

BOOK OF ABSTRACTS

**Published on the Occasion of a International Conference on
Cutting-Edge Strategies in Epidemiology and
Diagnostics of Infectious Diseases (CESEDID - 2025)**

Organizers

**Department of Microbiology, Centre for Infectious Diseases (CID),
Saveetha Dental College and Hospitals, SIMATS, Chennai**

**Editors: Rajesh Kanna Gopal, A.S. Smiline Girija, R.V. Geetha,
Sathish Sankar, J. Vijayashree Priyadharsini,
Pitchaipillai Sankar Ganesh & Priya Devi K.**

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Impaired metabolism in the exhausted CD8⁺ T-cell from people living with HIV

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In people living with HIV (PLWH), chronic viral replication and antiretroviral therapy (ART)-associated toxicity drive progressive T cell exhaustion—an immunological state marked by impaired effector functions and substantial metabolic reprogramming. These metabolic alterations compromise cellular energy homeostasis, functional persistence, and overall immune competence. A deeper understanding of the metabolic dysregulation underlying T cell exhaustion may reveal novel avenues to restore immune surveillance and enhance therapeutic efficacy in HIV management. In our study, we assessed the prevalence and metabolic gene expression profiles of exhausted CD8⁺ T cells across three clinically distinct PLWH cohorts: viremic treatment-naïve (TN), viremic treatment-failure (TF), and aviremic treatment-responders (TR). Our analysis revealed significantly elevated frequencies of exhausted and terminally differentiated CD8⁺ T cells in viremic TN and TF individuals compared to aviremic TR participants. Transcriptomic profiling using NanoString technology identified a broad downregulation of key metabolic genes in exhausted CD8⁺ T cells from viremic subjects, suggesting a shift toward a metabolically quiescent phenotype reminiscent of naïve T cells. Collectively, our findings underscore the role of impaired

metabolic programming in driving CD8⁺ T cell dysfunction in viremic PLWH and highlight metabolic pathways as potential targets for immune restoration strategies.

Keywords: T cell exhaustion, HIV, CD8⁺ T cells, Metabolic reprogramming, NanoString transcriptomics

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Emergence of Antifungal-Resistant *Candida auris*: A Global Public Health Concern

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Candida auris has rapidly spread worldwide as an antifungal-resistant organism which poses a major public health danger. Since its discovery in 2009 multiple countries have reported the presence of *C. auris*, which shows high mortality rates along with continuous colonization in healthcare environments. *C. auris* stands out among other *Candida* species because of its multidrug resistance (MDR) to standard antifungal medications like azoles, polyenes, and echinocandins which creates serious treatment limitations. The persistence of the pathogen on hospital surfaces combined with its regular misdiagnosis using standard lab tests presents additional challenges for infection control and prevention methods. Recent genetic research demonstrates that separate clonal outbreaks occurring on multiple continents indicate accelerated resistance development and evolutionary adaptation driven by widespread antifungal application and environmental stress factors. The scarcity of effective antifungal treatments demands immediate development of improved surveillance systems and innovative treatment methods to control *C. auris* outbreaks. Stringent hygiene practices and environmental decontamination combined with antimicrobial stewardship represent essential infection control measures that help to reduce transmission

rates. The development of effective antifungal treatments alongside improved outbreak management plans and stronger healthcare policies demands global cooperation to tackle this new infectious threat. The analysis presents information about the epidemiology of *C. auris* alongside resistance mechanisms and diagnostic challenges while proposing interventions for infection control that underline the urgency of a unified response.

Keywords

Candida auris, antifungal resistance, multidrug resistance, healthcare-associated infections, public health, epidemiology, infection control, diagnostics, global health crisis.

Gut Microbiome-Based Research on Health and Medicine

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The gut microbiome lives in the digestive tract and significantly impacts health through roles in immunity, digestion, and the gut–brain axis. The colon harbors the highest microbial density, mainly anaerobic bacteria from 30–40 key species. These microbes make up most of the faecal dry mass, and their combined gene pool is about 100 times larger than the human genome. Research indicates the microbiota-gut-brain axis enables two-way communication between the gut and brain. Imbalances in the gut microbiome, known as dysbiosis, are linked to neurodegenerative diseases like Alzheimer’s, potentially through mechanisms involving amyloid- β and tau protein production, neuroinflammation, and metabolic dysfunction. Although the gut microbiome’s role in Parkinson’s disease and other chronic conditions is not fully proven to reverse them, emerging evidence suggests that modifying the microbiome may help ease symptoms and possibly slow disease progression. Probiotics and prebiotics may help prevent cancers such as colorectal, breast, cervical, liver, bladder, and colon by boosting anti-inflammatory cytokine production, which plays a role in inhibiting cancer cell development. AI (Artificial Intelligence), especially machine learning and deep learning, enhances the analysis of complex gut microbiome data by

efficiently handling multi-omics datasets to identify key gut microbial markers linked to health and disease. This integration holds great promise for personalized healthcare and novel treatments. However, ethical considerations such as data privacy and informed consent must be prioritized. AI tools also support predictive modeling of gut microbial interactions and improve biomarker detection, helping to uncover disease causes and guide targeted therapies.

The Microbiome nexus in health and disease – Pivotal focus
and current trend

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The MICROBIOME plays a pivotal role in human biology, performing key functions in digestion, mood and behavior, development and immunity, and a range of acute and chronic diseases. Coexistence of microbial consortia bring about functionally balanced by symbiotic or antagonistic relationships. Antagonism is often characterized by the production of antimicrobials against other organisms occupying the same environmental niche. Microbial co-evolution in the gut has led to the development of specialized antimicrobials, which is attracting increased attention as these may serve as novel alternatives to antibiotics and thereby help to address the global problem of antimicrobial resistance. More than 1,000 species of bacteria have been identified in each topographical niche of humans and especially in the human mouth and gut. Understanding this incredibly diverse "microbiome" that can greatly impact health, and disease is pivotal and one of the hot trends in biological research. Because bacteria are routinely genetically engineered in labs, modifying genes of our intestinal and oral microbes to function more than just help digest our food. Among the major players in any microbiome, the Keystone

pathogens play a king function in modulation hence predispose to either health or disease state. Positive approach of host-pathogen interactions favor microbial harmony rather than dysbiotic infections. While in the recent past, since the microbiome keystone pathogens and the diversification of unique microbiome favors health, focusing on a synthetic intervention modulating host-pathogen interaction can empower the beneficial microbiome in to a “living medicine”.

The Hidden Conversation: Exploring Host-Microbiome Relationships Using Metagenomics

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The host microbiome constitutes a dynamic and integral component of health, immunity, and disease progression. With the emergence of high-throughput next-generation sequencing (NGS) technologies and advanced bioinformatics, it is now possible to explore the intricate “hidden conversation” between hosts and their microbial communities. In the context of infectious diseases, understanding microbiome composition, functional shifts, and host-microbe-pathogen interactions is increasingly critical for advancing epidemiological surveillance and diagnostic strategies. This presentation explores the role of Metagenomics particularly 16S rRNA-based community profiling in uncovering microbial diversity and functional potential. Tools such as QIIME enable culture-independent, rapid characterization of microbial populations from complex biological samples. We examine how microbiome dysbiosis correlates with disease susceptibility, modulates host immune responses, and offers novel biomarker candidates for diagnostics. Furthermore, we demonstrate how integrated bioinformatics pipelines and AI-enhanced data analysis support the identification of microbial patterns relevant to early detection, outbreak monitoring, and personalized therapeutics.

By bridging molecular biology, microbial ecology, and computational biology, this work underscores the critical role of microbiome research in transforming our approach to infectious disease diagnostics, prevention, and control.

Keywords: microbiome, metagenomics, infectious diseases, diagnostics, bioinformatics

Personalized Medicine: Role of Molecular Diagnostics

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Amico DX, Houston, Texas, USA.

Molecular diagnostics provides critical information about a patient's unique genetic makeup to enable tailored therapy, reduce adverse drug reactions, decrease costs, and improve patient outcome. From viral load testing where molecular disease monitoring made its debut to the current applications of liquid biopsy to assess cell-free DNA, molecular diagnostic techniques have become accepted as standard of care. This presentation will discuss the key aspects and trends of Molecular diagnostics in personalized medicine and how Molecular diagnostics is poised to revolutionize personalized medicine by enabling earlier and more accurate disease detection.

Epigenetics of antigen switching in host-pathogen interactions

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The epigenetic players contribute significantly to the fine-tuning of gene expression in eukaryotic organisms. The plasticity of genome organization and its functional outcomes are tightly regulated for the successful development of organisms. The epigenetic players that mediate gene silencing are conserved from lower eukaryotic organisms to multicellular organisms. The intracellular lower eukaryotic organisms, like protozoan pathogens, exploit host machinery to establish a successful infection. Similarly, the human malaria parasite is an obligate intracellular pathogen that extensively modulates its gene expression program in response to the host cells, including the liver and RBCs. One such mechanism adapted by the malaria parasite is antigen switching to escape from host immunity, which paves the way to the development of severe malaria. In my talk, I will highlight our recent work on epigenetic reader proteins that regulate the differential expression of variable surface antigenic genes in *P. falciparum* through selective interaction with modified chromatin. Such interaction tightly regulates the RIFIN (one of the VSA family), which is linked to the development of severe malaria.

Significant discoveries in infectious diseases, biological, and chemical sciences

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Significant discoveries in infectious diseases, biological, and chemical sciences include the development of antibiotics and vaccines, the discovery of DNA's structure, and the establishment of the germ theory of disease. These advancements have revolutionized medicine and public health, leading to significant reductions in mortality and morbidity from infectious diseases.

Significant inventions in infectious diseases include germ theory of disease, antibiotics, vaccines for eradicating infectious diseases, molecular genetics to understand the mechanisms of disease leading to targeted therapies and diagnostics, antimicrobial resistance, new drugs and alternative therapies, such as phage therapy, which uses viruses to target specific bacteria, infectious disease epidemiology helping to identify outbreaks and develop public health strategies, Koch's postulates to prove a specific microbe causes a specific disease. Significant inventions in biological sciences include structure of DNA, DNA replication and protein synthesis, genetic engineering, techniques like gene cloning and recombinant DNA technology have enabled scientists to manipulate genes and create new biological products, such as insulin for diabetes

treatment, evolutionary biology, synthetic biology for designing and building new biological systems, including creating synthetic genomes and viruses.

Significant inventions in chemical sciences include drug discovery and development for design of new drugs to treat a wide range of diseases, including infectious diseases, understanding chemical reactions in living organisms to understand the complex chemical reactions within cells and organisms, analytical chemistry techniques to identify and quantify biological molecules, aiding in disease diagnosis and treatment, chemical synthesis of biomolecules such as proteins and nucleic acids, which are essential for biological research and drug development. All the inventions mentioned in this paper have received noble prizes.

Current status of HIV epidemic in India and trends to achieve 2030 goals

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Since the first identification of HIV in India in 1986, India has achieved tremendous progress in reducing the burden of HIV as a major public health problem. The adult level HIV population level prevalence is estimated to be around 0.20%. New infections have decreased by around 44% as compared to the estimates of 2010. This has been made possible only by government commitment since the last three decades and concerted initiatives.

The HIV epidemic in India context remains a concentrated epidemic driven by key population. The average age of identification of new infections has been progressively decreasing over the last decade. Younger individuals spend more time accessing the internet, communicate by using online platforms, use virtual channels to find new partners and build networks / communities to indulge in high-risk behaviours leading to potential increase in new infections.

Combination prevention remains the most effective strategy to bring down the burden of new infections. In addition to the current programmatic interventions, there is an immediate need to de-stigmatise HIV, roll-out pre-exposure prophylaxis program for HIV and introduce integrated care health care delivery systems for STI / TB.

India is a signatory to achieve SDG goals by 2030 and is and is a strong votary of meeting UNAIDS 95-95-95 targets by 2030. Achieving the first 95 is the key to reaching these targets. Newer initiatives like enhancing public awareness using digital platforms, introduction of HIV self-testing, enhancing reporting through mandatory notification of the disease especially from the private sector health-care providers must supplement current laboratory programs under NACO.

India has around 2.5 million PLHIV and retention in care and motivation towards achieving virological suppression below transmissible levels, is essential to prevent transmission. Initiatives to identify-motivate ART defaulters, early laboratory identification of ART drug resistance cases is essential where newer targeted programs are being rolled out.

Current dictum for PLHIV is to be on oral ART for entire individuals' life-span. With increasing life expectancy, motivation to be adherent to treatment, requires periodic counselling through a government supported ART centres. With enhanced scientific knowledge about in biology and immunological aspects of HIV, newer insights are being developed to find cure for HIV which could happen in the force able future.

Biotechnological approaches for aquaculture vaccine
development

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Due to its delicious taste and high revenue generation on the global market, aquaculture is one of the most profitable food production industries. Utilizing a variety of culture techniques, aquaculture production has increased in recent decades. Unfortunately, the aquaculture industry has had significant issues with infectious diseases over the past 35 years, which has had an impact on production levels. Traditional disease treatment methods are ineffective and pose numerous environmental risks. Due to the huge economic losses and severe damages in the cultivable fin and shellfish species by microbial diseases, attention should be diverted to develop efficient treatment protocols including developing modern vaccine development protocols. Even traditional vaccines have been shown to provide immunity to the host animal against microbial pathogenesis; however, they have certain drawbacks, such as a weaker and shorter immunity, virulence reversion, ineffectiveness, heat liability, etc. In contrast to traditional vaccines, recombinant vaccines are a third-generation strategy that uses genetic engineering to create particular pathogen

components that increase robust and durable immunity. Finding the immune gene is crucial for effective vaccine development in order to provide strong and long-lasting immunity. Microbial biofilm, outer membrane proteins (OMP), virulent genes, viral capsid proteins, viral like particles (VLP), and other cell components are the best for robust and long-lasting immunity. A variety of development strategies, such as recombinant technology-based eco-friendly edible vaccines, recombinant subunit vaccines, DNA vaccines, genetically modified vaccines, RNA vaccines with RNA interference (RNAi), reverse vaccines, and phage-based vaccines, are very beneficial against viral and bacterial infections. The expression system is crucial for the effective and high- quality production of recombinant subunit vaccines. Baculoviral, yeast, mammalian cell and micro algae based expression produce strong and last lasting immunity in the cultivable fin and shellfish species.

Keywords: Aquaculture; Biotechnology tools; Recombinat DNA technology; Edible vaccine; RNA interference; Expression systems

A novel class of bacterial mobile genetic elements rich in
antiphage defense systems

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An arms race between bacteria and bacteriophages has driven the emergence of diverse bacterial immune strategies. Several bacterial immune systems against phages have been identified recently, but many remain functionally uncharacterized. Distribution of these defense systems within bacterial genome is also not well understood. We recently identified a widely distributed mobile genetic element, named as Gamma-Mobile-Trio (GMT) Island. This island serves as a bacterial survival toolkit by carrying a variety of functional genes including antiphage defense systems, type VI secretion system (T6SS) effectors and antibiotic resistance genes. We demonstrated that GMT-containing Islands are active mobile genetic elements. Within the GMT Island, we discovered four previously unknown antiphage defense systems. One such system, named GAPS1 (GMT-encoded Antiphage defense System 1), is activated upon detection of a phage capsid protein and induces cell dormancy to prevent phage replication. This work highlights the complex nature of bacterial defense and competition mechanisms in response to phage infection.

Impact of Climate Change in Zoonoses: Current Status,
Knowledge Gaps and Future Trends

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The outbreak of human zoonotic diseases has been initiated due to the complex interaction among humans, animals, environments and other vector organisms. The prevalence of zoonotic disease can be influenced by climatic conditions, that can regulate all the key factors including disease transmission, population dynamics, and their interactions. To control climate-associated zoonotic diseases in human, it is essential to understand the complex interconnections between climate conditions, human activities, wildlife health and seasonal-associated zoonotic diseases. Furthermore, surveillance system, and systematic analyses has been used to early diagnostic and therapeutic response. Recent zoonotic risk situations under extreme climate conditions and microbial evolution data are still limited. To emphasize this gaps, integrative approaches including disease epidemiology, climate science, and ecology analytics are essential. Notably, the One Health approach, interconnection of human, animal, and environmental health, should be adopted to predict and diminish future outbreaks. In addition, advanced technologies in genomic surveillance, predictive modelling and remote sensing are some of the

promising tools to strengthen early warning systems. Ultimately, proactive global collaboration and policy efforts will be a key effective activity to control threats and safeguard public health globally.

Keywords: Disease management, One Health approach, Human Zoonotic Disease, Global collaboration.

Hepatitis B Virus infection and Pathogenesis

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Introduction: Hepatitis B Virus is an infectious liver disease caused by Hepatitis B Virus. Hepatitis B Virus infects about two billion people worldwide. About 350 million are chronic carriers of HBV infection approximately one million individual die every year due to HBV related liver disease. **Outcome** of chronic Hepatitis virus infection leads to chronic Hepatitis, cirrhosis of liver, liver cell failure and hepatocellular carcinoma. **Severity** of Hepatitis B infection is related to host immune system. Cellular and humoral mediators are responsible for effective clearance and long term protection from HBV. **Mechanism** of virus host reaction depends on Various HBV Virulence factors like Protein molecule synthesis by virus, Kinetoplastid membrane protein, Nucleotidase, Viral secretion system and Biofilm formation. **Pathogenesis** contributed by cellular component of hepatocyte like cytoskeleton, microtubules, immune protein at endoplasmic reticular epithelial cell, capillary endothelial cell, fibroblast and sinusoidal cell. **Progression** to fibrosis, cirrhosis and hepatocellular carcinoma is mediated by mediators like TNF alpha, Interferon GAMA, interleukin which leads to pleiotrophic effects of stellate activation leads to chronic persistent inflammation, excessive connective tissue formation, irreversible fibrosis, cirrhosis and hepatocellular carcinoma.

