIYADARSHINI H, [3*]BHARATHI.B, [4]SARITHA.V

[1,2] II BSc MLT, MMM College of Health Sciences, Chennai

[3]Professor, Dept., of MLT, MMM College of Health Sciences, Chennai

[4]Assistant Professor, Dept., of MLT, MMM College of Health Sciences, Chennai

Email ID: bharathikarnan@gmail.com

Abstract

Deep learning, a specialized branch of Artificial Intelligence (AI), has revolutionized medical imaging by enabling rapid, accurate, and automated diagnosis of infectious diseases. The growing burden of infections such as tuberculosis, COVID-19, pneumonia, and malaria, coupled with increasing demand for timely diagnosis, has accelerated the adoption of AI-assisted imaging technologies in healthcare. This presentation explores the role of deep learning models, particularly Convolutional Neural Networks (CNNs), in enhancing infectious disease diagnosis through analysis of medical images including chest X-rays, computed tomography (CT) scans, magnetic resonance imaging (MRI), ultrasound, and microscopic blood smear images. Deep learning algorithms automatically extract complex image features, identify disease-specific patterns, and assist clinicians in detecting infections with high accuracy while reducing diagnostic delays and observer variability. The integration of imaging findings with laboratory data and clinical information further improves diagnostic precision and supports evidence-based clinical decision-making. In addition to improving patient outcomes, AI-powered medical imaging contributes to efficient disease surveillance, optimized healthcare resource utilization, and rapid response during infectious disease outbreaks. Despite challenges such as the need for large annotated datasets, data privacy concerns, infrastructure requirements, and regulatory considerations, deep learning continues to demonstrate significant potential in transforming diagnostic microbiology and radiology. Future advancements in explainable AI, cloud-based diagnostics, digital pathology, and AI-assisted telemedicine are expected to further strengthen infectious disease management. Overall, deep learning represents a promising tool that complements healthcare professionals by providing accurate, timely, and reliable diagnostic support, ultimately contributing to improved patient care and more resilient healthcare systems.

Keywords: Deep Learning; Artificial Intelligence (AI), Medical Imaging, Infectious Disease Diagnosis, Convolutional Neural Networks (CNNs), AI-assisted telemedicine.

Artificial Intelligence in Infectious Disease Prediction: Advancing Public Health Surveillance

JOSHIN R.S

Alagappa college of Technology Sardar Patel Rd, Anna University,

Guindy, Chennai, Greater Chennai, Tamil Nadu 600025

Email ID: joshinrs2005@gmail.com

Abstract

Infectious diseases continue to pose significant global health challenges, highlighting the need for timely prediction and effective outbreak management. This presentation explores the role of artificial intelligence (AI) in predicting infectious disease outbreaks by integrating epidemiological, environmental, and clinical data. Machine learning and deep learning approaches are discussed, along with their applications in forecasting disease spread, identifying high-risk populations, and supporting public health decision-making. Recent case studies demonstrate that AI-based models can improve prediction accuracy and enable earlier interventions compared with traditional surveillance methods. The presentation also addresses challenges such as data quality, model interpretability, privacy, and ethical concerns. Overall, AI has the potential to transform infectious disease surveillance and strengthen global public health preparedness.

Keywords: Artificial intelligence, Disease, Health, Public health

Artificial Intelligence in the Prediction, Early Detection, and Management of Tuberculosis

ADARSH A R[1], SAI RAMESH A[1*]

[1]Department of Bioengineering, Vels Institute of Science, Technology and Advanced Studies, Chennai 600117, India

Email ID: sairamesh.se@vistas.ac.in

Abstract

Tuberculosis (TB) is one of the leading infectious diseases worldwide and continues to cause significant mortality, particularly in developing countries. Conventional diagnostic methods, such as sputum microscopy and manual interpretation of chest X-rays, are often time-consuming and require experienced pathologists and radiologists. Recent advances in artificial intelligence (AI) have shown great potential in improving the speed and accuracy of TB diagnosis by assisting healthcare professionals in early detection and clinical decision-making. This review aims to evaluate the role of artificial intelligence in the prediction, early detection, and management of tuberculosis. The review was conducted by analyzing research and review articles on artificial intelligence in tuberculosis diagnosis and management. It mainly focused on machine learning, deep learning, convolutional neural networks (CNN), computer-aided diagnosis (CAD), and chest X-ray analysis to understand their applications and clinical significance. The reviewed studies showed that AI significantly improves the speed and accuracy of tuberculosis diagnosis. CNN- and deep learning-based models were examined to evaluate the significance of artificial intelligence in improving the accuracy and performance of TB detection from chest X-rays. One study reported a sensitivity of 97.94%, while another demonstrated that deep learning systems performed comparably to radiologists using chest X-ray datasets. Although systematic reviews highlighted the effectiveness of CAD systems, further clinical validation is required before their widespread clinical implementation. Overall, the use of AI in the detection, diagnosis, and management of tuberculosis has the potential to reduce the workload of radiologists and pathologists, support early diagnosis, and improve patient management and clinical outcomes.

Keywords: Tuberculosis, Artificial Intelligence (AI), Machine Learning, Deep Learning, Convolutional Neural Networks (CNN), Computer-Aided Diagnosis (CAD), Chest X-ray.

CRISPR-Driven Antimicrobial Technologies for Combating Multidrug-Resistant Pathogens

B R ADITHYA[1], G DHARSHINI[2], BHARATHI.B[3], SARITHA.V[4]

[1,2] II BSc MLT, MMM College of Health Sciences, Chennai

[3]Professor, Dept., of MLT, MMM College of Health Sciences, Chennai

[4]Assistant Professor, Dept., of MLT, MMM College of Health Sciences, Chennai

Email ID: bharathikarnan@gmail.com

ABSTRACT

Antimicrobial resistance (AMR) has emerged as one of the greatest global public health threats, significantly reducing the effectiveness of conventional antibiotics and contributing to the rapid spread of multidrug-resistant (MDR) bacterial infections. The increasing prevalence of pathogens such as methicillin-resistant Staphylococcus aureus (MRSA), vancomycin-resistant Enterococcus (VRE), carbapenem-resistant Klebsiella pneumoniae, extended-spectrum β-lactamase (ESBL)-producing Escherichia coli, and multidrug-resistant Pseudomonas aeruginosa necessitates the development of innovative and targeted antimicrobial strategies. This study highlights the emerging role of Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)-Cas technology as a promising next-generation approach for combating antimicrobial resistance. Unlike conventional antibiotics, CRISPR-based antimicrobial systems selectively target bacterial resistance genes or essential genomic sequences, thereby eliminating pathogenic bacteria or restoring antibiotic susceptibility while preserving the normal microbiota. Various delivery platforms, including engineered bacteriophages, conjugative plasmids, liposomes, and nanoparticle-based systems, have been investigated to facilitate efficient and precise delivery of CRISPR-Cas components into bacterial cells. Recent experimental studies have demonstrated the ability of CRISPR technology to eradicate MDR pathogens, disrupt biofilm formation, prevent horizontal transfer of resistance genes, and enhance the efficacy of existing antibiotics with high specificity and minimal off-target effects. Despite challenges related to delivery efficiency, potential off-target activity, regulatory approval, and large-scale clinical implementation, CRISPR-based antimicrobial therapy represents a transformative advancement in precision medicine. Continued research and clinical validation may establish CRISPR technology as a powerful therapeutic weapon against antimicrobial resistance, offering new hope in addressing the growing burden of drug-resistant bacterial infections in the post-antibiotic era.

Keywords: CRISPR-Cas System, Antimicrobial Resistance, carbapenem-resistant Klebsiella pneumoniae, MDR pathogens, off-target activity.

Malaria Prediction, Prevention, and Diagnosis: A Comparative Review of Conventional and AI-Based Methods

RAJ ROHAN K[1], SAI RAMESH A[1]

[1]Department of Bioengineering, Vels Institute of Science, Technology and Advanced Studies, Chennai 600117, India

Email ID: sairamesh.se@vistas.ac.in

Abstract

Malaria is a disease caused by the plasmodium falciparum parasite in mosquito that transmit the malaria from one person to another.The forecasting of malaria and the most common predictors are rainfall, relative humidity, temperature and the normalised difference vegetation index.In this review mosquito prevention method can effectively reduce the cause of disease especially the combination of two or three methods including insecticide treated bed nets (ITNs),Indoor Residual spraying (IRS) and topical repellents.diagnosis method of conventional and AI based methods.To review conventional methods which covers microscopy,rapid diagnostic testing (RDT) and polymerase chain reaction (PCR) are common traditional methods.The AI based methods which includes (ML) machine learning like (GB) gradient boosting, (SMOTE) systamatic minority oversampling technique and (RF) random forest.Among this conventional and AI based methods conventional methods are standardized technique in real world.AI is just used as a supporting technique in diagnosis and prevention of malaria disease. The drastical development of artificial intelligence in current affairs it is possible to implement the AI based tools as primary or above the supporting technique in the real world diagnosis of malaria.Conventional methods are time consuming but AI is faster according to some studies.Several studies have reported that AI-based techniques can give higher accuracy and sensitivity than the conversation methods under experimental conditions.Future work can focus on AI as a primary techniques and conventional methods as a supportive techniques.

Key words: Prediction, prevention, diagnosis of malaria conventional methods and ai based methods

AI-Integrated Salivary Biomarker Analysis for Early Detection and Prevention of Periodontitis

S.NISHAL[1], SAI RAMESH A[1*]

[1]Department of Bioengineering, Vels Institute of Science, Technology and Advanced Studies, Chennai 600117, India

Email ID: sairamesh.se@vistas.ac.in

Abstract

Periodontal disease is a chronic inflammatory condition affecting the gums and the supporting structures of the teeth, caused primarily by bacterial plaque accumulation. If left untreated, it progressively damages the periodontal tissue and bone, leading to tooth mobility and eventual tooth loss. It remains one of the most predominant oral health conditions worldwide, with a significant proportion of cases going undetected until the disease has already progressed, largely due to the limitations of conventional diagnostic methods that rely on visible clinical signs. This seminar focuses on how early prediction of periodontal disease can be achieved through the integration of salivary biomarkers with artificial intelligence. Saliva serves as a non-invasive diagnostic medium, carrying molecular indicators such as pro-inflammatory cytokines (IL-1β, IL-6, TNF-α), tissue-degrading enzymes (MMP-8, MMP-9), microbial DNA, oxidative stress markers, and emerging biomarkers like exosomes and microRNAs, each reflecting different aspects of disease activity. Since periodontal breakdown rarely correlates with a single biomarker, artificial intelligence plays a crucial role in analyzing these multi-marker profiles collectively, identifying subtle patterns and correlations that would otherwise be difficult to detect manually. This integration enables the prediction of disease risk at a much earlier stage.

Keywords: Periodontal, Inflammatory cytokines (IL-1β, IL-6, TNF-α), biomarkers, artificial intelligence, prediction.