Conclusion HBV is not a cytopathogenic virus itself. Cytokine plays a major role in liver injury. Host reaction is most significant pathogenesis in HBV infection. It is the host and not the virus responsible for pathogenesis.

***Helicobacter pylori* – Past, Present and Future**

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Introduction: The discovery of *Helicobacter Pylori* (H.p) by Warren and Marshal from the stomach mucosa in 1983 has changed the landscape of Acid Peptic Disease and stomach cancer. *H. pylori* infection occurs worldwide. **Prevalence** varies from 20% to 80%. Transmission of *H. pylori* occurs from person to person following oral –oral or fecal-oral route. *H. pylori* colonize in gastric mucosa. The **pathological events** depends on *H. pylori* strain virulence, host genotype and environmental epigenic and genetic factors. **Various tests** are available for diagnosis. Histology test is most specific and sensitive. The **treatments** are critically analyzed for Hp good and bad aspects. We collected information on 1. Effect of Hp on gastric and gut microbiome and 2. The effects of Hp eradication on gastric and gut microbiome. 3. The value of probiotic co-supplementation. We arranged this article in the following sequence. 1.brief

account of Hp, its pathogenesis and its therapy. 2.effect of Hp on gastric and gut microbiomes. 3.effect of Hp eradication therapy on gut microbiomes 4.effect of probiotics supplementation on gut microbiomes. 5.an overall review for future studies. Antibiotic resistance continues to be a major challenge molecular targets against essential bacterial proteins could be key to resolving antibiotic resistance.

Case Studies of Organophosphate Pesticide Poisoning due to Occupational and Environmental Exposure: An Indian Perspective

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Over the past decades, pesticide poisoning has drawn serious attention from the public, as it accounts for a significant number of deaths occurring each year. Organophosphate pesticides leading to the current trend and these are less frequently investigated. This review focusing on highly hazardous and widely used organophosphate pesticides in India such as phorate, monocrotophos, methylparathion, dichlorvos and triazophos. The extent of contamination has been found by the mortality rate of occupational poisoning, self-poisoning and food poisoning. This is the first case report of the above five highly hazardous organophosphate pesticide poisoning pertaining to India. This review emphasized the organophosphate pesticide exposure and appropriate poisoning cases in several part of India.

Keywords: Agricultural farmers; Human Exposure; Pesticide Poisoning; Case Studies; Health Effects

Molecular Characterization of β -lactamase Resistance Genes Among Gram-Negative Isolates from Cancer Patients

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Background: Antimicrobial resistance (AMR), particularly β -lactamase-mediated resistance in Gram-negative bacteria (GNB), poses a significant threat to immunocompromised cancer patients. This study aimed to characterize β -lactamase resistance genes (*bla*TEM, *bla*SHV, *bla*CTX-M, *bla*OXA) in clinically significant GNB isolates from cancer patients and correlate genotypic findings with phenotypic resistance profiles.

Methods: A prospective cross-sectional study was conducted at Malabar Cancer Centre, India, over four months (April–June 2025). Non-duplicate isolates of *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Acinetobacter baumannii* (n=101) from clinical specimens (urine, blood, exudates, respiratory, stool) were analyzed. Bacterial identification used MALDI-TOF MS, and antibiotic susceptibility

testing (AST) was performed via VITEK 2 Compact. Multiplex PCR detected β -lactamase genes.

Results: Urine (50.5%) and blood (24%) were the predominant sources. *K. pneumoniae* (75.2%) and *E. coli* (24.8%) were the most frequent isolates. The *bla*CTX-M gene was predominant (80% in *E. coli*, 78% in *K. pneumoniae*), often co-occurring with *bla*TEM (52%, 55%) and *bla*SHV (28%, 66%). Carbapenem resistance was high (*E. coli*: 100% meropenem resistance; *K. pneumoniae*: 89.4%). Tigecycline remained the most effective antibiotic (80% sensitivity in *E. coli*, 68.4% in *K. pneumoniae*).

Conclusion: High prevalence of ESBL and carbapenem resistance genes underscores the need for molecular surveillance in oncology settings to guide antibiotic stewardship and infection control.

Keywords: β -lactamase, ESBL, carbapenem resistance, Gram-negative bacteria, cancer patients, molecular surveillance, antimicrobial resistance.

Decoding Cross-Species Immune Signatures: An Integrated One Health Approach Reveals Novel Targets for Pan-Pathogen Defense

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Emerging and re-emerging infectious diseases often originate at the animal–human–environment interface, demanding a unified

One Health strategy. This study explores the immunological convergence across humans, domestic animals, and wildlife to identify conserved immune signatures critical for pan-pathogen defense. By integrating multi-omics datasets (transcriptomics, proteomics, and epigenomics) and immunological profiling from representative species, we reveal shared molecular pathways—including Toll-like receptor signaling, inflammasome activation, and interferon-stimulated gene networks—that are consistently mobilized in response to viral and bacterial threats. Notably, key mediators such as IRF7, MX1, and cGAS-STING were recurrently enriched across species, highlighting potential universal immune checkpoints. Environmental factors like microbiome diversity and pollutant exposure modulated these responses, underscoring the ecological complexity of immune regulation. Functional validation in cross-species cell models confirmed the broad-spectrum protective potential of select targets. These findings establish a blueprint for pan-pathogen immunological resilience and offer a foundation for next-generation vaccines and therapeutics that transcend species boundaries. This work reinforces the value of One Health-informed immunology as a transformative lens in global infectious disease preparedness.

Keywords: Cross-species immunology, Pan-pathogen resistance, One Health paradigm, Immune signaling pathways, Comparative omics analysis, Zoonotic disease defense, etc.

Filarial infection among the population ineligible for Mass Drug Administration (PieforM) in an endemic area: Implications for filariasis elimination program in India

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Lymphatic filariasis (LF), commonly known as elephantiasis, is a debilitating and severely disfiguring disease caused by helminths *Wuchereria bancrofti*, *Brugia malayi*, and *Brugia timori*. Global programme to eliminate LF as a public health problem is based on mass drug administration (MDA) of two or three drugs. MDA is administered to all the consenting population eligible for treatment. However, pregnant women, children below 2 years of age, and individuals with chronic diseases are considered as the **Population ineligible for MDA (PieforM)** and will not be covered during the MDA. The possible risk of contribution of this ineligible population as a source of infection in interrupting transmission is not known. In this study, a total of 36 villages were selected randomly out of 235 villages in Yadgir sub-district of Karnataka State, India. Family registers of community drug distributors were used to identify the PieforM and were

screened (n = 921) for filarial antigenemia using the Filariasis Test Strip (FTS). All the antigen-positive individuals were screened for microfilariae in the night blood smears. We observed high levels of filarial infection in comparison with the recommended thresholds for defining filarial endemicity in terms of antigenemia (2%) and microfilaraemia (1%) in all three categories of the PieforM. The PieforM will be a potential source of infection during the post-MDA period as these populations will never be treated and missed out during the MDA. Strategies such as “test and treat” individuals or evaluate and treat the community may be useful to prevent possible resurgence of infection after stopping MDA. The results will be presented during the Conference.

Keywords: Lymphatic filariasis, elephantiasis, *Wuchereria bancrofti*, mass drug administration

MATTAN TAILAM’A MEDICATED HERBO-MINERAL OIL

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‘*Mattan tailam*’, otherwise known as ‘Paccai ennay’ is a medicated herbo-mineral oil used in Siddha system of medicine. The preparation of tailams involve different oils in various medicines as the base material to extract the active chemicals from new drugs. The tailam is

used, externally for eczema and putrid ulcers, the tailam is also used in earache, accompanied by discharge of pus. The three ingredients which constitute the oil are Umattai ilia or leaf – *Datura metel* L. Tenkay enney – *Cocos nucifera* L. and Turucu – Copper sulphate. 5500 g, 1400 mL and 350 g respectively soaked for a period of one week.

Key words: Mattan tailam, herbal oil, datura, coconut, copper sulphate.

UHPLC-MS/MS based characterisation of Kyasanur forest virus disease (KFD) Envelope protein

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Kyasanur forest virus disease is a tick-borne zoonotic disease-causing public health concern in some south Indian states with fatality rate of 2-10%. KFD virus causes serious haemorrhagic fever or commonly called as “Monkey Fever” in human’s and clinical manifestations include headache, conjunctivitis, myalgia, vomiting, diarrhoea, and haemorrhagic fever. KFD is caused by Flaviviridae family virus called “Kyasanur forest disease virus’ (KFDV) and transmitted through ticks that harbour the Flavivirus viruses. *Haemaphysalis spinigera* ticks are the main vector and feeds on different hosts and predominant across India, Vietnam and Sri Lanka. KFD outbreaks are reported in last decade and

increase in new cases of KFD has been reported since 2012 in human and primates and mostly in Karnataka and few cases in Kerala, Tamil Nadu, Maharashtra and Goa. Since, specific treatment is not available for KFD virus infection except vaccination, it is very importance to diagnose early for the better management of disease and to contain epidemiological outbreaks. In order to identify and characterize the highly immunogenic proteins as antigens for diagnosis. UHPLC-MS/MS was used to identify the KFD ED domain III that can be useful as an antigen for the ELISA based detection for KFD virus.

Tackling Oral Biofilm Resistance: The Untapped Promise of *Selaginella bryopteris*

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Background:

Biofilm-related infections are a major challenge in dentistry, contributing to persistent periodontal disease, peri-implantitis, denture stomatitis, and delayed healing. Dual-species biofilms of *Staphylococcus aureus* and *Candida albicans* commonly colonize oral mucosa and prosthetic surfaces, where they resist routine antiseptics and promote antimicrobial resistance. Chlorhexidine remains the gold-standard oral antiseptic but has limited long-term biofilm efficacy at sub-inhibitory levels. *Selaginella bryopteris* ("Sanjeevini"), an ancient Indian herb known for its

potent antioxidant and stress-protective properties, remains untested as a biofilm-modulating agent in dentistry.

Aim:

To evaluate the effect of sub-inhibitory concentrations of chlorhexidine alone and in combination with *Selaginella bryopteris* extract on mono- and dual-species biofilms of *S. aureus* and *C. albicans*.

Materials

and

Methods:

Methanolic extracts of *S. bryopteris* will be prepared and characterized. Biofilms will be developed on polystyrene microtiter plates and treated with sub-MIC chlorhexidine, *S. bryopteris* extract, and their combination. Biofilm biomass will be assessed by crystal violet staining, metabolic activity by XTT assay, and structural changes visualized by light microscopy.

Results:

This is an ongoing study. Preliminary outcomes aim to show that *S. bryopteris* enhances the antibiofilm effect of chlorhexidine, offering a novel adjunct for managing oral biofilm-associated resistance.

Conclusion:

This study seeks to address the urgent need for innovative, evidence-based strategies to combat biofilm-associated antimicrobial resistance in dental practice. Demonstrating the benefit of combining a traditional phytochemical with a standard antiseptic could open new pathways for safer, more effective biofilm management and help dentists tackle hard-to-treat chronic oral infections with improved confidence and outcomes.

Influence of micronutrients on the growth of *Rhizopus Oryzae*

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Mucormycosis is the most common life-threatening secondary infection post covid. An increased incidence was observed among Diabetic and immunocompromised patients, which was explained on the basis of an increased availability of micronutrients and glucocorticoids as a treatment of choice. Though there are several effective antifungal drugs, resistance against these drugs is a major drawback. Spices are natural plant products enriched with the history of being used in herbal medicines for prevention and treatment of infectious diseases. India is the 'Land of Spices' and contributes for majority of medicinal spices cultivation. In the present study growth of mucor organisms under various micronutrients and indigenous spices has been assessed.

1.To evaluate the *In vitro* growth of mucormycosis in the presence of micronutrients.

2. To assess and evaluate the growth of mucor organisms in the media enriched with various indigenous spices

METHODOLOGY: *Rhizopus oryzae* quality control strain is used for the study. Inoculation of the strain at 37°C in the agar medium with micronutrients and spice extracts was done. The difference in colony forming units is compared with and without micronutrients, various spice extracts media and detailed assessment was done.

RESULTS: Zinc inhibits the growth, whereas iron supports the growth of *Rhizopus oryzae*. Comparing the indigenous spices of cinnamon, clove, pepper and turmeric. Antifungal properties is more in cinnamon compared to other spices.

Clinical benefit and re-suppression with TLD for the individuals who are failing with NNRTI based first-line HAART

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In Low- and Middle-Income Countries (LMIC), about 16 million people are currently receiving NNRTI-based first line therapy, of which 9 million are receiving TDF/3TC/EFV (TLE) or AZT/3TC/EFV (ZLE)-based first line therapy. Currently there is insufficient clinical evidence of individuals failing TLE to WHO recommended transition therapy TDF/3TC/DTG (TLD). Here, we report on the genotypic resistance profiles of patients who were failing NNRTI based first line HAART re-suppressed through recycling of TDF based NNRTI sparing transition to TLD in Chennai, India

We studied 300 participants attending YRG CARE, Chennai, who were failing NNRTI based 1stline HAART and their drug resistance mutations were grouped according to their TDF and AZT backbone. DRMs were interpreted using Stanford HIV drug

resistance database and its subtype was identified by REGA HIV-1 subtyping tool v3.0.

Subtype C was the predominant (97.3%). The median CD4 count and treatment duration among AZT vs TDF failing patients were [172 cells/ μ L (IQR 80-252) vs. 216 cells/ μ L (IQR 111-328) and 24 months vs. 61 months and it was found to be significant ($p < 0.0001$). High level of NRTI DRMs were observed in both AZT and TDF (78% & 81%) and K65R (25% vs. 2%), K70EG (21% vs. 2%), L74V (10% vs. 2%) and Y115F (13% vs. 1%) was higher among TDF ($p < 0.05$); whereas TAMs, M41L (30% vs. 15%, $p = 0.02$), L210W (8% vs. 1%, $p = 0.014$), T215Y (27% vs. 8%, $P = 0.0001$), K70R (24% vs. 9%, $P = 0.0026$), and K219QE (19% vs. 8%, $P = 0.0168$) were significantly higher in AZT group ($p < 0.05$). Genotypic predicted level of susceptibility to TDF were 63% and 77% in TLE and ZLE.

Conclusion: Individual failing with NNRTI based 1stline HAART can be resuppressed through recycling tenofovir in LMICs to the safe transition to more tolerable and affordable TLD.

Key words: Resistance, Dolutegravir, Low- and middle-income countries

Unveiling the potential of dried coconut (*Cocos nucifera*) haustorium as a nutraceutical

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Cocos nucifera (coconut) apple/haustorium has been traditionally consumed by people for its therapeutic potential. Despite its consumption, the complete nutrient profile was lacking. This study aimed to explore the nutritive value of dried coconut haustorium and analyze the phytochemicals by GC-MS analysis. The proximate composition of dried coconut reveals a high energy value due to the considerable number of proteins, fats, and carbohydrates. The amino acid profile shows a higher amount of essential amino acids, with cysteine and phenylalanine being more. In addition to sodium, dried coconut haustorium was found to be a potential source of minerals like calcium, magnesium, and potassium, along with trace elements like zinc, iron, and selenium. The vitamin C level was higher when compared to vitamins B₁ and B₂. By GC-MS analysis, 28 compounds were identified in the aqueous extract of coconut haustorium. The phytochemical composition revealed a greater number of fatty acids and their derivatives and other components with numerous therapeutic potentials. The results obtained provide a scientific validation for the consumption of coconut haustorium for many ailments due to its rich nutritional value and phytochemicals. Overall results indicate that coconut haustorium could be considered as a source of potential nutraceutical and therapeutic compounds that could find a place in food and pharmaceutical industries.

Keywords: Coconut (*Cocos nucifera*) haustorium; Proximate analysis; Minerals; Amino acids; GC-MS analysis.

Bioaccumulation of Chromium in *Phaseolus mungo* (L.) treated with titanium industry waste

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Contamination of soil, ground water, sediments, surface waters and air with trace metals is one of the major environmental problems. Owing to this study, this study focused on the investigation of the capability of the dried biomass of *Phaseolus mungo* (L.) to remove heavy metal (chromium) from titanium industry effluent. In *P. mungo* (2:1 ratio) maximum bioaccumulation of chromium was on the 60th day of exposure and the concentration were recorded as 0.623 ± 0.002 , 0.301 ± 0.028 and 0.224 ± 0.021 $\mu\text{g/g}$ in roots, stems and leaves. Chromium concentration was maximum in the phytal parts of *P. mungo* grown on titanium industry solid waste mixed with organic amendments (1:1, 2:1 and 3:1 ratio). From the results, it was confirmed that *P. mungo* can be effectively used for the treatment of heavy metal polluted industry effluent.

Keywords:

Seeds of *Phaseolus mungo*, Titanium industry waste, soil, sand and vermicompost.

An *in-vitro* study on the effect of *Vernonia arborea* fraction in reducing adhesion, quorum signals and invasion of enteric pathogens

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Enteric infections, caused by pathogens such as *Enterococcus faecalis* and *Salmonella typhi*, are of great public health concern due to the rising antimicrobial resistance. The anti-pathogenic potential of *Vernonia arborea* belonging to Asteraceae family, a plant with traditional medicinal properties, was assessed against these pathogens. The study demonstrates inhibitory activity of *V. arborea* fraction **against bacterial adhesion, quorum sensing, biofilm formation, and invasion**. The plant fraction showed significant anti-pathogenic activity at concentrations comparable or lower than standard antibiotics. The minimum inhibitory concentration of the fraction tested was 14 µg/ml against *E. faecalis* and 15 µg/ml against *S. typhi*. The minimum bactericidal concentration was found to be 14 µg/ml for *E. faecalis* and 20 µg/ml for *S. typhi*. The time kill kinetics showed, complete eradication of bacteria within 3-4 hours of treatment with the plant fraction at 2MIC concentration for *E. faecalis* and within 2 hours for *S. typhi*. In comparison to standard antibiotics ampicillin and ciprofloxacin, *V. arborea* revealed high reduction of both bacterial adhesion and biofilm forming potential. Further mode of action studies involving nucleic acid quantification

revealed a pattern similar to nucleic acid synthesis inhibitors like ciprofloxacin. These findings suggest a potential for *V. arborea* to be a source of effective, naturally acquired antimicrobial drug against enteric pathogens. Interference with pathogenic mechanisms also indicates possible usage as an additive compound with standard antibiotics, thus reducing the drug dependence and minimizing resistance development.

KEYWORDS - *Vernonia arborea*, Anti-pathogenic activity, Enteric pathogens, Quorum sensing inhibition, Biofilm reduction, antimicrobial resistance

Pharmaceutical Microbiology Applications of a Patent-Protected Glycolipid Biosurfactant from *Halomonas phoceae* MSJCR18: Dual Antimicrobial and Anticancer Therapeutic Potential

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A novel glycolipid biosurfactant produced by *Halomonas phoceae* MSJCR18 was characterized for pharmaceutical microbiology applications, focusing on emulsion stability, antimicrobial, and anticancer activities. The biosurfactant was purified using TLC and silica gel chromatography, demonstrating exceptional emulsification properties with 88.3% EI₂₄ index. This compound has been granted a patent for its superior emulsification activity and stability properties. Comprehensive antimicrobial screening against several Gram-positive, Gram-

negative bacteria, and fungal pathogens revealed significant therapeutic potential with MIC values. Anticancer evaluation using MCF-7 breast cancer cell lines through MTT assay demonstrated potent cytotoxicity with an IC₅₀ value of 43.86 µg/ml. The glycolipid structure proved critical for dual biological activities, combining antimicrobial efficacy with anticancer properties. These favourable pharmacological parameters indicate strong potential for pharmaceutical applications, including antimicrobial therapy and cancer treatment. The patent-protected emulsion stability properties further suggest utility in advanced drug delivery systems and pharmaceutical formulations. This multifunctional biosurfactant represents a promising candidate for biotechnological and therapeutic development in pharmaceutical microbiology, offering sustainable alternatives to synthetic compounds while providing dual-action therapeutic benefits for clinical applications.

Keywords: pharmaceutical microbiology, biosurfactant, MSJCR18, antimicrobial activity, anticancer activity, MIC, IC₅₀, *Halomonas phoceae*, glycolipid, MCF-7, drug delivery

Prevalence of Biofilm forming *A.baumannii* clinical isolates and the association with the resistant pattern of the bacteria

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Acinetobacter baumannii a Gram-negative bacteria responsible for hospital acquired infections. According to WHO, *A. baumannii* lists the top priority pathogens as it shows resistance to different class of antibiotics. Multidrug-resistant and extensively drug-resistant strains of *A. baumannii* that exhibit multiple drug resistance. Whereas the latter indicates resistance to at least five antibiotic categories, the former indicates resistance to at least three. Numerous virulence factors, such as porins, capsules, cell wall lipopolysaccharide, enzymes, biofilm formation, motility, and iron-acquisition systems, are indicative of *A. baumannii* pathogenesis. The present study aims to study the ability of biofilm formation and the development of multidrug resistance. The study was performed after obtaining institutional ethical clearance. The clinical isolates of *A. baumannii* were collected from the central laboratory, Sree Balaji Medical College and Hospital, Chennai. The biofilm formation of the isolates was screened using crystal violet staining and the prevalence of genes related to the biofilm formation and the Carbapenem resistant gene was studied using conventional PCR assay. Results showed the biofilm forming organism showed resistance to multiple drugs. *A. baumannii* was highly prevalent in urine sample and most of the sample showed

biofilm forming ability when compared with the samples collected from other sources like sputum, blood and pus.

Key words: *A. baumannii*, anti-microbial resistance, biofilm formation, PCR.

Identification of CviR inhibitors using ligand based-drug design and invitro analysis

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Phytochemicals from plant sources are abundant and easily available for clinical management. Designing inhibitors for quorum sensing and biofilm formation is a challenging task. *In-vitro* studies and clinical trials might take years to complete the drug design and discovery process. Bioinformatics approach has made finding suitable compounds through ligand-based structure design remarkable in the pharmaceutical industry and among researchers working on the formulation. The present study aims to optimize CviR protein inhibitors among analogs of hexadecanoic acid by pharmacophore, density functional theory, molecular dynamics simulations, and free energy binding. In addition, the gram staining and Minimum inhibitory

concentration is required to observe the anti-QS activity by the lead molecule.

Keywords: CviR; quorum sensing; inhibitors; analogs; drug design

Phytochemical profiling of green biosynthesis of silver nanoparticles using *Portulaca oleracea* leaves

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Plant extracts are widely used for synthesis of metal nanoparticles as they are non-toxic, economical and have a wide variety of phytochemicals. The current study explores the green synthesis of silver nanoparticles (AgNPs) using the aqueous leaf extract of *Portulaca oleracea*, a plant known for its rich phytochemical composition. The leaves of *Portulaca oleracea* were collected from Tambaram, Chennai. Qualitative phytochemical analysis revealed the presence of secondary metabolites such as proteins, saponins, alkaloids, and quinine, while steroids, flavonoids, tannins, terpenoids, cardiac glycosides, and phenols were absent. These bioactive compounds played a key role in reducing and stabilizing metal ions during nanoparticle synthesis. Silver nanoparticles were synthesized using aqueous extract of *Portulaca oleracea* leaves.

The colour change from green synthesized into greenish-gray indicates the synthesis of silver nanoparticles. Silver nanoparticles using *Portulaca oleracea* were successfully synthesized and characterized using UV-Vis spectroscopy (with an absorption peak at 265 nm for (AgNPs). The findings highlight the therapeutic potential of *P. oleracea*-mediated nanoparticles, offering a green, sustainable, and cost-effective approach for cancer treatment. Future studies should address environmental safety and scalability to ensure broader biomedical application and safer nanoparticle utilization.

KEYWORDS: *Portulaca oleracea*, Medicinal plants, Phytochemicals, Silver nanoparticles

Biopolymer production from microbiota of insectivorous plants – A novel sustainable approach

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Insectivorous plants, like *Drosera* and *Nepenthes*, present an intriguing yet underexplored habitat for the isolation of such microorganisms. These plants, which trap and digest insects, create a unique microenvironment enriched with diverse micro flora, potentially including bacteria capable of producing biopolymers. Insectivorous species such as *Nepenthes* and

Drosera were collected from diverse geographical regions, including Sri Lanka, Assam, and wetlands of Tamil Nadu. This work aimed to explore insectivorous plants and their associated microbiota for the sustainable production of biopolymers. Microorganisms associated with these plants were isolated under sterile conditions, leading to the identification of novel strains of *Bacillus* and *Pseudomonas*. These isolates were cultured in MRS broth, and biopolymer extraction was achieved using precipitation methods. The work successfully screened and characterized microbial strains capable of biopolymer production, laying the foundation for their application in bioplastic development. The study showed promising results in isolating efficient strains for biopolymer synthesis. Planned downstream activities include optimization of media, scale-up fermentation, composite development, and application testing for food wrapping and heavy metal absorption. Future directions involve biodegradability testing and commercialization prospects. The findings indicating significant scientific and societal impact in promoting sustainable, biodegradable alternatives to synthetic plastics.

Keywords:

Insectivorous plants, *Nepenthes*, *Drosera*, *Bacillus*, *Pseudomonas*, Biopolymer, Biodegradation

**Biosynthesis of silver nanoparticles from bacteriocin producing
Lactobacillus casei and its antibacterial efficacy against food
borne pathogens**

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Nanotechnology offers transformative solutions in food safety and preservation, particularly through the application of biologically synthesized nanoparticles. In this study, *Lactobacillus casei* var. Shirota—a probiotic bacterium isolated from the commercially available fermented milk drink Yakult®—was employed for the eco-friendly biosynthesis of silver nanoparticles (AgNPs). The bacterium was cultivated on de Man, Rogosa and Sharpe (MRS) agar, and its identity was confirmed through gram staining (Gram-positive rods) and catalase testing (catalase-negative). Cell-free supernatant (CFS) containing antimicrobial bacteriocins was extracted, pH-adjusted to neutralize organic acids, and evaluated for antimicrobial activity using the disk diffusion method. The CFS exhibited significant inhibition against two major foodborne pathogens: *Escherichia coli* and *Staphylococcus aureus*, indicating the presence of bioactive peptides such as bacteriocins.

Silver nanoparticles were synthesized by incubating the neutralized CFS with 0.1 M aqueous silver nitrate (AgNO_3) at room temperature for 72 hours in dark conditions. A distinct color change from pale yellow to dark brown indicated the successful reduction of silver ions (Ag^+ to Ag^0), mediated by

microbial enzymes, likely nitrate reductases. The biogenic AgNPs synthesized through this green route represent an environmentally sustainable alternative to chemically synthesized counterparts. These nanoparticles, in conjunction with the bacteriocins, may offer synergistic antimicrobial activity and have potential applications in food packaging, preservation, and as novel antimicrobial agents in the food and healthcare industries. Further characterization and toxicity assessment will enhance the understanding of their practical utility.

Keywords: *Lactobacillus casei* var. *Shirota*, Bacteriocins, Foodborne pathogens, Probiotics, Antimicrobial peptides

Larvicidal activity of *Bacillus thuringiensis israelensis* (Bti) and its enhanced activities with selected aqueous plant extracts

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Mosquitoes adversely affect human health because they act as vectors for a wide variety of dreadful diseases. Now-a-days mosquito control is facing a threat due to the emergence of resistance to synthetic insecticides. The present study is a preliminary work to control mosquito larvae with the use of bio-pesticides in combination with easily available plant extracts. *Bacillus thuringiensis israelensis* (Bti) is a natural biological enemy of mosquito larvae that is safe for humans and all creatures except fungal gnats, black flies and a few very closely

related insects. *Bti* is only activated in the gut of insect but it's not as effective for all kinds of mosquito. *Culex* and *Anopheles* larvae are most susceptible while *Aedes* are less susceptible. There is also a greater chance that mosquito may build resistance to it, and resistance has already been reported in some areas through scientist are already working on ways of preventing the problem. Hence in this study we have used integrated pest management control of *Bti* in combination with selected plant extracts (*Ocimum basilicum*, *Vitex negundo*, *Azadirachta indica* and *Mentha piperita*). The efficacy was determined through bioassay method as per WHO guidelines with slight modifications. Mortality percentage and LC50 were calculated after monitoring the treatment sets for a period of 96 hours. *Vitex negundo* showed high mortality rate with 2.5 LD50 and LC50 of 0.77

Index Terms: *Bacillus thuringiensis israelensis*, Larvae, Bio assay, Mortality, LC₅₀, LD₅₀

Case Studies of Organophosphate Pesticide Poisoning due to Occupational and Environmental Exposure: An Indian Perspective

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Over the past decades, pesticide poisoning has drawn serious attention from the public, as it accounts for a significant number of deaths occurring each year. Organophosphate pesticides lead

to the current trend, and these are less frequently investigated. This review focusing on highly hazardous and widely used organophosphate pesticides in India such as Phorate, Monocrotophos, Methylparathion, Dichlorvos and Triazophos. The extent of contamination has been found by the mortality rate of occupational poisoning, self-poisoning and food poisoning. This is the first case report of the above five highly hazardous organophosphate pesticide poisoning pertaining to India. This review emphasized the organophosphate pesticide exposure and appropriate poisoning cases in several part of India.

Keywords: Agricultural farmers; Human Exposure; Pesticide Poisoning; Case Studies; Health Effects

Novel Nano Bioremediation strategy and there of

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Background: We all knew well that water resources are mainly contaminated by heavy metals and disease causing pathogens due to increasing industrialization and various anthropogenic activities. These contaminations have posed a serious threat to the environment, animals, and humans. Thus, it becomes very important to develop a cost-effective, non- toxic novel nano bio-product. **Methodology:** The various methods of bio-molecular

and nano technology step by step process were involved in the production of novel nano bio-molecules. The produced nano bio-molecular particles were given for various characterization analyses like FTIR, HR-SEM, EDAX, HR-TEM, SAED Pattern and XRD to ensure its physical, chemical and biological features. Then the nano bio- molecules were utilized for various applications. **Results and Discussion:** The synthesized nano bio-molecules reveals good results in characterization analyses like FTIR, HR-SEM, HR-TEM, SAED Pattern and XRD results and various applications. **Conclusion:** So I conclude that the prepared nano bio-molecules are the excellent source of antimicrobial agent to disease causing pathogens and also to remove water contaminant, heavy metals.

Key words: Nano, non-toxic, contaminations, heavy metals, pathogens.

Electrochemical sensing of glucose by ZnS modified graphene

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A simple and novel nanocomposite of Graphene, ZnS nanoparticles were successfully prepared and used for the modification of carbon paper-based glucose biosensor. Interestingly, the presence of ZnS nanoparticles decorated

graphene sheets increase the electrocatalytic activity of electrodes, leading to enhanced sensitivity of the glucose biosensor. XRD, SEM, TEM was implemented to characterize the morphology and composition of the nanocomposites. Furthermore, glucose oxidase (GOx) was immobilized on to the ZnS/G modified carbon paper electrode for the determination of glucose. This ZnS/G/GOx/CPE has been characterized using cyclic voltammetry. CV results indicated a direct electron transfer between the enzyme and the electrode surface. The proposed biosensor showed rapid response, high sensitivity, wide linear range and low detection limit. Furthermore, our ZnS/G modified carbon paper electrode showed excellent selectivity, repeatability, and long-term stability over a month's period.

Keywords: Graphene; Glucose biosensor; Glucose Oxidase, ZnS nanoparticles; Carbon paper electrode

Synthesis of rGO for supercapacitor application

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This work presents the synthesis of GO in Room temperature with low cost, simpler method and reduction of GO through safer, Hazardous free nature friendly method. Reduced Graphene oxide formed was studied and confirmed by XRD and Raman Spectra. The d spacing was calculated from XRD data. Morphology of the rGO sheets was analyzed from the SEM images. UV-VIS spectrometer results suggested excellent optical

response in rGO sheets. Electrochemical properties of the rGO electrode were analyzed by cyclic voltammetry Method by which the capacitive behavior of the material was confirmed. This Study focuses on the significance of Synthesizing rGO sheets using reduction method in eco-friendly manner, that contributes to supercapacitor applications.

Key words: graphene, electrochemical, electrode

Identification of 3',4',5,7-Tetrahydroxyisoflavanone as a Potential Anti-Breast Cancer Agent via Molecular Docking and Dynamics Simulation Studies

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Cancer is the second threatened disease causing high mortality worldwide. The most common cancer and with greatest fatality rate is breast cancer. Chemotherapy is a most common treatment for cancer which contains various harmful substances that affects patient's quality of life. As a result, there is still an urge for identifying natural substances with fewer side effects and potential anticancer effects. In this research work, anti-breast cancer targets from *Syzygium aromaticum*, *Artemisia absinthium*, *Mentha piperita* and *Juglans nigra* extracts were analyzed through *in silico* analysis. Phytocompounds from ethanolic extracts of *Syzygium aromaticum* buds, *Artemisia absinthium* and *Mentha piperita* leaves, *Juglans nigra* shell and

nuts were analysed using GC-MS and LC-MS techniques. The phytocompounds identified were docked using SeeSAR-9.2 with breast cancer receptors includes estrogen (PDB ID: 3ERT) and progesterone (PDB ID: 4OAR). From the docking results, the best hit molecule was selected and proceeded for pharmacokinetic (ADMET) analysis using pkcsn tools and molecular dynamic simulation studies using GROMACS. About 58 and 53 compounds were tentatively identified from the extracts through GC-MS and LC-MS analysis respectively. The best hit molecule identified from docking is 3',4',5,7-Tetrahydroxyisoflavanone (THIF) which showed best binding with the receptors and falls into the optimum drug-likeness compound.

Keywords: Breast cancer, Estrogen, Progesterone, Molecular docking, 3',4',5,7-Tetrahydroxyisoflavanone

Biopython-assisted in-Silico profiling and antimicrobial evaluation of chitosan nanoparticles against antibiotic-resistant pathogenic bacteria from lake ecosystems

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Freshwater bodies in urban areas are emerging as reservoirs of antibiotic-resistant pathogenic bacteria, posing a growing threat to environmental and public health. This study explores the

antimicrobial potential of chitosan nanoparticles (CNPs) against multidrug-resistant (MDR) bacteria isolated from lake water samples collected across Chennai. Bacterial strains, including, *Ralstonia picketti*, *Aeromonas caviae*, *Coronobacter sakazakii*, *Bacillus subtilis* were isolated and identified using standard microbiological and molecular techniques. Their resistance profiles were determined through antibiotic susceptibility testing. To understand resistance mechanisms at the molecular level, Biopython was employed to perform genomic and transcriptomic data analysis of resistance genes NDM-1. In-silico molecular docking studies were conducted to assess the binding efficiency of chitosan molecules to key resistance-related bacterial proteins. Chitosan nanoparticles were synthesized and characterized, then evaluated for their antibacterial efficacy through assays such as MIC determination, bacterial viability. The results reveal that CNPs exhibit strong inhibitory effects against MDR isolates, indicating their potential as eco-friendly bioremediation agents. The integration of computational and experimental approaches underscores the value of nanoparticle-based strategies in mitigating antimicrobial resistance in aquatic environments.

Keywords: Lake water, MDR bacteria, Chitosan nanoparticles, Biopython, Molecular Docking.

**Microbial Flora Associated with *Limnodrilus hoffmeisteri*
Claparède, 1862: Isolation and Identification of Bacterial and
Fungal Pathogens from a Commercially Important Aquatic
Oligochaete (Tubifex worm)**

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Limnodrilus hoffmeisteri (Tubifex worm), a commercially valuable aquatic oligochaete widely used as live feed for ornamental fishes, was collected from the Kodungaiyur Swamp (13°08'48"N, 80°15'51"E) in Chennai during October 2024. Microbial flora from both the worms and the swamp water were isolated using pure culture techniques. Bacterial identification was performed via partial 16S rRNA gene sequencing and similarity analysis using the NCBI BLASTn algorithm. The 16S rRNA sequences from water-derived isolates showed 100% similarity with *Aeromonas hydrophila*, *Pantoea agglomerans*, and *Acinetobacter* spp. Additionally, an 18S rRNA gene sequence from a fungal isolate exhibited 99% similarity with *Aspergillus terreus*. All sequences were submitted to GenBank (accession numbers: PQ817788, PQ817809, PQ817848, PQ219291).