Targeting NF-κB Signaling to Combat Antimicrobial Resistance: A Molecular Approach

[1] Dr.K.MAHALAKSHMI, [2]DANAPOORNIMA.B, [2]JANANI.V, [2]SUVASHINI.M

[1]Asst Professor [2]M.Sc., PG Dept of Biochemistry

Bhaktavatsalam Memorial College for Women, Korattur, Chennai-600050.

Email: mahalais@gmail.com

Abstract

Antimicrobial resistance (AMR) has emerged as one of the greatest threats to global health, compromising the effectiveness of antibiotics and increasing the risk of prolonged infections, treatment failure, and mortality. While extensive research has focused on microbial resistance mechanisms, growing evidence highlights the critical role of host immune signaling in influencing disease progression and therapeutic success. Among these pathways, nuclear factor-kappa B (NF-κB) functions as a master regulator of inflammatory and immune responses by orchestrating the expression of cytokines, chemokines, and antimicrobial mediators. Although transient NF-κB activation is essential for pathogen clearance, sustained activation promotes excessive inflammation, tissue injury, and a microenvironment that favors the persistence of resistant pathogens. This review explores the molecular interplay between NF-κB signaling and antimicrobial resistance, emphasizing the potential of host-directed therapeutic strategies. Selective modulation of NF-κB, when used alongside conventional antibiotics, offers a promising approach to restoring immune balance, limiting inflammation-induced tissue damage, and improving antimicrobial efficacy. Furthermore, advances in natural bioactive compounds, selective small-molecule inhibitors, and nanotechnology-based drug delivery systems provide innovative avenues for targeted intervention. By integrating host immune modulation with antimicrobial therapy, targeting NF-κB represents a promising strategy to combat antimicrobial resistance and improve clinical outcomes, paving the way for next-generation precision therapies against infectious diseases.

Keywords: Master Regulator, Cytokines, Inhibitor, Orchestrating, Precision therapies.

Production of eco-friendly antifungal liquid hand wash by using plant extract

KALIAMOORTHI RAMYA[1*],HARINI B[2]

Assistant Professor, Department of Microbiology, School of Life Science, Vels Institute of Science Technology and Advanced Studies, Pallavaram, Chennai.

PG Student, Department of Microbiology, School of Life Science, Vels Institute of Science Technology and Advanced Studies, Pallavaram, Chennai.

Email: ramyak.sls@vistas.ac.in, ramyakuzhaly@gmail.com

Abstract

This study aimed to develop an eco-friendly antifungal liquid hand wash using Acalypha indica and Tridax procumbens plant extracts. The formulation was prepared with natural ingredients and evaluated for its phytochemical composition, physicochemical properties, antimicrobial activity, and skin safety. The herbal hand wash exhibited good stability, a skin-friendly pH, effective antifungal and antibacterial activity, and no signs of skin irritation. The presence of bioactive compounds such as flavonoids, tannins, saponins, and phenols contributed to its antimicrobial effectiveness. Overall, the developed formulation is a safe, biodegradable, and effective natural alternative to synthetic hand wash products, with potential applications in personal hygiene and sustainable healthcare.

Keywords: Antifungal, Herbal Hand Wash, Health Care, Plant Extract.

Studies on the Virulence and Biofilm Inhibitory Potentials of 3-Formylchromone Against *Acinetobacter baumannii*

R. SAM JABARAJ

Department of Microbiology,

Dwaraka Doss Goverdhan Doss Vaishnav College (Autonomous)

Arumbakkam, Chennai – 600106

Email: samjabarajr14@gmail.com

Abstract

Acinetobacter baumannii (A. baumannii) is an opportunistic, Gram-negative, non-motile, and aerobic bacillus commonly found in natural environments as well as in healthcare settings such as hospitals and long-term care facilities. It is recognized as a major nosocomial pathogen due to its ability to form biofilms and exhibit multidrug resistance (MDR). In this study, the anti-biofilm and anti-virulence potentials of 3-formylchromone (3-FC), a natural chromone derivative, were investigated against clinical and reference strains of *A. baumannii*. The study demonstrated that 3-FC effectively inhibits biofilm formation by disrupting the synthesis of exopolysaccharides (EPS), an essential component of the biofilm matrix, and impairs quorum sensing (QS) regulated virulence factors without impacting bacterial growth at sub-inhibitory concentrations. These effects were evidenced through quantitative biofilm assays, EPS quantification, motility inhibition, and microscopic visualization, indicating a disruption of bacterial communication and colonization processes. The data suggest that 3-FC acts as a QS inhibitor, attenuating the pathogenesis and persistence mechanisms of A. baumannii. Given the challenges posed by MDR and biofilm-mediated infections, 3-FC presents a promising antivirulence candidate for adjunctive therapeutic development. Further research is warranted to elucidate its molecular targets and evaluate clinical applicability.

Keywords: Acinetobacter baumannii, biofilm, 3- formylchromone, quorum sensing

Antibacterial properties of Rhodococcus rhodochrous assisted silicon dioxide nanoparticles synthesized by sol gel method

RESHMA.B*, DR.S. NARENDHRAN

Department of Microbiology, Ethiraj college for women, Chennai, Tamil Nadu 600008

Email: reshmabalamurugan7@gmail.com

Abstract

The rapid emergence of antibiotic resistance demands a novel antimicrobial agent and sustainable approaches in their utilization. Actinomycetes remain one of the most renowned sources of secondary metabolites with antimicrobial activity and pharmaceutical applications. Actinomycetes are unicellular, aerobic, non-motile spore forming organisms that produce potent secondary metabolites having antimicrobial, anti-inflammatory and anti-carcinogenic properties. In this study, actinomycetes having antimicrobial properties were isolated from soil and evaluated for potential application in the green synthesis of silica nanoparticles. The silica nanoparticles were then characterized to determine their structure, morphology, physio-chemical characteristics, anti-oxidant and anti-bacterial activity against predominant drug-resistant pathogens. This study highlights the role of actinomycetes in providing novel antimicrobial agents as well as synthesizing silica nanoparticles using a greener approach, serving as an important milestone in combining microbiology and nanotechnology to combat antimicrobial resistance.