Homogenized worm samples yielded three bacterial isolates, with no detectable fungal growth. Biochemical characterization revealed that these bacterial isolates were phenotypically identical to the species identified in the water. Antibiofilm profiling demonstrated high efficacy of Enrofloxacin, Meropenem, and Ciprofloxacin against these pathogens. These findings underscore the necessity of disinfecting wild-caught Tubifex worms prior to their use as feed in aquaculture systems to prevent disease transmission and support effective health management of ornamental fishes.

Key words: *Limnodrilus hoffmeisteri*, Kodungaiyur

Identification of a Natural Protease Inhibitor from Hot Spring Actinomycetes with Antiviral Potential against Dengue Virus

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Abstract

Dengue virus (DENV) remains a significant global health challenge, primarily affecting tropical and subtropical regions. The increasing incidence of DENV infections underscores the

urgent need for novel antiviral therapies. Proteases, critical for the life cycle of numerous pathogenic viruses, offer a compelling target for therapeutic intervention. This study aimed to identify and characterize a protease inhibitor (PI) with antiviral activity against DENV, leveraging the unique bioactive compound potential of hot spring actinomycetes. By exploring the understudied ecological niche of Rajgir hot springs, we successfully isolated a potent *Streptomyces* sp., designated as VITARB4 (Accession No. PQ339659). Plate assays and quantitative analyses demonstrated that *Streptomyces* sp. VITARB4 produces a strong inhibitor of cysteine proteases. Advanced analytical techniques, including UPLC, GC-MS, and FTIR, identified diethyl phthalate as the primary compound responsible for the observed protease inhibitory activity. Molecular docking studies revealed that diethyl phthalate exhibited high binding affinity and significant interactions with the NS5 protein, a critical target for DENV replication. Further *in silico* assessments of its drug-likeness and ADME/T properties confirmed its favorable pharmacokinetic and safety profile. Functional assays, including focus-forming unit (FFU) assays, demonstrated significant antiviral activity of the compound, with evaluations conducted at concentrations maintaining high cell viability (>90%). *In vivo* toxicity evaluations were conducted through acute and sub-acute studies at varying doses of diethyl phthalate in rodent models. No significant adverse effects or mortality were observed, confirming its safety profile across tested concentrations. This study highlights the potential of diethyl phthalate as a promising therapeutic candidate against DENV and underscores the value of hot spring actinomycetes as a source of bioactive compounds. These findings pave the way for further development of targeted antiviral therapies through *in vitro*, *in silico*, and *in vivo* approaches.

Keywords: Dengue virus (DENV), Hot Spring actinomycetes, Antiviral activity, NS5 protein

Characterization and virulence of *Candida spp* , synergism with *S. mutans* in pediatric dental caries

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Early childhood caries is a significant global health issue with a complex microbial basis. The co-existence of *Streptococcus mutans* and *Candida spp.*, especially *C. albicans*, enhances virulence through robust biofilm formation, acidogenicity, and tissue invasion, contributing to severe carious lesions in children.

Aim: This study aimed to isolate and characterize *Candida spp.* from pediatric dental caries patients and to evaluate their virulence traits and synergistic interaction with *S. mutans*.

Methods: Plaque samples were collected from children diagnosed with dental caries. *Candida spp.* and *S. mutans* were isolated on selective media and confirmed by phenotypic and molecular methods. Virulence factors such as phospholipase and proteinase activity, hyphal transition, and biofilm formation were assessed. Mono- and dual-species biofilms were quantified by crystal violet staining. Biofilm structure and microbial interactions were visualized by Scanning Electron Microscopy (SEM). **Result:** Apart from *C. albicans*, *C. glabrata*, *C. tropicalis* has been isolated. High prevalence of *C. albicans* co-isolated with *S. mutans* was observed. *Candida* isolates demonstrated significant enzyme activity and hyphal formation, indicating high

virulence. Dual-species biofilms showed significantly higher biomass and dense matrix structures compared to mono-species biofilms ($p < 0.05$).

Keywords: *Candida* spp., *Streptococcus mutans*, biofilm, synergism, pediatric dental caries

Targeting Breast Cancer with Beta-Glucans from Seaweed-Derived Endophytic Yeasts: A Microbial-Based Drug Discovery Approach

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According to the World Health Organisation (WHO), breast cancer is the most common malignancy among women worldwide, accounting for the highest cancer incidence in 157 of 185 countries. Resistance to treatment accounts for 90% of breast cancer fatalities, highlighting the critical need for innovative therapeutic options. This study examines the potential of seaweed-associated endophytic yeasts as a source of bioactive beta-glucans with antioxidant and anticancer properties. Seaweeds were gathered along the Tamil Nadu coastline in India, and their endophytic yeasts were extracted, morphologically characterized, and identified using 18S rRNA sequencing. Beta-glucans were isolated from yeast biomass and structurally analysed to validate their identity. Various assays

were employed to evaluate antioxidant activity, and the MTT assay was utilized to investigate cytotoxic effects on MCF-7 breast cancer cells. Beta-glucans are recognized for their immunomodulatory and anticancer effects, and they possess significant therapeutic potential. Furthermore, beta-glucans can act as novel drug delivery vehicles, encapsulate therapeutic compounds, and allow for targeted administration. This study highlights the untapped potential of seaweed-derived endophytic yeasts as sustainable sources of beta-glucans, paving the path for targeted breast cancer treatments. The findings demonstrate the viability of combining beta-glucans with traditional chemotherapies or immunotherapies to boost treatment efficacy while minimizing side effects, providing a new perspective in the fight against breast cancer.

Key words: Breast cancer, seaweed endophytic yeast, beta-glucan, Antioxidant, MTT assay.

Pathogenic microorganisms associated with Inflammatory Bowel Disease (IBD)

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Inflammatory Bowel Disease (IBD), encompassing Crohn's disease and ulcerative colitis, is a chronic, relapsing inflammation of the gastrointestinal tract with multifactorial

etiology. While genetic predisposition and immune dysregulation are central to its pathogenesis, increasing evidence suggests a significant role of infectious pathogens in triggering or exacerbating IBD. Bacterial species such as *Escherichia coli* (adherent-invasive strains), *Clostridium difficile*, *Mycobacterium avium* subspecies *paratuberculosis*, and viral agents including cytomegalovirus have been implicated in the onset and flares of IBD. These pathogens may disrupt mucosal barriers, alter host immune responses, or cause dysbiosis, contributing to chronic intestinal inflammation. Furthermore, IBD patients, particularly those on immunosuppressive therapies, are more susceptible to opportunistic infections, complicating diagnosis and treatment. The overlap of infection-induced inflammation with autoimmune activity poses diagnostic challenges, requiring careful microbiological investigation to distinguish primary infectious colitis from IBD flares. Understanding the complex interplay between pathogens and host immunity is crucial for developing targeted therapies and infection prevention strategies in IBD management. This review explores current evidence on pathogenic contributors to IBD, mechanisms of microbial-induced inflammation, and clinical implications for treatment and prognosis.

Keywords: Pathogens, autoimmune disorder, IBD

Inhibition of Dengue virus fusion and entry into the host cell by small molecule natural compounds

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Currently, there is no antiviral drug, or vaccine is available to treat Dengue virus infection and reduce Dengue-related morbidity and mortalities. Considering health and economic burden of Dengue, and challenges in vaccine development, this study aimed to identify novel anti-Dengue compounds from medicinal plants. A curated library of 1453 natural compounds were screened against β OG pocket of the Dengue virus envelope (E) protein. The lead compounds identified were subjected to Induced-fit docking and Molecular Dynamic (MD) simulations using the Schrödinger suite. The drug like properties were predicted using the Molinspiration web tool. The antiviral activity

of the lead compounds was evaluated using Cytopathic effect (CPE) reduction assays and Quantitative Real-time PCR. The molecular docking and MD simulations revealed that Rosmarinic acid and Dihydromyricetin formed stable interactions with β OG pocket of the Dengue virus E protein. Both compounds exhibited well-defined drug-like properties. Rosmarinic acid inhibited the Dengue virus induced CPE in Vero cells by reducing the viral copy numbers. ADME profiles of these compounds support their potential as a safe and effective antiviral agent. This study findings conclude that Rosmarinic acid is an promising antiviral candidate against Dengue virus.

Antioxidant potential of *Glycyrrhiza glabra* extract and its nanoparticles against infectious pathogens

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Glycyrrhiza glabra is one of the useful medicinal plants from the ancient days, which belongs to the Leguminosae family and is native to the Mediterranean and certain areas of Asia especially India. *G. glabra* is a typical herbaceous perennial, growing to 1 m in height, presenting pinnate leaves with a length of 7 to 15 cm. The flowers are purple to pale whitish blue, being arranged in a hermaphrodite inflorescence, whereas the fruit is an oblong legume with 2 to 3 cm of length and containing several seeds. *Glycyrrhiza glabra* is a plant with strong ethno-botanical history and the rhizome parts of this plant are used as a folk medicine.

G. glabra is one of those ancient plants, which have been used in the traditional pharmacopoeias for its multifaceted activities against variety of systematic and nonsystematic ailments. *G. glabra* extracts have been shown to possess lot of medicinal properties like antimicrobial, antioxidant, anti-inflammatory, antiulcer, anticancer properties due to presence of so many bioactive components, triterpene, saponins, flavonoids, alkaloids. The aim of the study was to analyze anti-microbial resistance of the microorganism against the extract and antioxidant potential of *Glycyrrhiza glabra* extract and its nanoparticles against infectious pathogens. Assay such as DPPH· radical, superoxide radical, phosphomolybdenum reduction and Fe^{3+} reducing power assays were carried out for antioxidant activity. The antibacterial and antifungal activity was tested by well diffusion method against pathogens such as *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Candida albicans*, *Candida tropicalis*, *Candida krusei* and the zone of inhibition was measured and compared with standards.

Keywords: Medicinal properties, Antimicrobial, pathogens, Antioxidant potential.

Acknowledgement: Sivaraj. C, Justin Pakia Jacob

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Persistence of Anti-SARS-CoV-2 IgG Antibodies up to 24 Months Post-Vaccination Among Healthcare Workers in Central India

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Healthcare workers (HCWs) remain at sustained risk of SARS-CoV-2 exposure due to their occupational roles, underscoring the importance of evaluating the durability of vaccine-induced immunity in this high-risk group. This cross-sectional study investigated the persistence of anti-SARS-CoV-2 IgG antibodies up to 24 months post-vaccination among 251 HCWs at a tertiary care hospital in Central India. All participants had completed the primary COVID-19 vaccination schedule, and 94.8% had received at least one booster dose. Serological analysis using an ICMR-approved ELISA revealed that 75.3% of participants remained IgG seropositive. The highest seropositivity was observed in the 40–49 years age group (86.7%) and among those who had received a booster dose (76.9%). In contrast, seropositivity among participants without a booster was markedly lower (46.2%). Notably, individuals with prior SARS-CoV-2 infection exhibited higher antibody levels (median OD: 0.903), while all infection-naïve participants were seronegative. These findings highlight the role of booster vaccination and hybrid immunity in sustaining long-term antibody responses and reinforce the need

for periodic serological surveillance to guide targeted immunization strategies for HCWs.

Keywords: SARS-CoV-2, healthcare workers, IgG antibodies, vaccine durability, booster dose, hybrid immunity

Clinical and Molecular Insights into Chronic Hepatitis B in Central India: A Cross-Sectional Hospital-Based Study

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Background:

Chronic hepatitis B virus (HBV) infection is a major public health concern in India. HBV genotype distribution and clinical manifestations vary across regions. This study aimed to characterize the molecular and clinical profile of chronic HBV patients in Central India.

Methods:

A hospital-based cross-sectional study was conducted at a tertiary care centre in Central India. Adult patients with confirmed chronic HBV infection were enrolled. HBV DNA and

genotyping were performed by using real-time PCR and nested PCR. Liver fibrosis was assessed by using APRI and FIB-4 scores.

Results:

A total of 214 patients were included (mean age: 36.0 ± 14.0 years; 68.7% male). Genotyping was successful in 132 cases, with genotype D detected in 98.5% and mixed A&D in 1.5%. Significant fibrosis (APRI ≥ 1.5) and advanced fibrosis (FIB-4 ≥ 3.25) were observed in 8.9% and 9.8% of patients, respectively. Patients with advanced fibrosis had higher transaminase levels, lower serum albumin and platelet counts, and higher HBV DNA levels compared to those without fibrosis, suggesting more advanced liver disease.

Conclusions:

Genotype D found to be the predominant HBV strain along with a notable proportion of patients demonstrated significant hepatic fibrosis, emphasizing the importance of early detection and intervention.

Green Synthesis of Berberine-Loaded Copper oxide Nano formulation Using *Solanum torvum*: A strategic advancement in lung cancer therapy and wound healing

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This study aimed to synthesized berberine-conjugated copper oxide nanoparticles (BBR-CuONPs) using *Solanum torvum* for lung cancer therapy. Berberine chloride and copper sulfate were precursors, and *S. torvum* extract acted as the reducing agent. Characterization of BBR-CuONPs formation was confirmed by UV-vis, FTIR, and TEM (10–50 nm) and berberine-CuO interactions. In A549 lung cancer cells, BBR-CuONPs showed dose-dependent cytotoxicity ($IC_{50} = 32.35 \pm 2 \mu\text{g/ml}$) with better efficacy than berberine or CuONPs alone. High viability in HEK cells and significant inhibition of cell migration in wound healing assays support their biocompatibility and therapeutic potential. Further in vivo evaluation is recommended.

Key words: Berberine, *Solanum torvum*, Copper oxide nano formulation, Anti-cancer activity, Lung cancer therapy, A549 cell lines.

New insights to address antimicrobial resistance by co-cultivation of Potential *Bacillus* species from soil environment: a narrative review

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Antimicrobial resistance (AMR) has emerged as a critical issue due to the overuse and improper usage of antibiotics and antifungals for the management of prevalent microbial infections, leading to a growing depletion of effective therapeutic drugs. Microorganisms serve as pivotal producers of chemically diverse specialized metabolites, which are produced during the late or stationary phase of their growth cycle. These metabolites possess considerable importance in chemical, pharmaceutical, and agro-industrial sector. This review aims to explore the co-cultivation of distinct *Bacillus* species from soil environments to induce the production of novel bioactive compounds as well as to stimulate interspecies interactions and activate silent biosynthetic pathways.. The objective is to assess how co-culture techniques can activate silent biosynthetic gene clusters and thus contribute to combating AMR. Numerous bioactive metabolites has been isolated from Gram-positive endophytes obtained from agriculture, forest, mangrove, and medicinal plants. These interactions are regulated by

intercellular communication mechanisms such as quorum sensing. The co-culture strategy presents a novel and effective method to explore microbial metabolic potential, providing a sustainable and innovative solution to address the urgent problem of antimicrobial resistance. This approach can lead to the discovery of new antimicrobial agents, helping to replenish the reduced production of effective therapeutics.

Keywords: Antimicrobial resistance, Co-cultivation, *Bacillus*, Horizontal gene transfer, Quorum sensing, metabolites.

New insights to address antimicrobial resistance by co-cultivation of Potential *Bacillus* species from soil environment: a narrative review

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Keywords: Antimicrobial resistance, Co-cultivation, Bacillus, Horizontal gene transfer, Quorum sensing, metabolites.

Title: Antimicrobial and Anticancer Efficacy of Selenium Nanoparticles Synthesized Using *Amomum subulatum* (Black Cardamom) Extract.

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The rise in multidrug-resistant bacteria and lung cancer cases underscores the need for novel bioactive agents with dual therapeutic potential. In this study, selenium nanoparticles (SeNPs) were biosynthesized using *Amomum subulatum* (black

cardamom) aqueous extract and evaluated for their antimicrobial and anticancer activities. The green synthesis approach yielded stable, spherical SeNPs, confirmed through UV-Vis spectroscopy, FTIR, and TEM. Antibacterial efficacy was tested against *Staphylococcus aureus*, *Pseudomonas aeruginosa*, and *Escherichia coli* using the agar well diffusion method and minimum inhibitory concentration (MIC) assays. The SeNPs exhibited significant antibacterial activity, with the largest inhibition zones observed against *S. aureus*, followed by *P. aeruginosa* and *E. coli*, indicating broad-spectrum effectiveness. The anticancer potential was assessed in vitro against A549 (lung adenocarcinoma) and H460 (large cell lung carcinoma) cell lines using MTT assay and morphological analysis. The SeNPs induced dose-dependent cytotoxicity, reduced cell viability, and triggered apoptotic features, indicating effective anticancer activity. These findings highlight the therapeutic promise of black cardamom-mediated selenium nanoparticles as potent antimicrobial and anticancer agents. This biogenic approach offers a sustainable and efficient pathway for future pharmaceutical applications.

Keywords: Selenium nanoparticles, Black cardamom, Antimicrobial, A549, H460, *S. aureus*, *Pseudomonas*, *E. coli*, Green synthesis.

**Molecular and Functional Evaluation of Rutin as a Resistance-
Breaking Adjuvant for MRSA and TRSA**
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Biotechnology, Nehru Arts and Science College, Coimbatore.