Keywords: Antibiotic resistance, actinomycetes, silica nanoparticles, green synthesis, antimicrobial agent

Isolation and characterization of endophytic bacteria from Ocimum sanctum (Tulsi) and Murraya koenigii (Curry leaves) for their antimicrobial potential against foodborne pathogens

MAYURIKAA. N[1*], SHINEY JENITA Y.M[2]

Assistant Professor, Department of Microbiology, VELS Institute of Science, Technology and Advanced Studies.

Post Graduate Student, Department of Microbiology, VELS Institute of Science, Technology and Advanced Studies.

Email: mayurikaan98@gmail.com

Abstract

The present study was undertaken to isolate, characterize, and evaluate the bio-preservative potential of endophytic bacteria obtained from the medicinal plants *Ocimum sanctum* (Tulsi) and *Murraya koenigii* (Curry leaves). Healthy leaf samples were surface sterilized to eliminate epiphytic microorganisms, and endophytic bacteria were isolated using homogenization and serial dilution techniques. Three distinct bacterial isolates, designated as T10-1, T10-2, and CL10-1, were obtained and subjected to morphological, microscopic, biochemical, and enzymatic characterization. Gram staining revealed that all isolates were Gram-positive, with T10-1 and CL10-1 appearing as rod-shaped bacilli and T10-2 as cocci. Endospore staining confirmed spore formation in T10-1 and CL10-1. Biochemical profiling showed that all isolates were catalase positive, while citrate utilization was observed only in T10-1. Enzymatic assays demonstrated that T10-2 and CL10-1 possessed amylase, protease, and gelatinase activities, indicating strong extracellular hydrolytic potential. The antimicrobial activity of the isolates was evaluated against *Escherichia coli* and *Staphylococcus aureus* using the agar well diffusion method. No measurable zones of inhibition were observed under the tested conditions, suggesting that the antimicrobial metabolites may be intracellular, produced in low concentrations, or expressed only under specific environmental conditions. Despite the absence of direct antimicrobial activity, the pronounced enzymatic capabilities and endospore-forming nature of the isolates highlight their potential role in competitive exclusion, nutrient depletion, and sustainable food bio-preservation. The study demonstrates that medicinal plants harbor functionally diverse endophytic bacteria with promising applications in food microbiology and biotechnology.

Keywords: Endophytic bacteria, Ocimum sanctum, Murraya koenigii, Bio-preservation, Extracellular enzymes

CRISPR-Cas Systems as Dual-Purpose Tools Against AMR in WHO Priority Pathogens: Bridging Rapid Resistance Diagnostics and Emerging Gene - Editing Therapeutics

[1]DHANYASRI Y, [*]DR. ANUSHA BALASINGH

[1]PG student, [*]Associate Professor

Department of Microbiology, Ethiraj college for Women, Chennai - 600008

Email: divyasenthilkumr27@gmail.com

Abstract

Antimicrobial resistance (AMR) among WHO priority pathogens continues to erode antibiotic efficacy, driving demand for faster diagnostics and alternative countermeasures. CRISPR-Cas systems, originally a bacterial antiviral defence, have been repurposed along two tracks: Cas12a/Cas13a-based diagnostics for culture-independent resistance-gene detection, and Cas9-based gene editing delivered via conjugative plasmids or engineered phages to resensitize or eliminate resistant strains. This review finds diagnostic platforms achieving strong clinical performance — e.g., a Cas12a assay for carbapenem-resistant Klebsiella pneumoniae reported 91.2% sensitivity and 84.1% specificity within 60 minutes — positioning them near point-of-care use. Therapeutic applications remain mechanistically validated but variable, with resensitization efficacy ranging from 4.7% to 100% across studies and progress limited by narrow host range, physiological instability, and escape mutations. Recent delivery advances including a conjugative plasmid eliminating over 99.9% of resistant E. coli in a mouse gut model and an engineered phage cocktail now in clinical evaluation — suggest the translational gap is narrowing. Overall, CRISPR-Cas is a rapidly maturing dual-use platform against multidrug-resistant pathogens, with diagnostics nearer clinical deployment than therapeutics.

Keywords: CRISPR-Cas, antimicrobial resistance, WHO priority pathogens, diagnostics, therapeutics, conjugative plasmids, engineered phages

In Silico Design and Evaluation of a Multi-Epitope Vaccine Against Bluetongue Virus

FATHIMA MUNAVAR AHAMED BASHEER

Department of Microbiology, Saveetha Dental College & Hospitals, Chennai, India

Email: fathima.munans@gmail.com

Abstract

Bluetongue virus (BTV) is a vector-transmitted virus that infects ruminant livestock and wildlife, resulting in economic losses relating to its impact on animal health and trade. To design a BTV vaccine targeting the non-structural protein of the virus, optimized with allele profiling. Conserved viral sequences were taken and checked for MHA, cytotoxic T-cell & B-cell responses. These sequences were evaluated for their antigenicity, toxicity and allergenicity. The vaccine design was created using universal linker sequences; the stability of the vaccine was also demonstrated. The Molecular Docking of the vaccine design was performed on NS5 protein. Popularity coverage of the vaccine was performed via similar HLA alleles. The constructed vaccine demonstrated antigenicity and non-allergenicity; CAI score =0.90 & the estimated half-life demonstrated >10 hours for Escherichia coli (in vivo). The vaccine was found to be structurally stable and the Ramachandran analysis showed 96.0% favoured score. The Molecular Docking performed resulted in the binding energy to be -5669.49. This study establishes the theoretical and computational efficiency against the Blue Tongue Virus, providing a point for subsequent experimental validation against the animal virus.