A serious threat to public health is the rising incidence of methicillin- and trimethoprim-resistant *Staphylococcus aureus* (MRSA/TRSA). To restore the effectiveness of methicillin and trimethoprim/sulfamethoxazole against resistant *S. aureus* strains, this study examines the adjuvant potential of rutin, a naturally occurring flavonoid. Strong and consistent interactions between Rutin and important resistance-related targets, such as penicillin-binding protein 2a (PBP2a) and dihydrofolate reductase (DHFR), were shown by in-silico molecular docking and molecular dynamics simulations. Additionally, simulations showed that Rutin exhibited positive membrane-associative behaviour, progressively assimilating into the bacterial lipid bilayer without causing the membrane structure to become unstable. ADMET and toxicity predictions suggested favourable drug-like and safety profiles. In-vitro assays confirmed significant antibacterial synergy between Rutin and both methicillin and trimethoprim, with marked reductions in minimum inhibitory concentration (MIC) values. Time-kill kinetics and biofilm inhibition studies further supported Rutin's ability to enhance bacterial susceptibility. Additional mode-of-action investigations revealed reduced virulence factor production (staphyloxanthin, hemolysin), oxidative stress sensitization, loss of membrane stability, extracellular protein leakage, and disruption of surface hydrophobicity. Fluorescence-based live/dead staining

confirmed dose-dependent bacterial cell death in treated groups. These findings position Rutin as a promising adjuvant molecule capable of resensitizing multidrug-resistant *S. aureus* to conventional antibiotics through multiple complementary mechanisms.

Key words: MRSA, Rutin, Simulation, Nanoemulsion

Biosurfactants from Actinomycetes: A Green Solution for Pharmaceutical Innovations

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Actinobacteria are a diverse group of organisms known for producing a wide range of bioactive compounds that have shown applications in the medicinal and pharmaceutical industries. Biosurfactants, which are amphiphilic compounds produced by microbes, have received a lot of interest due to their environmental friendliness and versatility in sectors such as medicines, bioremediation, and detergents. Compared to their chemical equivalents, they exhibit qualities that include lower toxic levels, increased biodegradable properties, and unique physicochemical properties. Due to these traits, biosurfactants have become attractive substitutes for synthetic surfactants in the pharmaceutical industry in areas like cancer studies, wound healing, and drug development. In this study, actinomycetes were isolated from hydrocarbon-contaminated soil and screened for the production of biosurfactants with various tests like the

drop collapse method, emulsification assay, and oil displacement efficiency. Biochemical assays and molecular approaches, including 16S rRNA sequencing, were used to characterize the selected strains to identify potential biosurfactant producers. An optimization study was carried out to see which temperature, pH, salinity, carbon source, and nitrogen source showed the highest yield of biosurfactants. The chemical structure and composition of biosurfactants were investigated using GC-MS techniques.

Keywords: Actinomycetes, Biosurfactants, 16S rRNA Sequencing, Anti-Bacterial, Antioxidant.

Identification of a Natural Protease Inhibitor from Hot Spring Actinomycetes with Antiviral Potential against Dengue Virus

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and characterize a protease inhibitor (PI) with antiviral activity against DENV, leveraging the unique bioactive compound potential of hot spring actinomycetes. By exploring the understudied ecological niche of Rajgir hot springs, we successfully isolated a potent *Streptomyces* sp., designated as VITARB4 (Accession No. PQ339659). Plate assays and quantitative analyses demonstrated that *Streptomyces* sp. VITARB4 produces a strong inhibitor of cysteine proteases. Advanced analytical techniques, including UPLC, GC-MS, and FTIR, identified diethyl phthalate as the primary compound responsible for the observed protease inhibitory activity. Molecular docking studies revealed that diethyl phthalate exhibited high binding affinity and significant interactions with the NS5 protein, a critical target for DENV replication. Further *in silico* assessments of its drug-likeness and ADME/T properties confirmed its favorable pharmacokinetic and safety profile. Functional assays, including focus-forming unit (FFU) assays, demonstrated significant antiviral activity of the compound, with evaluations conducted at concentrations maintaining high cell viability (>90%). *In vivo* toxicity evaluations were conducted through acute and sub-acute studies at varying doses of diethyl phthalate in rodent models. No significant adverse effects or mortality were observed, confirming its safety profile across tested concentrations. This study highlights the potential of diethyl phthalate as a promising therapeutic candidate against DENV and underscores the value of hot spring actinomycetes as a source of bioactive compounds. These findings pave the way for further development of targeted antiviral therapies through *in vitro*, *in silico*, and *in vivo* approaches.

Keywords: Dengue virus (DENV), Hot spring actinomycetes, Antiviral activity, NS5 protein

Biofilm Formation by Drug-Resistant Nosocomial Bacteria *Enterococcus* Isolates from Chronic Periodontitis Patients

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Chronic periodontitis is a common inflammatory condition characterized by gradual degradation of the periodontal ligament and alveolar bone, which can lead to tooth loss if not treated. The persistence and recurrence of infection are frequently related to the presence of opportunistic pathogens such as *Enterococcus* species, which are recognized for their intrinsic resistance to various antibiotics and ability to form biofilms. Biofilms provide increased resistance to both host immune responses and antimicrobial treatments, making infections more difficult to cure. The purpose of this study was to assess the antibiotic resistance patterns and biofilm-forming capacities of *Enterococcus* isolates collected from subgingival plaque samples from patients with chronic periodontitis. The isolates were identified using established microbiological and biochemical techniques. CLSI criteria were followed for conducting antimicrobial susceptibility testing utilizing the Kirby-Bauer disk diffusion technique. Biofilm formation was measured quantitatively using the crystal violet microtiter plate test. A high majority of the isolates were resistant to common used antibiotics, such as ampicillin, erythromycin, and ciprofloxacin. Furthermore, 82.3% of the isolates showed moderate to high biofilm development. Notably, multidrug-resistant (MDR) isolates were associated with a significantly higher biofilm-forming

capacity compared to non-MDR strains,, indicating a link between antibiotic resistance and increased biofilm production. These data highlight the clinical significance of *Enterococcus* spp. in periodontal infections, particularly in terms of chronicity and resistance to conventional treatment. This research indicates the urgent need for novel therapeutic approaches that target both biofilm disintegration and antimicrobial resistance to effectively manage drug-resistant periodontal pathogens.

Key words: Periodontal infections, *Enterococcus* spp, Biofilm formation, Antibiotic resistance, Multidrug-resistant (MDR) strains

Molecular Characterization of Actinomycetes from Forest and Marine Habitats

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The isolation and characterization of actinomycetes have gained significant attention due to their crucial role in natural product biosynthesis and their implications for biotechnological applications. This study focuses on the systematic isolation of diverse actinomycete strains from soil samples collected from selected forest areas and marine regions using serial dilution and spread plate techniques. Optimal growth conditions were established at 28-30°C on Starch Casein Agar (SCA), for a duration of 7-14 days to enhance the growth recovery rate. The

isolation process adhered to standard microbiological procedures.

The isolated strains were screened for antimicrobial activity against a range of pathogenic microorganisms, including *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Escherichia coli*, and *Klebsiella pneumoniae*. Thin-layer chromatography was employed to analyse the presence of secondary metabolites. The isolated strains exhibited sensitivity to Erythromycin, Vancomycin, Tobramycin, and Chloramphenicol, indicating susceptibility to these antibiotics. However, resistance to Gentamycin was observed, suggesting an inherent acquired resistance mechanism.

The strains were further subjected to molecular characterization through 16S rRNA sequencing to determine their phylogenetic relationships. Analysis was performed using bioinformatics software, which confirmed the identity of the isolates as *Streptomyces griseus* and *Streptomyces albus*. BLAST analysis supported this identification. A phylogenetic tree was constructed, placing our isolates in close proximity to other *Streptomyces* species.

Targeting Breast Cancer with Beta-Glucans from Seaweed-Derived Endophytic Yeasts: A Microbial-Based Drug Discovery Approach

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According to the World Health Organisation (WHO), breast cancer is the most common malignancy among women worldwide, accounting for the highest cancer incidence in 157 of 185 countries. Resistance to treatment accounts for 90% of breast cancer fatalities, highlighting the critical need for innovative therapeutic options. This study examines the potential of seaweed-associated endophytic yeasts as a source of bioactive beta-glucans with antioxidant and anticancer properties. Seaweeds were gathered along the Tamil Nadu coastline in India, and their endophytic yeasts were extracted, morphologically characterized, and identified using 18S rRNA sequencing. Beta-glucans were isolated from yeast biomass and structurally analysed to validate their identity. Various assays were employed to evaluate antioxidant activity, and the MTT assay was utilized to investigate cytotoxic effects on MCF-7 breast cancer cells. Beta-glucans are recognized for their immunomodulatory and anticancer effects, and they possess significant therapeutic potential. Furthermore, beta-glucans can act as novel drug delivery vehicles, encapsulate therapeutic compounds, and allow for targeted administration. This study highlights the untapped potential of seaweed-derived endophytic yeasts as sustainable sources of beta-glucans, paving the path for targeted breast cancer treatments. The findings demonstrate the viability of combining beta-glucans with traditional chemotherapies or immunotherapies to boost treatment efficacy while minimizing side effects, providing a new perspective in the fight against breast cancer.

Key words: Breast cancer, seaweed endophytic yeast, beta-glucan, Antioxidant, MTT assay.

**Characterization and virulence of *Candida* spp , synergism with
S. mutans in pediatric dental caries**

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Early childhood caries is a significant global health issue with a complex microbial basis. The co-existence of *Streptococcus mutans* and *Candida* spp., especially *C. albicans*, enhances virulence through robust biofilm formation, acidogenicity, and tissue invasion, contributing to severe carious lesions in children.

Aim: This study aimed to isolate and characterize *Candida* spp. from pediatric dental caries patients and to evaluate their virulence traits and synergistic interaction with *S. mutans*.

Methods: Plaque samples were collected from children diagnosed with dental caries. *Candida* spp. and *S. mutans* were isolated on selective media and confirmed by phenotypic and molecular methods. Virulence factors such as phospholipase and proteinase activity, hyphal transition, and biofilm formation were assessed. Mono- and dual-species biofilms were quantified by crystal violet staining. Biofilm structure and microbial interactions were visualized by Scanning Electron Microscopy (SEM). **Result :** Apart from *C.albicans*, *C.glabrata*, *C.tropicalis* has been isolated. High prevalence of *C. albicans* co-isolated with *S. mutans* was observed. *Candida* isolates demonstrated significant enzyme activity and hyphal formation, indicating high virulence. Dual-species biofilms showed significantly higher biomass and dense matrix structures compared to mono-species biofilms ($p < 0.05$).

Keywords: *Candida* spp., *Streptococcus mutans*, biofilm, synergism, pediatric dental caries

Development and Characterization of Papain-Infused Antibiotic Coatings for Urinary Catheters: Enhancing Antibacterial Efficacy and Reducing Biofilm Formation

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Catheter-associated urinary tract infections (CAUTIs) pose several clinical challenge due to biofilm formation by uropathogenic bacteria such as *Escherichia coli* and *Klebsiella pneumoniae*. These biofilms shield bacteria from antibiotics and immune responses, contributing to treatment failure and antibiotic resistance. This study introduces a novel multifunctional urinary catheter coating composed of Ofloxacin (a broad-spectrum fluoroquinolone), Papain (a biofilm-degrading proteolytic enzyme), and Polyvinyl Alcohol (PVA), a biocompatible hydrogel facilitating sustained agent release. The coating achieved significant biofilm inhibition, reducing *E. Coli* by 95.8% and *K. pneumoniae* by 96.3%, compared to uncoated catheters. Zone of inhibition (ZOI) assays revealed expanded antimicrobial activity, increasing from 10 mm to 28 mm for *E. coli*, and 19 mm to 40 mm for *K. pneumoniae*. The PVA matrix also reduced catheter swelling by 63% for *E. coli* and 44% for *K. pneumoniae* minimizing surface roughness and bacterial adhesion. In vitro studies confirmed sustained Ofloxacin release over 72 hours, promoting prolonged antimicrobial action and reducing resistance risk. This advanced coating offers a promising strategy to enhance urinary catheter safety and efficacy by preventing biofilm-associated infections and mitigating antibiotic resistance, addressing key limitations of current antibiotic-impregnated devices.

Keywords- Biofilm, antibiotic resistance, Urinary tract infection, Polyvinyl Alcohol (PVA)

To evaluate anticancer effect of probiotics & bee venoms on SiHa cell lines

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Bee venom (BV), a complex natural toxin secreted by *Apis mellifera*, has gained increasing attention for its therapeutic potential, particularly in cancer treatment and tissue repair. This study aimed to evaluate the cytotoxic and wound healing properties of BV on SiHa cervical cancer cells using MTT and scratch assays. In the MTT assay, SiHa cells were treated with varying concentrations of BV (0.5%, 10%, 20%, 40%, and 80% v/v) for 24 hours. A dose-dependent decrease in cell viability was observed, with a significant reduction starting at 10% BV ($p < 0.05$). The highest concentration (80%) resulted in only 12.5% cell viability. The IC_{50} was calculated to be approximately 21.5%, indicating potent cytotoxic activity. These results align with existing literature suggesting that melittin, the primary bioactive component of BV, induces apoptosis through membrane disruption, caspase activation, and reactive oxygen species (ROS) generation, leading to mitochondrial dysfunction and cell death. To assess the wound healing potential, a scratch assay was conducted. BV-treated groups (10% and 20%) showed significantly enhanced cell migration and wound closure.

compared to the control group. At 48 hours, the 20% BV-treated group achieved up to 95% wound closure, while the control showed only 68%. This suggests that BV promotes rapid re-epithelialization, likely through upregulation of growth factors such as TGF- β and VEGF, as well as by enhancing collagen synthesis. Additionally, the anti-inflammatory and antimicrobial properties of BV may contribute to a favorable environment for tissue regeneration.

In conclusion, BV demonstrates dual biological activity: cytotoxic effects against cervical cancer cells and the ability to accelerate wound healing. These findings support the potential development of BV-based formulations for cancer therapy and wound management. Further in vivo and mechanistic studies are warranted to validate its clinical applicability and safety.

**Biogenic Synthesis of Copper Oxide Nanoparticles from Anethum graveolens; In vitro Analysis of Antibacterial, anticancer Potential
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In this study, copper oxide nanoparticles (CuONPs) were prepared using a green and eco-friendly route with *A. graveolens* (dill) seed aqueous extract as a reducing and stabilizing agent. Synthesis was revealed by colour change from light green to dark green and also confirmed by UV-Visible spectroscopy, which

showed broad surface plasmon resonance (SPR) peaks at 342-380 nm. XRD FTIR, SEM and TEM, were used to perform morphological and structural analyses. XRD also confirmed the crystallinity of CuONPs, and TEM images revealed uniformly distributed particles with an average particle diameter of 45.26 ± 22.7 nm. Large clusters (>300 nm) were formed due to the aggregation of nanoparticles as revealed by SEM. The CuONPs exhibited strong antibacterial activity against *Staphylococcus aureus*, *Escherichia coli*, and *Pseudomonas aeruginosa*, with increasing efficacy at higher concentrations. Furthermore, it showed potential anticancer properties against A549 lung cancer cells, with low cytotoxicity toward HEK normal cells. These findings highlight the potential of dill seed-mediated CuONPs as an eco-friendly approach towards the development of novel antimicrobial and anticancer agents. Additional research is required to discover its anticancer activities under an in vivo system.

Keywords: *Anethum graveolens*, Copper oxide nanoparticle, Antibacterial, Anticancer activity.

Antibiofilm Strategies Targeting Quorum-Sensing Molecules in *Candida tropicalis*

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Quorum sensing (QS) plays a vital role in *C. tropicalis* by controlling key physiological processes, especially biofilm formation, hyphal growth, and virulence factor production. QS is a cell-density-dependent communication system where microbial cells regulate gene expression via small signalling molecules. The primary QS molecules identified in *C. tropicalis* include farnesol and tyrosol, which modulate morphological transitions between yeast and hyphal forms, a critical step in establishing mature biofilms. Disruption in QS signalling directly affects the structural integrity, biomass, and antifungal resistance associated with biofilms. Targeting QS has emerged as a novel anti-biofilm strategy. Various methods have been explored to inhibit QS pathways, including the use of natural plant-derived compounds (such as flavonoids, terpenoids, and phenolic extracts), essential oils (garlic, clove, cinnamon oil) and synthetic QS inhibitors (Farnesol Analogues, furanones, synthetic benzimidazoles). These agents either degrade QS molecules, block receptor binding, or interfere with signalling cascades, ultimately impairing biofilm development without affecting fungal viability, reducing the risk of resistance development. This review highlights the mechanism of QS in *C. tropicalis*, its direct connection to biofilm formation, and explores promising anti-QS agents as potential adjunctive therapies for controlling biofilm formation in *C. tropicalis*.

Keywords: Quorum sensing, *Candida tropicalis*, Biofilm, Antifungal resistance, Farnesol, Tyrosol

Prevalence of multidrug-resistant bacterial patterns from Diabetic Foot Ulcer patients and detection of resistance genes by Multiplex PCR.

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Diabetic Foot Ulcers (DFUs) are a severe complication of diabetes, often leading to chronic infections and non-traumatic lower limb amputations. The rise of multidrug-resistant (MDR) bacteria in DFUs poses a major challenge to effective treatment and recovery. This study aimed to isolate and identify key bacterial pathogens, *Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas aeruginosa*, and *Klebsiella pneumoniae* from DFU patients and assess their antibiotic resistance profiles. From June 2022 to April 2023, pus samples from 75 DFU patients in Tambaram hospitals were collected and processed using standard microbiological methods. Among 143 bacterial isolates, 102 were isolates of interest subjected to antibiotic susceptibility testing through the Kirby-Bauer disc diffusion method using 21 different antibiotics from 10 classes. Multiplex PCR was conducted to detect eight β -lactam resistance genes. Results revealed 81% (81/102) of isolates were MDR. *P. aeruginosa* showed the highest resistance (97%), followed by *K. pneumoniae* (85%), *E. coli* (76%), and *S. aureus* (47%). Gel electrophoresis confirmed the presence of resistance genes in MDR isolates. The

study highlights the alarming prevalence of MDR pathogens in DFUs and underscores the urgent need for regular antimicrobial resistance monitoring and personalized antibiotic therapy for improved patient recovery.