Keywords: Cytotoxic T-cells, Antigenicity, Vaccine, Molecular Docking

Comparative Bioinformatic Profiling of Human microRNAs Targeting Nipah and Hendra Virus Genomes

REVATHY. M

Department of Microbiology, Saveetha Dental college and hospital, Chennai, India

Email: revathymurugan1445@gmail.com

Abstract

Nipah virus (NiV) and Hendra virus (HeV) are highly pathogenic zoonotic viruses belonging to the Henipavirus genus. They pose significant public health concerns because of their high case-fatality rates and the lack of specific antiviral therapies. Human microRNAs (miRNAs) are small non-coding RNAs that regulate gene expression and have been predicted to influence viral infections by binding to viral RNA genomes. This study aimed to comparatively predict human microRNAs capable of targeting the genomes of Nipah and Hendra viruses using an in silico bioinformatics approach.Complete genome sequences of Nipah and Hendra viruses were analyzed using the RNA22 v2 prediction tool to identify potential human miRNA binding sites. The predicted interactions were examined based on binding positions, complementary pairing, and the prediction scores generated by RNA22 v2. A comparative analysis was performed to identify miRNAs predicted to target both viral genomes. RNA22 v2 predicted multiple human miRNAs with potential binding sites in both Nipah and Hendra virus genomes. Several miRNAs were predicted to interact with comparable regions of the two viral genomes, suggesting possible shared miRNA–viral RNA interactions. These findings indicate potential host miRNAs that may influence both viruses and provide candidates for further computational and experimental investigation. This comparative bioinformatics analysis identified several human miRNAs predicted to target both Nipah and Hendra viruses. Although these findings are based on computational prediction, they provide a useful foundation for future validation using additional bioinformatics tools and laboratory studies. Such investigations may contribute to the development of miRNA-based antiviral strategies against henipavirus infections.

Keywords: Bioinformatic analysis, non-coding, miRNA, Zoonotic

Bioelectricity generation from banana and tomato waste using microbial fuel cell

SHOBANA SHREE
Dwaraka Doss Goverdhan Vaishnav College
Arumbakkam, Chennai – 600 106, Tamilnadu
Email: shobanashrie18@gmail.com

Abstract

The accumulation of organic waste, such as banana and tomato residues, presents significant environmental challenges, necessitating sustainable management strategies. This study investigates the potential of Microbial Fuel Cell (MFC) technology to convert these wastes into bioelectricity, leveraging their high organic nutrient content to support microbial metabolism and electron generation. The primary objective was to evaluate the efficiency of banana and tomato waste as substrates for electricity production while monitoring key parameters including voltage, pH, dissolved oxygen, and biological oxygen demand (BOD). Banana and tomato wastes were processed into a slurry and introduced into an anode chamber under anaerobic conditions, where indigenous microorganisms broke down the organic matter, releasing electrons transferred via an external circuit to a cathode chamber. Voltage output was measured using a multimeter. Results demonstrated effective bioelectricity generation from the fruit wastes, confirming their viability as low-cost, renewable substrates. This MFC approach not only yields a sustainable energy source but also aids waste valorisation, reducing environmental pollution. Our findings further validates by integrating bioenergy production with organic waste management, promoting eco-friendly alternatives to conventional energy systems.

Keywords: Bioelectricity, Bioenergy, Organic waste, Microbes

From Reactive to Predictive: Integrating Artificial Intelligence and One Health Frameworks for Zoonotic Disease Surveillance in India

DIVYADHARSHINI S[1] AND DR VIDHYA C V[2]

[1]Postgraduate, Applied Microbiology, Department of Microbiology,
Ethiraj College for Women

[2]Associate Professor, Department of Microbiology, Ethiraj College for Women

Email: divyasenthilkumr27@gmail.com, vidhya_cv@ethirajcollege.edu.in

Abstract

Globally, nearly 75% of emerging infectious diseases are zoonotic in origin, making spillover prevention a major One Health priority. In India, this risk is amplified by close human–animal contact, environmental change, and the presence of endemic and high-impact threats such as rabies, scrub typhus, leptospirosis, Nipah virus, and avian influenza. While international models focus on food-chain traceability, India requires a customised approach to resolve inter-ministerial data silos (linking IHIP, NADRES, and environmental networks), address rural primary health disparities and navigate complex biodiversity fringes. To bridge this gap, AI must enable multimodal data fusion—synthesising satellite environmental metrics, metagenomic sequencing, livestock mobility, and grassroots syndromic reporting. Deploying privacy-preserving AI architectures, alongside "frugal AI" applications for frontline health workers, is vital. Aligned with India's National One Health Mission (NOHM), this AI-driven framework will enable epidemiologists and microbiologists to detect spillover risks at the forest-wildlife edge, shifting the paradigm from chasing epidemics to preventing spillover before it occurs. This review evaluates the integration of Artificial Intelligence (AI) and Machine Learning (ML) into the One Health paradigm to establish predictive early-warning systems tailored to India's socio-ecological landscape.

Keywords: One Health, Zoonotic Surveillance, Artificial Intelligence, Predictive Epidemiology, National One Health Mission (NOHM).

Pro Wheat: A Functional Probiotic Drink with Antimicrobial Potential

R. RAMYA

Department of Microbiology,

Dwaraka Doss Goverdhan Doss Vaishnav College (Autonomous)

Arumbakkam, Chennai – 600106

Email: ramyamalathi2005@gmail.com

Abstract

Probiotics are beneficial microorganisms that contribute to human health by improving gut microbial balance and inhibiting pathogenic organisms. The present study aimed to develop a non-dairy probiotic beverage, “Pro Wheat,” using wheat milk fermented with Lactobacillus species. The increasing demand for functional foods and the growing prevalence of lactose intolerance have highlighted the need for plant-based probiotic alternatives. Lactobacillus species were isolated and characterized using standard microbiological and biochemical techniques. Wheat milk was prepared and inoculated with the selected probiotic culture under controlled fermentation conditions. The antimicrobial activity of the fermented product was evaluated against Escherichia coli using the agar well diffusion method. The fermented beverage exhibited inhibitory activity against the test organism, indicating its potential role in suppressing harmful microorganisms. The developd probiotic drink demonstrated desirable characteristics as a functional food with added health benefits. In addition to being lactose-free, the product may contribute to maintaining gut health and enhancing microbial balance. The findings suggest that “Pro Wheat” can serve as a promising, affordable, and nutritious probiotic beverage suitable for individuals seeking plant-based dietary options. This study highlights the potential application of probiotic microorganisms in the development of innovative functional foods with antimicrobial properties, thereby contributing to the advancement of microbiology and public health.

Keywords: Pro Wheat, Probiotics, Wheat Milk, Lactobacillus spp., Antimicrobial Activity, Escherichia coli, Functional Food.

Exploring the Antimicrobial and Wound-Healing Potential of *Mimosa pudica*

PRIYADHARSHINI. S[1], PRIYADHARSHINI. L.K[1], SURESH DHANARAJ[2], PRIYA SUNDARARAJAN[3*]

[1]Post Graduate Student, Department of Microbiology, School of Life Sciences, Vels Institute of Science, Technology and Advanced Studies (VISTAS), Chennai, Tamil Nadu, India.

[2]Professor, Department of Microbiology, School of Life Sciences, Vels Institute of Science, Technology and Advanced Studies (VISTAS), Chennai, Tamil Nadu, India.

[3*]Assistant Professor, Department of Microbiology, School of Life Sciences, Vels Institute of Science, Technology and Advanced Studies (VISTAS), Chennai, Tamil Nadu, India.

Email: priyasundararajan2509@gmail.com

Abstract

The increasing prevalence of antimicrobial-resistant wound pathogens has intensified the search for safe, effective, and plant-based therapeutic alternatives. Mimosa pudica (sensitive plant), a medicinal herb renowned in traditional medicine, possesses a rich repertoire of bioactive phytochemicals with promising antimicrobial and wound-healing properties. This study evaluated the phytochemical composition, antimicrobial efficacy, and in vitro wound-healing potential of ethanolic Mimosa pudica extract against major wound-associated bacterial pathogens. Fresh plant material was shade-dried, powdered, and extracted by cold maceration using ethanol. Qualitative and quantitative phytochemical analyses confirmed the presence of alkaloids, flavonoids, phenolics, tannins, saponins, and terpenoids. The extract was further characterized using UV–Visible spectroscopy, FTIR, HPLC, and GC–MS to identify its bioactive constituents. Antibacterial activity was assessed against Staphylococcus aureus, Escherichia coli, and Pseudomonas aeruginosa using agar well diffusion assays at different extract concentrations. The ethanolic extract demonstrated concentration-dependent antibacterial activity, with the highest inhibition observed at 100% concentration, particularly against Staphylococcus aureus. The abundance of phenolic and flavonoid compounds suggests their contribution to the observed antimicrobial and antioxidant effects, which are closely associated with tissue repair and wound regeneration. Spectroscopic analyses further supported the presence of functional groups and phytochemicals linked to therapeutic activity. Overall, the findings highlight Mimosa pudica as a promising natural source of antimicrobial and wound-healing agents with potential applications in the development of eco-friendly phytopharmaceuticals and advanced wound-care formulations. Further in vivo investigations and clinical validation are warranted to establish its efficacy and safety for therapeutic use.

Keywords: Antimicrobial resistance, Phytochemicals, Mimosa pudica, Antimicrobial activity, Wound healing activity.

Efficient adsorptive removal of heavy metals using sugarcane bagasse ash and chitosan composite biosorbent

YUVASREE.D.S
Department of Microbiology,
Dwaraka Doss Goverdhan Doss Vaishnav College (Autonomous)
Arumbakkam, Chennai – 600106
Email: samjabarajr14@gmail.com

Abstract

Freshwater scarcity and the increasing discharge of industrial effluents have made heavy metal contamination a pressing environmental challenge. Conventional treatment methods, though effective, often generate secondary pollutants or involve high operational costs, highlighting the need for sustainable alternatives. Biosorption, using low-cost and eco-friendly materials, has emerged as a promising approach. In this study, a composite biosorbent was developed by combining microwave-activated sugarcane bagasse ash (SCBA), an agro-industrial byproduct, with chemically modified chitosan (MISCBA). The biosorbent was prepared through microwave incineration, acid activation, Schiff-base modification, and bead formation. Optimisation experiments established that adsorption efficiency was influenced by dosage, contact time, and pH. with maximum uptake observed under specific conditions. Characterization using Fourier Transform Infrared Spectroscopy (FTIR) and Scanning Electron Microscopy (SEM) confirmed the presence of functional groups and porous surface morphology responsible for metal binding. Laboratory studies demonstrated a strong affinity of MISCBA for multiple heavy metals, while validation with textile industry wastewater confirmed its practical applicability. Atomic Absorption Spectroscopy (AAS) analysis showed that the biosorbent effectively reduced toxic metal concentrations, supporting its role as a reliable treatment option. Overall, the findings highlight MISCBA A as as a cost-effective, sustainable, and environmentally friendly biosorbent capable of addressing heavy metal pollution in industrial wastewater. This work contributes to circular economy principles by transforming agricultural waste into a valuable product for environmental remediation.