Keywords: Diabetic Foot Ulcer, Microbial resistance, Diabetic mellitus, susceptibility testing.

Biofilm Busters: Harnessing Dark Honeys and *Ixora coccinea* to Disarm *Streptococcus mutans*

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Dental caries, mainly caused by the formation of biofilms and acid production from *S. mutans*, remains a major public health issue. Natural products like honey, known for their antibacterial, antifungal, and anti-inflammatory effects, present promising alternatives to conventional treatments. Oral samples collected from local dental clinics were cultured on Mitis-Salivarius agar, leading to the identification of characteristic *Streptococcus mutans* isolates through standard microbiological techniques. The presence of black colonies on Congo Red Agar after 24-48 hours confirmed biofilm formation, which was also verified using Christensen's Congo Red tube method. Antimicrobial susceptibility was assessed using the Kirby-Bauer disk diffusion method against various antibiotics, including tetracycline, erythromycin, clindamycin, penicillin, gentamicin, chloramphenicol, ciprofloxacin, cefoxitin, and ceftriaxone. Different types of honey and extracts from leaves, flowers, and

roots of the *Ixora coccinea* plant were evaluated against *S. mutans* using well-diffusion assays, with ethanolic leaf extracts showing marked inhibitory effects. Molecular confirmation of *S. mutans* was achieved through PCR, targeting *spaP* and *comE* genes, along with 16S rRNA Sanger sequencing. Marthandam honey was analyzed using GC-MS to identify bioactive compounds like 5-HMF. In vitro microdilution and biofilm assays indicated that dark honeys (buckwheat, honeydew) and Manuka honey had the most potent bactericidal effects, significantly reducing *S. mutans* growth and biofilm formation. Focusing on genetic factors such as *spaP* & *comE* could enhance the effectiveness of these natural treatments. Future clinical trials and formulation studies are crucial to evaluate the safety, efficacy, and best delivery methods before these natural agents can be incorporated into preventive or therapeutic dental care.

Phytochemical and bioactivity assessment of *Halophila sp.*

Seagrass extracts:

A pharmacological perspective

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Oceans cover over 70% of our planet and hold a vast, largely untapped pharmacopeia of bioactive compounds. While marine organisms like algae, sponges, and microbes have been extensively studied, seagrasses particularly *Halophila sp.* a group

of submerged marine angiosperms, are increasingly acknowledged not just for their ecological functions, but as bio factories of high-value secondary metabolites with untapped therapeutic, nutraceutical, and agrochemical potential. In this study, we employed a comparative multi-solvent extraction strategy (methanol, ethanol, dichloromethane, aqueous, petroleum ether, acetone, and hexane) to investigate the phytochemical diversity, antioxidant capacity, and broad-spectrum antimicrobial efficacy of seagrass extracts. Phytochemical profiling revealed a rich repertoire of terpenoids, flavonoids, phenolic acids, alkaloids, phytosterols, cardiac glycosides, and polyphenols, reflecting diverse biological modalities. GC–MS analysis identified a range of bioactive phytoconstituents including phytol, phenolic phosphite, benzohydrate analogues, fatty acid esters (e.g., hexadecanoic acid), and siloxane derivatives, each with known pharmacodynamic properties such as radical scavenging, cytotoxicity, anti-inflammatory, antimicrobial, and anticancer mechanisms. Functional evaluation through antioxidant assays (DPPH, ABTS, and Total Antioxidant Capacity) demonstrated that ethanolic and methanolic extracts exhibited robust redox-modulating activity (IC_{50} values $\sim 13 \mu l$; TAC $> 29 \mu l$), correlating with high phenolic content. In parallel, antibacterial screening via agar well diffusion revealed pronounced inhibitory zones, particularly in ethanol, acetone, and methanol (upto 20 mm) against *Listeria*, *Staphylococcus* and *Pseudomonas* species, suggesting strong efficacy against both Gram-positive and Gram-negative pathogens. While non-polar extracts such as hexane and petroleum ether showed cytotoxic or selective antimicrobial activity, they lacked broader bioefficacy. These findings support future mechanistic in vitro studies to evaluate their pro-

apoptotic and anticancer potential, especially in the context of natural product-based drug development.

Keywords : *Halophila spp.*, Marine phytochemicals, Antioxidant activity, Antimicrobial efficacy, GC–MS analysis.

**Genomic Insights into the Clinical Isolates of Multidrug-Resistant
Klebsiella pneumoniae: The Superbug**

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Drug resistance leads to prolonged illnesses, increased healthcare costs, and higher mortality rates. It also intensifies the risk of treatment failures and dissemination of resistant strains. India's high mortality rate from infectious pathogens is attributed to inadequate antimicrobial stewardship, fueling the emergence of multidrug-resistant superbugs in both community and healthcare settings. The WHO has endorsed *Klebsiella pneumoniae* as a high-priority pathogen. This study aimed to evaluate the phenotypic and genotypic characterization of multidrug-resistant *Klebsiella pneumoniae* isolated from various clinical samples. Clinical strains of *Klebsiella pneumoniae* (n=117) were included in the current study. Based on the antibiogram results, 79 strains (67.5 %) were found to be multidrug-resistant (MDR). Multidrug-resistant isolates were further screened by phenotypic and genotypic methods for Extended-Spectrum Beta-Lactamase, Amp-C and Carbapenemase production. Preliminary and confirmatory methods have been

employed to evaluate the prevalence of beta-lactamase enzyme production. The current study reported 41.8%, 11.99% and 54.7% positive results by phenotypic methods for ESBL, AmpC and Carbapenemase enzymes, respectively. Among the genes assessed by PCR, *bla*TEM 54.4% was the most prevalent, followed by *bla*OXA48 39.2% and *bla*KPC 22.7% The AmpC encoding gene *bla*MOX (0%) was not detected. Thus, the current study revealed a higher rate of multidrug resistance among *Klebsiella pneumoniae* strains, highlighting a concerning resistance rate underscoring the importance of appropriate antibiotic stewardship and recommending a proper surveillance to mitigate healthcare crises.

A comparative investigation into the green synthesis and characterization of copper oxide and zinc oxide nanoparticles utilizing *Hemidesmus indicus* root extract.

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This research examines the green synthesis of copper oxide (CuO) and zinc oxide (ZnO) nanoparticles using the root extract of *Hemidesmus indicus*. The nanoparticles were examined using UV-Vis, FTIR, XRD, and FE-SEM techniques. The UV-Vis analysis confirmed the successful creation of the nanoparticles, while FTIR spectra revealed the presence of phytochemical functional groups involved in reduction and capping processes. The X-ray diffraction patterns confirmed the crystalline characteristics of

both types. The CuO nanoparticles had an irregular morphology, while the ZnO nanoparticles had more distinct nanostructures. The study highlights the potential of *Hemidesmus indicus* as a bioresource for environmentally friendly metal oxide nanoparticle synthesis, with potential applications in antimicrobial agents, environmental remediation, and biomedical sciences.

Keywords: Green synthesis, Copper oxide nanoparticles, Characterization, Zinc oxide nanoparticles, *Hemidesmus indicus*

Metagenomic Study of Chicken Bedding Reveals AMR Gene Abundance and Microbial Diversity

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Antimicrobial resistance (AMR) is a growing global health concern, with poultry farms acting as key reservoirs due to the frequent use of antibiotics. Chicken bedding, which accumulates feces and organic matter, supports diverse microbial communities and may harbor antimicrobial-resistant bacteria and genes. In this study, we performed Whole Metagenome Sequencing (WMS) of chicken bedding material to investigate microbial diversity and the prevalence of AMR genes. Total DNA was extracted and libraries were prepared using the Twist NGS Kit (Cat. No. 104119) with an average insert size of 384 bp. Sequencing was carried out on the Illumina NovaSeq 6000 platform (2×150 bp), generating approximately 12 GB of data per

sample (~146.62 million paired-end reads). De novo assembly with MEGAHIT produced 239,596 scaffolds (~310.4 Mb), and gene prediction with Prodigal identified 472,313 genes. Alpha diversity indices indicated high microbial richness (Chao1: 9,931) and diversity (Shannon: 6.07; Simpson: 0.99). Kaiju-based taxonomic annotation revealed dominant phyla including *Actinomycetota*, *Bacillota*, and *Pseudomonadota*. Functional annotation indicated enrichment in amino acid metabolism, carbohydrate metabolism, and antibiotic-related pathways. A total of 18,270 AMR genes were identified using the CARD database, with common resistance to tetracyclines, beta-lactams, and macrolides. These findings highlight the significant AMR gene burden in poultry environments and the importance of routine surveillance.

Therapeutic prospects of *Dictyota sp.* extracts in liver disease and its molecular insights

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Seaweeds have been consumed as a whole food since ancient times and used to treat several diseases, even though the mechanisms of action were unknown. During the last decades, research has demonstrated that those unique compounds express beneficial properties for human health. The current

study focused on examining the therapeutic potential of *Dictyota sp.*, a brown seaweed collected from the Gulf of Mannar, India, emphasizing its anti-cirrhotic, and antimicrobial properties. Extraction was performed using six different solvents, like ethanol, isopropyl alcohol, acetone, hexane, toluene and petroleum ether. Qualitative phytochemical screening confirmed the presence of multiple bioactive compounds, including terpenoids, phytosterols, flavonoids, polyphenols, alkaloids, saponins, steroids, carbohydrates, etc. Functional groups analyzed by FT-IR spectroscopy of selected extracts indicate the presence of alcohol stretching, alkane and anhydride groups. GC-MS profiling identified 12 compounds across these extracts, the ethanolic fractions predominantly comprising Cholesta-6,22,24-triene, 4,4-dimethyl- and Cholesta-8,24-dien-3-ol, 4-methyl-, (3 β ,4 α), both noted for their antimicrobial, anti-inflammatory, and anticancer properties. In the antioxidant activities of DPPH, ABTS, Nitric acid scavenging and superoxide scavenging assay, the ethanol extraction shows the highest antioxidant activity among the other extractions. Similarly, antibacterial screening further revealed that the ethanol extract most effectively inhibited both *Escherichia coli* and *Staphylococcus aureus*. Molecular docking studies of two major compounds from the ethanolic extracts exhibited strong binding affinities to PPAR α (2P54) and PPAR γ (2PRG) receptors. These interactions suggest the potential modulation of AMPK and PPAR signaling pathways, implicating the extract's possible role in reversing liver cirrhosis. These findings indicate that *Dictyota sp.* ethanolic extract showed strong antioxidant, antibacterial, and anti-cirrhotic effects, but further in vitro and mechanistic studies are needed for validation.

Key words: *Dictyota sp*, Bioactive metabolites, Antioxidant, Anti-microbial, Molecular interactions, liver cirrhosis.

**Lycorine induces oxidative stress-mediated DNA damage in
*Saccharomyces cerevisiae***

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Lycorine (LYC) is a natural alkaloid that induces cytotoxicity at very low concentrations and with high specificity against several cancers. Here, we have collected evidence suggesting that lycorine induces DNA damage, probably ROS-mediated. Utilizing yeast, *Saccharomyces cerevisiae*, we investigated the cellular response of lycorine on the strains lacking antioxidant and DNA-damage response genes. LYC sensitizes yeast mutants lacking DNA repair and oxidative stress response pathway genes. Also, binding assay demonstrated that LYC intercalates into DNA, which suggests direct genotoxic potential. In addition, we explore the mechanisms associated with the cytotoxicity by measuring ROS generation, ROS-mediated DNA damage, DNA damage checkpoint activation, change in gene expression and induction of apoptosis by LYC. Further, we show that LYC can be synergistically used with a known DNA-damaging agent, bleomycin (BLM), at low concentration, which made the mutant more sensitive. Our results indicate LYC can cause DNA level

toxicity, which could be valuable for designing future selective anticancer therapies.

Green Synthesis and Antimicrobial Evaluation of Zinc Oxide Nanoparticles Mediated by *Annona muricata* Leaf Extract
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The increasing prevalence of antimicrobial resistance necessitates innovative, eco-friendly solutions in nanomedicine. This study focuses on the green synthesis of zinc oxide (ZnO) nanoparticles using aqueous leaf extract of *Annona muricata* (soursop) and evaluates their antimicrobial efficacy against clinically relevant pathogens. The biosynthesis was achieved through a simple, non-toxic method utilizing the phytochemical-rich extract as a reducing and stabilizing agent. Characterization of the synthesized ZnO nanoparticles was performed using UV-Visible Spectroscopy, Scanning Electron Microscopy (SEM), and Energy Dispersive X-ray Spectroscopy (EDAX), confirming their morphology and elemental composition. Antimicrobial activity was assessed via the disc diffusion method against *Escherichia coli*, *Staphylococcus aureus*, and *Candida albicans* with standard samples (ATCC). Results demonstrated notable inhibitory zones, underscoring the potential of *Annona muricata*-mediated ZnO nanoparticles as biocompatible agents in antimicrobial formulations. This study advances sustainable nanotechnology and supports the integration of plant-based synthesis in combating microbial infections.

KEYWORDS - Antimicrobial, Zinc oxide (ZnO) nanoparticles, *Annona muricata*, characterization, clinical, method.

Restoring oral symbiosis: antibacterial effects of fermented rice water on dysbiotic salivary microbiota

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Background:

Oral dysbiosis, an imbalance in microbial communities, contributes to dental caries periodontal disease and varies oral diseases. Natural interventions to restore microbial symbiosis are gaining attention.

Objective:

To assess the antibacterial effects of fermented rice water from five Indian rice varieties on key oral pathogens.

Methods

Rice varieties (parboiled, raw, red, black, Mapillai samba) were fermented for 16 hours. Fermented and non-fermented rice water samples were incubated with dysbiotic saliva broth after 24 hr incubation with Muller Hilton Broth. Post-incubation, DNA was extracted, and bacterial load was assessed using quantitative PCR targeting *S. mutans*, *F. nucleatum*, *T. forsythia*, and *P. gingivalis*.

Results:

Fermented rice water showed enhanced antibacterial activity compared to non-fermented samples. Black and Mapillai samba

rice demonstrated 100% inhibition of *S. mutans* and *F. nucleatum*, and significant suppression of *P. gingivalis*. Fermented red and parboiled rice were also effective, particularly against *T. forsythia*.

Conclusion:

Fermented rice water, especially from black and Mapillai samba varieties, exhibits strong antibacterial action against oral pathogens, suggesting its potential in managing oral dysbiosis and promoting microbial symbiosis.

**The Microbiome Connection: Evaluating Knowledge Levels
among Healthcare professionals on Gut-Lung Axis and Dysbiosis
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Abstract:

The human microbiome primarily mediates the gut-lung axis, which is becoming more widely acknowledged as a vital pathway connecting intestinal and respiratory health. Via systemic communication and immunological regulation, dysbiosis, or microbial imbalance, in the gut can affect lung disorders. The level of knowledge and comprehension of this connection among healthcare professionals is still unknown, despite mounting scientific evidence.

The purpose of this study is to evaluate healthcare professionals' understanding of the gut-lung axis, the microbiome, and the effects of dysbiosis on general health, with an emphasis on respiratory conditions. Healthcare professionals (n=250) (physicians, nurses, and allied health personnel) from a few chosen medical institutions participated in a cross-sectional survey. Participants' understanding of the gut-lung axis, the microbiome, and the clinical consequences of dysbiosis was assessed using a validated questionnaire. Knowledge gaps and related demographic characteristics were examined using descriptive and inferential statistics.

Findings suggests that participants have a moderate understanding of the fundamentals of the microbiome, but there are notable knowledge gaps regarding the gut-lung axis and the clinical significance of dysbiosis, particularly with regard to respiratory health. Variations in knowledge levels were noted according to years of experience, occupation, and previous exposure to education about the microbiome. The study highlights a pressing need for targeted educational interventions among healthcare workers to bridge gaps in knowledge regarding the gut-lung axis and dysbiosis. Raising understanding of microbiome-mediated health and disease could enhance evidence-based practice and enable integrative approaches to patient management.

Key Words: Gut Microbiome, Gut- Lung Axis, Dysbiosis, Health Care Professionals.

Identification and Characterisation of Isolated probiotic from gut microbiome of *Labeo rohita*

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Indian major carp *Labeo rohita* is one of the important species used in polyculture. Probiotics are live microorganisms which provide wide benefits to the aquatic animals. The probiotics are isolated from the gut of intestine and used as supplements for the better health of animals and humans. The potential probiotic *Bacillus albus* was isolated from the intestine of *Labeo rohita*. The isolate was initially identified based on the morphological and gram staining method, and the species was confirmed through molecular characterization of the 16S rRNA gene sequence and phylogenetic analysis. The isolated probiotic was subjected to the in-vitro activity against the aquatic pathogens. The isolated probiotic showed antagonistic to aquatic pathogens *Aeromonas hydrophila* and *Vibrio parahaemolyticus*. In the study, the experimental pathogenicity of the aquatic pathogens was also done which gave the results of 100% mortality in *V. parahaemolyticus* and 66% mortality in *A. hydrophila*. The in-vivo pathogenicity of the study showed the clinical symptoms like reddish lesions, exophthalmic eyes, haemorrhages on the skin and tail fin rot and scale loses. Overall, the study demonstrated that the isolated probiotic *Bacillus albus* MCCC 1A02146 has a potent activity against the aquatic pathogens which helps in the management to prevent the possibility for the diseases in aquaculture.