Keywords: Biosorption, Sugarcane Bagasse Ash (SCBA), Chitosan Composite (MISCBA), Heavy Metal Removal, Industrial Wastewater Treatment.

Digital Epidemiology: AI and social media for disease outbreak prediction

[1]SRIDEVI.M & [2]BHARATHI.B

[1]II MSc MLT, MMM College of Health Sciences, Chennai

[2]Professor, Dept., of MLT, MMM College of Health Sciences, Chennai

Email: sridevim4919@gmail.com

Abstract

Digital epidemiology has emerged as a transformative approach to disease surveillance by utilizing digital data sources such as social media, search engine queries, wearable devices, and mobile health applications. Artificial Intelligence (AI), particularly Machine Learning (ML) and Natural Language Processing (NLP), enables real-time analysis of these large-scale datasets to detect early signs of infectious disease outbreaks. Unlike conventional surveillance systems that often experience reporting delays, AI-driven digital epidemiology provides rapid outbreak prediction, geographical hotspot identification, and trend analysis. Recent studies have demonstrated the effectiveness of AI models using platforms such as X (formerly Twitter), Reddit, Google Trends, and health forums for monitoring diseases including COVID-19, Influenza, Dengue, and Mpox. However, challenges such as misinformation, data privacy, sampling bias, and ethical concerns remain significant obstacles. This paper reviews recent advancements (2023–2026) in AI-powered digital epidemiology, discusses current methodologies, highlights innovative applications of Large Language Models (LLMs) and multimodal AI, and explores future research directions for improving global public health surveillance.

Keywords: Digital Epidemiology, Artificial Intelligence, Machine Learning, Social Media Analytics, NLP, Disease Surveillance, Outbreak Prediction.

Isolation and characterization of antimicrobial compound from soil derived Streptomyces and its application

S. MUKESH

Department of Microbiology,

Dwaraka Doss Goverdhan Doss Vaishnav College (Autonomous)

Arumbakkam, Chennai – 600106

Email: mukeshshunmugam@gmail.com

Abstract

The rapid emergence of antimicrobial resistance necessitates the exploration of novel microbial resources for bioactive secondary metabolites. In the present study, Streptomyces species were isolated from twelve soil samples collected across six ecologically diverse environments and systematically screened for antimicrobial potential. A total of 24 isolates were recovered, of which 16 exhibited inhibitory activity during primary screening, while isolate AIA 24 consistently demonstrated the strongest broad-spectrum antibacterial activity throughout sequential screening assays. Cell-free metabolites of AIA 24 produced inhibition zones of 12 mm against Escherichia coli and 18 mm against Staphylococcus aureus, leading to its selection for further characterization. Morphological, biochemical, chemotaxonomic, and 16S rRNA analyses identified the isolate as Streptomyces albus. Bioactive metabolites obtained through ethyl acetate extraction and silica gel column chromatography displayed characteristic UV absorption peaks at 330.8, 347, and 356 nm, while FTIR, GC–MS, and NMR analyses confirmed the presence of structurally diverse antimicrobial compounds. The purified metabolite exhibited broad-spectrum antibacterial activity with MIC values ranging from 12.5–50 µg/mL, together with strong antioxidant (85% DPPH radical scavenging) and anti-inflammatory (98% inhibition of protein denaturation) activities. Collectively, these findings identify Streptomyces albus AIA 24 as a promising reservoir of multifunctional bioactive metabolites with significant potential for future therapeutic development.

Keywords: Antimicrobial resistance, Bioactive metabolites, 16S rRNA

HLA-optimized multi-epitope vaccine design against nipah, marburg, lassa, ebola, and crimean-congo hemorrhagic fever viruses

POOJA. S

Department of Microbiology, Saveetha Dental college and hospital, Chennai, India

Email: poojasubramonian@gmail.com

Abstract

Emerging zoonotic viruses such as Nipah virus, Marburg virus, Lassa virus, Ebola virus, and Crimean-Congo hemorrhagic fever virus (CCHFV) are associated with high mortality rates, epidemic potential, and the absence of widely available, broadly protective vaccines. The extensive genetic diversity of Human Leukocyte Antigen (HLA) molecules significantly influences antigen presentation and T-cell-mediated immune responses, making population-specific vaccine design an important strategy for maximizing vaccine efficacy. Immunoinformatics enables the identification of conserved immunogenic epitopes across multiple viral pathogens, facilitating the rational design of broad-spectrum multi-epitope vaccines with improved population coverage. To design a broad-spectrum multi-epitope vaccine against Nipah virus, Marburg virus, Lassa virus, Ebola virus, and Crimean-Congo hemorrhagic fever virus by identifying conserved immunogenic epitopes from selected viral proteins and optimizing the vaccine construct for Indian HLA allele profiles using immunoinformatics approaches to maximize antigenicity, immunogenicity, and population coverage. Conserved viral sequences were screened for cytotoxic T lymphocyte (CTL), helper T lymphocyte (HTL), and B-cell epitopes. Selected epitopes were evaluated for antigenicity, allergenicity, toxicity, IFN-γ induction, and binding to dominant Indian HLA alleles. The final vaccine construct incorporated these epitopes linked with an adjuvant and a PADRE sequence. Evaluation included population coverage, structural modeling, molecular docking with immune receptors, normal mode analysis, immune simulation, and in silico cloning. The vaccine construct demonstrated high antigenicity and non-toxicity, achieving 99.6% coverage across Indian populations. Structural analysis confirmed a stable 3D conformation, supported by a 96.67% Raman favoured score. Docking with the TLR4 receptor revealed high thermodynamic stability, evidenced by a binding energy of -5556.28 kcal/mol and 0.00 clash score. Immune simulations predicted robust cellular and humoral responses, while codon optimization confirmed excellent compatibility for bacterial expression. This study establishes the theoretical efficacy and safety of an HLA-tailored multi-epitope rabies vaccine, providing a robust candidate for subsequent experimental validation.

Keywords: Zoonotic viruses, vaccine, IFN-γ, cytotoxic T lymphocyte

Metabolomic and Bioinformatic Insights into Chia Seed–Fortified Synbiotic Yoghurt: A Dietary Intervention for Preventing Emerging Infectious Diseases

U. BHAVATHAARANI[1] AND A. SUBHASHINI *

[1]PG Student,* Associate Professor

Department of Microbiology, Ethiraj College For Women, Chennai 600008

Email: ubhavathaarani16@gmail.com

Abstract

The rapid emergence of infectious diseases and the growing prevalence of antimicrobial resistance have increased the need for complementary dietary strategies that support immune function and gut health. Functional foods, particularly synbiotic dairy products, have gained considerable attention due to their ability to modulate the gut microbiota and promote the production of health-beneficial metabolites. Chia seeds (Salvia hispanica L.) are rich in dietary fiber, omega-3 fatty acids, proteins, polyphenols, and antioxidants, making them an ideal natural prebiotic ingredient for functional yogurt development. This study explores the fortification of synbiotic yogurt with chia seeds (1% and 2%) and evaluates its physicochemical, nutritional, microbiological, and sensory properties alongside advanced metabolomic and bioinformatic analyses. Chia seed supplementation enhanced protein, dietary fiber, omega-3 fatty acids, viscosity, and probiotic viability while maintaining acceptable sensory quality, with the 1% formulation showing the highest consumer acceptance. Untargeted metabolomic profiling using LC–MS, GC–MS, and NMR is proposed to identify fermentation-derived metabolites, including organic acids, amino acids, peptides, short-chain fatty acids, vitamins, and phenolic compounds that contribute to the functional properties of the yogurt. Bioinformatic analysis using databases and platforms, enables metabolic pathway reconstruction, and network analysis to elucidate interactions between chia-derived bioactive compounds and probiotic metabolism. The integration of metabolomics and bioinformatics provides a comprehensive understanding of fermentation dynamics, postbiotic production, and metabolic pathways associated with immune modulation and gut microbiota health. This integrative approach also offers valuable insights for the development of next-generation functional dairy products with scientifically validated health benefits.

Keywords: Chia seeds (Salvia hispanica L.), Synbiotic yogurt, Functional foods, Dietary intervention, Metabolomics, Bioinformatics, LC–MS, GC–MS, NMR, Gut microbiota, Postbiotics, Emerging infectious diseases, Immune modulation.

Comparative Evaluation of Citrus reticulata- mediated Carbon Dots and Chitosan Nanoparticles as Potential Nanoparticles for Salivary α-Amylase-Based Forensic Biosensing

Dr. RANJANA N.I

Department of Forensic Odontology, Saveetha Dental college and hospital, Chennai, India

Email: 152539001.sdc@saveetha.com

Abstract

Saliva is an important forensic evidence that links individuals, objects, and crime scenes. However, conventional saliva detection methods are laboratory-based and time-consuming. Nanoparticles offer favourable physicochemical and optical properties, making them promising analytical materials for forensic saliva detection. This study aimed to synthesise and compare C. reticulata-mediated Carbon Dots and Chitosan Nanoparticles by evaluating their physicochemical characteristics using UV–Vis, FTIR, DLS, zeta potential analysis, and SEM, followed by an in vitro α-amylase inhibition assay to investigate their potential for future forensic saliva biosensing. Preparation and physicochemical characterization of C. reticulata-mediated Carbon Dots and Chitosan Nanoparticles were performed via UV-Vis, FTIR, DLS, zeta potential determination, and SEM. Analytical evaluation was conducted via an in vitro α-amylase inhibition assay (10-50 µg/mL). Both nanoparticles were successfully synthesised and exhibited distinct physicochemical properties, including differences in surface charge, particle morphology, hydrodynamic size, and colloidal stability with concentration-dependent α-amylase inhibitory activity. The C. reticulata-mediated Carbon Dots showed slightly better overall performance and represent a reliable nanoparticle from agricultural waste. These findings support the continued development of eco-friendly nanoparticle-based approaches for future forensic saliva biosensing.

Keywords: Biosensor, Carbon dots, Chitosan, Nanoparticles, Saliva

Saveetha Platform Advancing Research Commercialization

Where ideas transform into innovations.....

Join us to explore the unexplored areas in the field of Medicine, Dentistry, Bio and Life Science Research