Keywords: Probiotics, *Labeo rohita*, antagonistic, Pathogenicity

In vitro* activity of combination antimicrobials against carbapenem resistant *Acinetobacter baumannii

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Antimicrobial resistance is a major concern. Carbapenem Resistant *Acinetobacter baumannii* (CRAB) is increasingly becoming resistant. Carbapenem resistance rates in Southeast Asia, China, India, and South Korea are upto 70%. The present work was undertaken to study the invitro activity of combination antimicrobial as a treatment alternative for CRAB. The objective of the study is to determine the in vitro activity of combination antimicrobial agents against CRAB and to study the effectiveness of combination antimicrobial agents between CRAB and non-CRAB strains. Prospective study was conducted in a tertiary care teaching hospital, Eluru, Andhra Pradesh, during the period from January 2024 to April 2025. A total of 163 *Acinetobacter baumannii* isolates were taken in this study. The samples include all types of respiratory samples. Samples were processed and isolates were identified as per standard protocol. Antibiotic susceptibility of isolates was determined by the standard Kirby Bauer disc diffusion method as per Clinical laboratory standards institute (CLSI) guidelines 2017. MIC test was performed to determine the MIC of antibiotics. Out of the total 163 *Acinetobacter* isolates, 126 (77%) of isolates were multidrug resistant organisms and all were extended spectrum β -lactamase producers, 91 (55.8%) of isolates were carbapenem resistant. Male- female ratio is 2:1. The effectiveness of cefipime-sulbactam, cefeperazone-sulbactam, piperacillin-tazobactam

was compared for both CRAB and non-CRAB strains. Cefipime-sulbactam showed better antimicrobial activity against CRAB whereas very slight difference between cefeperazone-sulbactam and piperacillin-taobactam. Based on our study we can say that Cefepime/sulbactam can be considered as a reliable option.

Keywords: *Acinetobacter baumannii*, carbapenem resistant, sulbactam,

Co-occurrence of DIM, NDM and OXA-48 like carbapenemase in a pan drug resistant *Klebsiella pneumoniae* patient isolate from South India.

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Recently, emergence of pan drug resistance (PDR) hinders the ability to treat the infections caused by *K. pneumoniae*. We performed whole genome sequencing to understand the characteristics of PDR *K. pneumoniae*. The patient isolate was subjected to AST, carbapenemase gene detection using PCR and WGS. The bacterium was resistant to all the antibiotics tested. *bla*_{NDM} and *bla*_{OXA-48} like carbapenemases were identified using

PCR. *K.pneumoniae* ST231 on MLST analyses, carried almost 42 ARGs including *aac*, *aad*, *ant*, *aph* and *arm* (aminoglycosides) gene clusters, beta lactamases gene(s) such as *bla*_{CMY} (2), *bla*_{CTX-M} (4), *bla*_{DIM-1}, *bla*_{NDM-1}, *bla*_{OXA-10}, *bla*_{OXA-232} etc, fluoroquinolones resistance genes, sulfonamide resistance genes and phenicol resistance genes. Other resistance genes include *dfrA12*, *ARR-2* and *tet(I)*. Virulence factors *ompA*, *ent* etc were found. Plasmid replicons such as *ColKP3*, *IncFIB(pQil)* and *IncFII(pAMA1167-NDM-5)* and Insertion elements like *ISKpn19*, *IS Sty2*, etc., were found. Integrons and mobile genetic elements was identified including *bla*_{TEM-1B} and *qnS1* associated with *IS Kpn19*, *bla*_{SHV-28} and *bla*_{SHV-106} with *IS Sty2* and *bla*_{OXA-232} located in the plasmid *ColKp3*. Virulence factor *tarT* was identified in the plasmid *IncFII(K)*. Phylogeny study revealed that the isolate used in the study was distant, forming a distinct clade, to the same STs found in the same region and internationally.

Keywords: Carbapenemase, ST231, antimicrobial resistance, virulence, mobile genetic elements

Assessment of Sleep Quality and Psychological Distress Among Government Hospital Nurses in Puducherry: A Cross-Sectional Study

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Sleep deprivation and psychological distress are significant occupational health concerns for staff nurses. This can negatively impact both personal well-being and professional performance in the healthcare sector. This study aimed to determine the prevalence of Sleep distress, stress, anxiety, and depression among nurses in tertiary hospitals in Puducherry. A descriptive pilot study was conducted among 120 nurses aged 20 to 60 in the Government tertiary care hospitals of Puducherry. The participants were recruited through systematic random sampling. Sleep quality was assessed using the Pittsburgh Sleep Quality Index, and psychological distress using the Depression, Anxiety, and Stress Scale- 21. Participants had a mean age of 45 years. 56.7% had poor sleep quality. 56.66% had limited 5-6

hours of sleep, 45% had moderate to high sleep latency, and 75.33% had good sleep efficiency. Regarding psychological distress, 30% had stress, 34.5% had anxiety, and 20.2% had depression symptoms. The study highlights that nurses experience sleep problems, anxiety, depression, and stress. Similar patterns are seen in international studies. Poor sleep and mental health can affect clinical performance and patient safety. More interventional research is needed to support mental health and improve sleep hygiene among nursing professionals.

Keywords: Sleep Quality, Nurses, Stress, Anxiety, Depression, PSQI

**Prevalence of Clinically Important Antibiotic-Resistant Pathogens
and Antimicrobial Resistance Genes in Wastewater from a
Tertiary Hospital in Coimbatore, India**

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Hospital sewages are hotspots in disseminating several MDR organisms. In this study, waste waters from a tertiary care

hospital is screened for gram-negative bacteria exhibiting resistance to carbapenem, colistin and gentamicin. Disc diffusion method and Modified Hodge test were applied to study the phenotype of selected isolates. Genotyping for the presence of carbapenemase genes – *bla_{NDM}*, *bla_{OXA}*, *bla_{KPC}*, *bla_{VIM}*, *bla_{IMP}*; colistin resistant genes– MCR 1-10 and 16S rmtase genes – *armA*, *rmtA-D*, *npmA* was performed. A total of 302 isolates were obtained out of which 82 exhibited colistin, 125 meropenem and 95 gentamicin resistance. AST revealed 84 isolates to be multi-drug resistant and 76 to be extremely drug resistant. 123 isolates were capable of producing carbapenemase enzymes in which 35% were from effluent. The most detected genes were in the order *bla_{NDM}*– 103 isolates (68%), *bla_{OXA}*–88 (58%), *bla_{KPC}*–29 (19%), *bla_{VIM}*–15 (9.9%). The genes mcr 2&9 were present in 2 isolates both were from clinical influent. The most prevalent 16S rmtase genes were *armA* in 23 isolates followed by, *rmtB* – 13, *npmA*–7, *rmtD*– 6. Stringent and novel purification methods have to be applied to tackle the dissemination of AMR organisms in to the environment from these water sources.

Keywords – Antimicrobial resistance, carbapenem, colistin, gentamicin, beta-lactamase

Development and Evaluation of a Multiple Essential Oil-Loaded Nanoemulgel Against *Enterococcus faecalis*, a Resilient Endodontic pathogen: A Novel Antibiofilm Strategy
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Persistent endodontic infections represent a significant clinical challenge, with *Enterococcus faecalis* frequently identified as a primary causative agent due to its exceptional ability to survive harsh conditions, penetrate dentinal tubules, and form resilient biofilms. The increasing incidence of antimicrobial resistance highlights the need for effective, biocompatible alternatives to conventional agents such as chlorhexidine. In the present study, a multiple essential oil loaded nanoemulgel was formulated and evaluated for its potential to combat *E. faecalis*. Nanoemulsions were prepared using varied oil, surfactant, and aqueous phase ratios guided by a pseudoternary phase diagram and optimized through Response Surface Methodology (RSM). The optimized nanoemulsion was characterized for particle size, polydispersity index (PDI), zeta potential, electrophoretic mobility, conductivity, turbidity, and pH. Structural and chemical features were confirmed via Fourier-transform infrared spectroscopy (FTIR) and field emission scanning electron microscopy (FE-SEM). The formulation exhibited potent antibacterial and antibiofilm activity against *E. faecalis*, with superior efficacy observed in comparison to standard chlorhexidine. Biofilm

disruption was further confirmed through scanning electron microscopy (SEM). The formulation also demonstrated significant antioxidant activity (DPPH assay). Incorporation into a Carbopol 940-based nanoemulgel enhanced stability and application properties, confirming its potential as a natural, effective alternative for the management of *E. faecalis*-associated dental infections.

**Anti-Mycobacterial Activity and Synergistic Effects of
Selected Siddha and Ayurvedic Formulations**
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Background: The Indian system of medicine (ISM) has been used alongside allopathic treatments for a long time. There are reports implicating that Homeopathy formulations were noted to synergise with anti-TB drugs. This study aimed to generate scientific evidence to determine whether certain Siddha and Ayurvedic treatments can be effective against *Mycobacterium tuberculosis*.

Aim: To assess the anti-mycobacterial efficacy, cytotoxicity, and synergistic role played by Siddha and Ayurveda polyherbal and herbo-mineral formulations against drug-sensitive and multidrug-resistant isolates of *Mycobacterium tuberculosis*.

Methodology: A total of 30 formulations from the Siddha system and 5 formulations from the Ayurveda system of medicine were selected as per the recommended treatment options provided

by the Standard Siddha Treatment Guidelines (prepared by National Institute of Siddha, 2019) and Ayurvedic Standard treatment guidelines (1st Edition, 2017) by Ministry of AYUSH. The formulations were procured commercially, and their efficacy was tested by the microbroth dilution method against *Mycobacterium tuberculosis* (Mtb) H37Rv and stored clinical isolates of both multidrug-resistant (MDR-TB) and sensitive isolates of Mtb (DS-TB). Synergism between the potent formulations (as per the efficacy testing) and Rifampicin (RMP) was attempted by checkerboard assay. The ex-vivo cytotoxicity of the selected formulations in Human leukemia monocytic cell lines (THP-1) were assessed by a resazurin reduction assay.

Result: Notably, the Minimum inhibitory concentration (MIC) for Gowrichinthamani Chenduram (GC) and Thalaka Chenduram (TLKC) were 250 µg/ml and 62.5 µg/ml respectively versus MtbH37Rv and were effective against 4 out of 6 MDR clinical isolates and for all the DS-TB isolates. Among Ayurvedic formulations, increased potency was observed for Bringarajaseva (BNS) against Mtb H37Rv (MIC: 3.9 µg/ml). Potency of BNS ranged between 62.5- 500 µg/ml for MDR-TB and 31.25–62.5µg/ml for DS-TB isolates (Table-1). The checkerboard test demonstrated synergism between GC and RMP (FICI-0.07), whereas additive effect noted for TLKC [Fractional Inhibitory Concentration index (FICI)-0.56] and BNS (FICI-0.62) with RMP. FICI value of less than 0.5 indicates synergism and values between 0.5 and 1.0 is indicative of additive effect. All three formulations considerably lowered the MIC of RMP from 0.25 µg/ml to 0.0019 µg/ml for GC, 0.015 µg/ml for TLKC, and 0.03 µg/ml for BNS (Table-2). There was no cytotoxicity observed in THP-1 cells ex-vivo at levels up to three times the MIC (Table-3, Figure-1)

Conclusion: The study provided insights into the efficacy of three traditional formulations namely GC, TLKC, and BNS which demonstrated synergistic effects with rifampicin, suggesting their potential as adjunct therapies in tuberculosis management. These preliminary findings, based on testing against six MDR-TB and a few DS-TB clinical isolates, warrant further validation in larger sample sizes for improved clinical relevance. The results lay the foundation for future preclinical development of these formulations and may inform policy-level decisions for integrating traditional medicine into TB care, pending further safety and efficacy evaluations.

Key Words: *Mycobacterium tuberculosis*, Mtb H37RV, MDR-TB and DS-TB, Bringarajaseva, Gowrichinthamani Chenduram, Thalaka Chenduram.

Estimation of Interleukin 6 levels as a potential Biomarker among Pulmonary Tuberculosis Patients for Assessing Disease Severity

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Pulmonary tuberculosis (PTB), a major public health concern, frequently worsens due to a poor immune response and delayed diagnosis. Interleukin-6 (IL-6), a pro-inflammatory cytokine, is linked to illness development and may serve as a biomarker. The purpose of this study was to assess IL-6 levels in newly diagnosed sputum-positive PTB patients and determine their relationship to clinical severity and treatment outcomes. A prospective laboratory-based study was undertaken on 80 microbiologically confirmed PTB patients at a tertiary care institution from December 2022 to December 2023. Serum IL-6 levels were measured using ELISA. Demographic, radiological, and clinical data were gathered and analyzed. The majority of the participants (81.25%) were males aged 31 to 60. Diabetes was among the most common comorbidities (26.25%). Elevated IL-6 levels (6.64-151.91 pg/mL) were substantially linked to higher sputum smear grades, radiographic abnormalities, and concomitant diseases. Treatment outcomes showed that 55% were cured, 36.25% were treated, and 8.75% died. Patients with severe illness and poor outcomes had higher levels of IL-6. IL-6 levels in PTB are associated with disease severity and may serve as a useful biomarker for prognosis and treatment monitoring. Further large-scale research are required to validate IL-6 as a therapeutic aid in tuberculosis care.

Key words: Pulmonary tuberculosis, Interleukin 6, Inflammatory markers, ELISA.

**Comparative Evaluation of Virulence Factors of Uropathogenic
Escherichia coli and Commensal *Escherichia coli*.**

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Urinary tract infections (UTIs) are among the most prevalent bacterial infections, primarily caused by uropathogenic *Escherichia coli* (UPEC), which possess distinct virulence traits that are absent in commensal strains. This study aimed to compare the phenotypic and genotypic virulence profiles of UPEC with those of commensal *E. coli* strains. A total of 180 UPEC isolates obtained from clinically confirmed UTI cases were included, and 30 commensal *E. coli* isolates from healthy individuals served as controls. Phenotypic analysis revealed that UPEC isolates exhibited significantly higher expression of hemolysin (48.88%), hemagglutination (57.77%), cell surface hydrophobicity (52.77%), and serum resistance (26.11%) compared to commensal strains ($p < 0.001$), while no significant differences were noted in adhesion and gelatinase production. Among various UTI subtypes, hemolysin was commonly associated with cystitis (55.44%), hemagglutination with pyelonephritis (93.54%), and hydrophobicity with catheter-associated UTIs (64.28%) and recurrent infections (63.63%).

Genotypic analysis identified *fyuA* (100%) and *traT* (98.33%) as the most prevalent virulence genes in UPEC, followed by significant presence of *hlyA*, *papGII*, *sfa/focDE*, and *iutA* ($p < 0.05$). No significant differences were observed in the distribution of *papC*, *papGIII*, *aer*, and *usp*, and *cvaC* was absent in all isolates. These findings highlight the distinct virulence characteristics of UPEC strains and emphasize their role in the pathogenesis of UTIs, providing valuable insights for the development of targeted diagnostic and therapeutic strategies.

Keywords: Uropathogenic *Escherichia coli*, Virulence factors, UTIs, Phenotypic traits, Genotypic profiling, Commensal *E. coli*.

Isolation, Identification and Characterisation of probiotic bacteria from gut microbiome of *Labeo rohita* and its efficiency

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Labeo rohita is one of the important Indian major carp species used in polyculture. Probiotics are live microorganisms which provide wide benefits to the aquatic animals. The probiotics can be isolated from the gut and used as supplements for the betterment of aquatic animals. In the present study, a probiotic bacterium *Bacillus albus* was isolated from the intestines of *L. rohita*. The isolate was identified through morphological and gram staining techniques. It was further confirmed through molecular and phylogenetic analysis. The *in vivo* pathogenicity studies with the aquatic pathogens showed mortality of 100% in *Vibrio parahaemolyticus* and 66% in *Aeromonas hydrophila*.

Further, clinical manifestations such as reddish lesions, exophthalmia, haemorrhages on the skin and tail, and scale loss were observed. The probiotic isolate showed *in vitro* antibacterial activity against the aquatic pathogens. A zone of inhibition of 14.5 ± 0.5 mm (*A. hydrophila*) and 17.83 ± 0.76 mm (*V. parahaemolyticus*) were observed at 200 µg/mL. Further, *B. albus* was used to treat *A. hydrophila* infections in *L. rohita*. The survival rate of 100% was observed in the treated fishes. This study demonstrated that *Bacillus albus* is antagonistic against the aquatic pathogens which helps in the management to prevent the possibility for the diseases in aquaculture.

Keywords: Probiotics, *Labeo rohita*, antagonistic, Pathogenicity

Comparative Genome-Based Resistome Profiling of
Fusobacterium

nucleatum: Insights from 77 Complete Genomes
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Fusobacterium nucleatum is a gram-negative anaerobe that colonizes the human oral cavity, gut, and other mucosal surfaces. As an opportunistic pathogen, it's linked to periodontitis, preterm birth and colorectal cancer. Despite its pathogenic potential, a comprehensive understanding of the antimicrobial resistance (ARGs) landscape in *F. nucleatum* remains limited. This study aims to characterize the functional diversity of ARGs across the complete *F. nucleatum* genomes. We analyzed the diversity of 77 *F. nucleatum* genomes, using whole-genome and 16S phylogeny. Comparative genomic analysis using curated databases to reveal ARG abundance, diversity, and functional categories. Phylogenetic analysis revealed three major clusters, indicating genomic divergence. Resistance mechanisms revealed that the majority of core ARGs were linked to antibiotic target alteration, conferring vancomycin resistance and three strains associated with antibiotic inactivation and target protection, conferring tetracycline, lincomycin and erythromycin resistance. ARG profiling showed broad resistance against multidrug classes

which includes aminoglycosides, fluoroquinolones, and sulfonamides, with notable strain-level variation in peptide antibiotics (n = 28), macrolides (n = 8) and elfamycins (n = 2). Heavy metal resistance was conserved, while efflux pumps and bile hydrolysis genes (n = 35) showed strain-level variation. This study reveals diverse functional categories of ARGs in *F. nucleatum*, including both common and rare ARGs. Their association suggests potential gene transfer, highlighting the need for surveillance and targeted strategies to control antimicrobial resistance.

Keywords: *Fusobacterium nucleatum*, Opportunistic Pathogen, Phylogeny, Resistome, Antimicrobial Resistance, Vancomycin, Heavy Metal Resistance

Biopython-assisted in-Silico profiling and antimicrobial evaluation of chitosan nanoparticles against antibiotic-resistant pathogenic bacteria from lake ecosystems

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Freshwater bodies in urban areas are emerging as reservoirs of antibiotic-resistant pathogenic bacteria, posing a growing threat to environmental and public health. This study explores the antimicrobial potential of chitosan nanoparticles (CNPs) against multidrug-resistant (MDR) bacteria isolated from lake water samples collected across Chennai. Bacterial strains, including, *Ralstonia picketti*, *Aeromonas caviae*, *Coronobacter sakazakii*, *Bacillus subtilis* were isolated and identified using standard microbiological and molecular techniques. Their resistance profiles were determined through antibiotic susceptibility testing. To understand resistance mechanisms at the molecular level, Biopython was employed to perform genomic and transcriptomic data analysis of resistance genes NDM-1. In-silico molecular docking studies were conducted to assess the binding efficiency of chitosan molecules to key resistance-related bacterial proteins. Chitosan nanoparticles were synthesized and characterized, then evaluated for their antibacterial efficacy through assays such as MIC determination, bacterial viability. The results reveal that CNPs exhibit strong inhibitory effects against MDR isolates, indicating their potential as eco-friendly bioremediation agents. The integration of computational and experimental approaches underscores the value of nanoparticle-based strategies in mitigating antimicrobial resistance in aquatic environments.

Keywords: Lake water, MDR bacteria, Chitosan nanoparticles, Biopython, Molecular Docking.

Phylogenomics and Resistome Profiling of *Corynebacterium diphtheria* reveal Emerging Multidrug Resistance
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Corynebacterium diphtheria, a gram-positive bacterium that primarily colonizes the upper respiratory tract, skin, and mucous membranes. While historically associated with diphtheria, non-toxicogenic and cutaneous strains are increasingly implicated in invasive infections. The emergence of multidrug-resistant (MDR) strains underscores the need for ongoing genomic surveillance. To investigate the antimicrobial resistance gene (ARG) profile, 76 complete genomes of *C. diphtheriae* were retrieved from public databases and analyzed using *in-silico* annotation tools. Phylogenetic analysis and antibacterial resistome profiling were conducted to assess genomic diversity and ARG distribution. Resistance genes belonging to nine antibiotic drug classes were identified, with eight strains classified as MDR. Notably, resistance to macrolides, a key therapeutic class was detected in

five strains. All three cutaneous isolates carried macrolide resistance genes (*ermX*) and exhibited a higher abundance of ARGs, suggesting their potential role as reservoirs, likely driven by increased environmental exposure and microbial gene exchange. Multiple sequence alignment of the *ermX* gene revealed an Isoleucine-to-Leucine (I→L) substitution at position 21, a conservative mutation that may indicate reduced resistance but requires phenotypic validation. These findings emphasize the need for continued genomic monitoring of *C. diphtheriae*, particularly for community-associated and cutaneous strains, to better understand and mitigate the spread of antimicrobial resistance.

Keyword: *C. diphtheria*, Multi drug resistance, *ermX*, Mutation

Biofilm Formation and Phenotypic Traits of Clinical Carbapenem resistance *Acinetobacter baumannii* Isolates

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Acinetobacter baumannii is an opportunistic Gram-negative pathogen and a leading cause of healthcare-associated infections, particularly in intensive care units. Its clinical relevance stems from its ability to develop multidrug resistance and form biofilms, enhancing its persistence and virulence. This study phenotypically characterized 120 clinical isolates of *A.*

baumannii to assess antimicrobial susceptibility, hemolytic activity, and biofilm-forming ability. Antimicrobial susceptibility testing (AST), with a focus on carbapenem resistance, was performed using the VITEK automated system. Hemolysis was evaluated on 5% sheep blood agar. Biofilm formation was assessed using the crystal violet microtiter plate assay. AST revealed a high prevalence of carbapenem resistance, especially against imipenem and meropenem, indicating widespread CRAB (Carbapenem-Resistant *A. baumannii*) strains. Hemolysis testing showed no alpha-hemolytic isolates, three (2.5%) beta-hemolytic, and 117 (97.5%) gamma-hemolytic isolates. Regarding biofilm production, 82 isolates (68.3%) were strong producers, 12 (10%) moderate, and 26 (21.7%) non-biofilm formers. The combined presence of carbapenem resistance and strong biofilm-forming ability among the isolates underscores the threat posed by *A. baumannii* in hospital settings. These findings highlight the urgency for stringent infection control measures and ongoing surveillance to prevent the spread of CRAB strains.

KEYWORDS: Biofilm, antimicrobial resistance, phenotypic characterization, crystal violet assay

Characterization of bacteria isolated from *Oreochromis mossambicus* with reference to Antimicrobial-resistance

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Aquaculture has become one of the fastest-growing food production sectors, now exceeding livestock and poultry in global protein supply. *Oreochromis mossambicus*, a widely consumed freshwater fish, is cultivated extensively due to its rapid growth, environmental adaptability, and high consumer demand. In response to increased food requirements farmers have shifted from traditional cultivation to intensive and semi-intensive aquaculture practices. These practices have increased the spread of disease-causing pathogens thereby leading to incorporation of antibiotics in feeds for prevention of diseases. This led to the emergence of Antibiotic-resistant organism (AR) harbouring AR genes. These AR genes can enter the human body via food chain. This preliminary study involves isolation of antibiotic-resistant bacteria from *Oreochromis mossambicus* to study its antibiotic resistance profile and pathogenicity. Molecular characterisation by 16s rRNA sequencing confirmed the presence of *Micrococcus luteus* in the fish and its resistance profile was confirmed by performing antibiotic susceptibility test against 10 commercially important antibiotics. Its pathogenic effect was also studied and symptoms like redness on its operculum, decolourisation of scales, loss of scales and yellow lesions on the skin were noted. These findings highlight the pathogenic role of *M. luteus* and the need to address AR bacteria to mitigate their impact on fish health and human safety.

Keywords: *Oreochromis mossambicus*, *Micrococcus luteus*, Antibiotic resistance, Pathogenicity, Antibiotic resistance genes

Evaluation of Multidrug-Resistant Tuberculosis in *Mycobacterium tuberculosis* using the Bactec MGIT 960 System

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Tuberculosis is an infectious disease caused by the bacillus *Mycobacterium tuberculosis*. Multidrug-resistant TB remains a public health crisis. *M. tuberculosis* strains resistant to isoniazid and rifampicin are defined as multidrug-resistant tuberculosis. Linezolid is an effective antibiotic to treat patients with MDR-TB treatment failure. The aim of the study is to determine the phenotypic resistance to Linezolid among MDR TB patients. A total of 187 sputum samples from patients with clinical suspicion of MDR-TB were processed following WHO guidelines using the NALC-NaOH decontamination procedure. The decontaminated samples were inoculated into both BACTEC MGIT 960 tubes and Lowenstein–Jensen (LJ) medium for primary isolation of *Mycobacterium tuberculosis* complex (MTBC). The growth was identified as MTBC using MPT64Ag ICT (SD Bio line) and further subjected to DST for SIRE and PZA. After the antimicrobial mixture of PANTA was added, the samples were entered in the MGIT 960 instrument using the standard 14-day protocol for

Linezolid and Moxifloxacin as per the manufacturer's guidelines. A total of 187 MDR TB samples were tested for Linezolid resistance by MGIT from Jan 2024 to December 2024. Out of 187, four (2.1%) isolates were resistant to Linezolid and 184 were susceptible to Linezolid. This rate of resistance (approximately 2.1%) is concerning, as LZD is a crucial treatment option for patients with limited therapeutic alternatives. Individualised regimens with newer medications, adequate management of related adverse effects, early detection of LZD resistance using DST and sequencing, and stronger indicators of treatment failure would contribute to better outcomes for TB patients with LZD resistance.

Key Words Mycobacterium tuberculosis complex, LJ medium, Immunochromatographic test (ICT), MPT 64 Ag, DST, MGIT, Linezolid.

**Personal Listening Device (PLD) Usage and Auricular Dysbiosis:
Microbial Shifts, Antimicrobial Resistance, and Herbal
Disinfection Strategies**

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The widespread use of Personal Listening Device (PLD), particularly among younger populations and delivery agents, has prompted concerns regarding their impact on both auditory health and the auricular microbiome. Prolonged usage has been associated with early signs of noise-induced hearing loss (NIHL) and microbial colonization of the external auditory canal (EAC) by potential pathogens such as *Staphylococcus aureus*, *Pseudomonas spp.*, and *Aspergillus spp.*, several of which exhibit antimicrobial resistance (AMR). The occlusive environment created by PLDs, coupled with poor hygiene, favors biofilm formation and microbial dysbiosis. This review consolidates evidence linking earbud use with both auditory and microbiological alterations, emphasizing the urgent need for eco-friendly intervention. Herbal disinfectants including *Azadirachta indica* (Neem), *Ocimum sanctum* (Tulsi), *Melaleuca alternifolia* (Tea Tree), and *Allium sativum* (Garlic) demonstrate potent antimicrobial and antifungal activity and offer sustainable alternatives to chemical disinfectants. Current literature lacks integrated studies correlating auditory threshold changes with microbiota profiling and in vivo testing of herbal agents. Future directions include longitudinal clinical studies combining metagenomic sequencing with resistance profiling and herbal

formulation validation. This review highlights a pressing need for preventive strategies combining hearing protection and antimicrobial hygiene, especially among habitual PLD users.

Nature's Defense: Algae and Herbal Extracts Disrupt Oral and Nosocomial Biofilms

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The study examined the effects of selected algae and herbal infusions on biofilms associated with oral and nosocomial infections. Biofilm suppression was evaluated after treatment of the isolates. LC-MS, MALDI-TOF, and GC-MS were used to assess the impact of bioactive components. The findings suggest that natural infusions could serve as alternative antifungal agents.

Study On Drug Resistance *Pseudomonas Aeruginosa*: A Focus On Esbl, Ampc, And Mbl Production

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Multidrug resistant *Pseudomonas aeruginosa* is an alarming and emerging public health problem globally. *Pseudomonas aeruginosa* is still a major cause for nosocomial infection and

approx 10-20% of these patients are admitted to the ICU's. The aim of the present study was to evaluate the production of β -lactamases (ESBL, MBL, AmpC) in multi drug resistant *Pseudomonas aeruginosa* isolated from a tertiary care hospital.

Factors Affecting Diagnostic and Treatment Delays in Tuberculosis: A Cross-Sectional Study from South India

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Background:

Tuberculosis (TB) continues to be a significant public health threat in low- and middle-income countries, particularly in India, which bears the highest global TB burden. Timely diagnosis and initiation of treatment are critical to reducing transmission and mortality. This study aimed to assess the duration from symptom onset to diagnosis and identify key factors associated with diagnostic and treatment delays among TB patients.

Methods:

A community-based cross-sectional study was conducted from January to June 2025 among 331 microbiologically confirmed TB patients at PKTB Sanatorium, Mysore, Karnataka. A semi-structured questionnaire was administered through face-to-face interviews. Sociodemographic data, symptom onset, healthcare-seeking behavior, and barriers to early diagnosis were collected. Descriptive statistics and multivariate logistic regression were used to analyze factors associated with delay.

Results:

A total of 331 TB patients were studied, with most aged 20–60 years (77.9%), male (76.4%), residing in rural areas (63.4%), and living below the poverty line (88.5%). Pulmonary TB was predominant (95.8%), and 90.3% were newly diagnosed cases. Delays in tuberculosis diagnosis and treatment were primarily attributed to poor symptom awareness (68.9%), stigma (62.5%), and economic hardship. A majority (82.5%) consulted multiple healthcare providers, and 91.2% were diagnosed in private facilities. Patient delays were linked to self-medication and cultural beliefs, while provider delays resulted from low clinical suspicion and misdiagnosis. Treatment delays arose from reluctance, long distances, and limited knowledge.

Conclusion:

Delays in TB diagnosis and treatment were substantial and multifactorial. Both patient- and provider-related barriers contribute significantly to these delays. Targeted interventions focusing on awareness, stigma reduction, and health system strengthening are urgently needed to improve early detection and control of TB in high-burden settings.

Key Words: TB, Diagnostic Delays, Treatment Delays, Tuberculosis

Oral Signs of Re-emerging Infectious Diseases: Bridging Public Awareness and Dental Practice

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Introduction:

Emerging and re-emerging infectious diseases have become a growing concern worldwide, influenced by factors such as globalization, climate change, and microbial adaptation. Many of these diseases exhibit early signs and symptoms in the oral cavity, including mucosal lesions, ulcers, and other atypical presentations. Dentists, often being the first point of contact in the healthcare system, are in a key position to detect these oral manifestations. Early recognition by dental professionals can lead to timely diagnosis and better patient outcomes.

Aim and Objective:

The aim of this study was to assess public awareness of the oral manifestations associated with re-emerging infectious diseases and to understand their perception of the role of dentists in identifying and managing systemic conditions. The objective was to evaluate the public's knowledge of oral signs and symptoms linked to re-emerging infectious diseases and to explore the factors that influenced public perception of the connection between oral and systemic conditions.

Material and Methods:

This cross-sectional study employed a structured questionnaire to collect data from participants who were recruited through both online platforms and in-person surveys. The questionnaire consisted of 20 multiple-choice questions that aimed to evaluate participants' awareness of oral

symptoms, perceptions of the role of dentists, and the significance of oral health during infectious disease outbreaks. Adults aged 18 years and older who provided informed consent were eligible to participate.

Results:

This survey on *"Oral Signs of Re-emerging Infectious Diseases: Bridging Public Awareness and Dental Practice"* aimed to assess public awareness about infectious diseases, re-emerging diseases, and the role of oral signs and symptoms in identifying systemic illnesses. Most respondents (67.2%) correctly identified infectious diseases as those caused by bacteria, viruses, or fungi. Additionally, 56% understood "re-emerging diseases" as those that were previously controlled but are becoming more common again, with measles and dengue (58.6%) recognized as examples. Many (42.2%) attributed the re-emergence of diseases to antibiotic resistance. Regarding dentists' role, 75% of people believed dentists are important in controlling infectious diseases, and 73.3% agreed that dentists should identify symptoms and refer patients to specialists. It's been found that 28% said general physicians don't usually check the mouth for signs of systemic illness. Most respondents (56%) thought oral signs can indicate systemic diseases, with 51.3% highlighting unexplained tongue alterations as a reason to see a dentist. The survey also showed interest in increasing awareness about the link between oral conditions and infectious diseases, with 57.3% wanting educational programs on the signs and symptoms of these diseases. Overall, the findings suggest a growing awareness of the role played by dentists in managing infectious diseases. The results also highlighted the need for enhanced public health initiatives.

Conclusion:

The results of this study provides insights into the public's understanding of the oral manifestations of re-emerging infectious diseases and the role of dentists in their management. These findings guide the development of targeted oral health education programs and foster stronger collaborations between dental practice and public health to effectively combat infectious diseases.

Evaluation of relationship between dental caries in non-diabetic, good controlled and poorly controlled diabetics using microbiological studies

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To evaluate the relationship between dental caries and diabetes status by comparing microbiological profiles in three groups of patients based on HbA1C levels. Non-diabetic patients (HbA1c- 4-6%), Known Diabetic patients with Good control (HbA1c- 6%-7%) and Known Diabetic patients with Poor control (HbA1c- 8% and above).The study will assess the composition, diversity, and activity of oral microbiota among these three groups to determine how diabetes-related factors influence the development of dental caries.

To assess and compare microorganisms causing Dental caries in Non-Diabetic Patients (Group A), Dental caries in Good Controlled Diabetic Patients (Group B), Dental caries in Poorly

controlled Diabetic Patients (Group C) using DMFT values, HbA1c levels and Microbiological studies.

Detailed case history, DMFT indices, HbA1c level were recorded. Saliva samples were collected in all the 3 groups and cultured onto Robertson Cooked Meat Media, Blood Agar, MacConkey Agar and Mitis Salivarius and organisms were identified based on colony characteristics. Further gram staining was done and organisms were confirmed using antibiotic sensitivity test for gram positive organisms and biochemical test for gram negative organisms. test was applied to analyze the distribution of organisms among the three groups. There was highly significant difference between proportions of Gram-positive organisms like *Streptococcus Mutans* ($p < 0.044$), *Streptococcus Pneumoniae* ($p < 0.04$), *Enterococcus species* ($p < 0.04$), in Group C compared to Group A and B. There was also highly significant difference between proportions of Gram-negative organisms like *Klebsiella Pneumoniae* ($p < 0.024$) and Gram negative cocci ($p < 0.041$) in Group C compared to Group A and Group B. The present study highlights elevated blood sugar levels, DMFT values, and complex and diverse microbial milieu in poor controlled diabetes which confirms a link between diabetes mellitus and increased risk of dental caries with shift in the microbiota from gram positive to gram negative organisms.

Identification and quantification of streptococcus species and lactobacillus species among anemic and non-anemic individuals - a cross sectional study

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Background:

Dental caries is a microbial disease influenced by the presence of acidogenic bacteria such as Streptococcus and Lactobacillus species. An altered oral environment, as seen in anemic individuals, may promote the growth of these cariogenic bacteria.

Aim:

To identify and quantify Streptococcus and Lactobacillus species in the saliva of anemic and non-anemic individuals and compare their bacterial loads.

Materials and Methods:

A total of 20 unstimulated saliva samples were collected and divided into two groups: Group A (anemic, n=10) and Group B (non-anemic, n=10). Saliva samples were cultured on selective media to isolate and quantify Streptococcus and Lactobacillus species.

Results:

Group A showed a consistently higher count of both Streptococcus and Lactobacillus species when compared to Group B. The increase was observed across all samples from the anemic group.

Conclusion:

Anemic individuals exhibited a greater prevalence of cariogenic bacteria, indicating a potentially higher risk for dental caries. These findings underscore the importance of integrating caries risk assessment and preventive dental care in individuals with underlying hematological conditions like anemia.

BRUSHING UP ON TUBERCULOSIS :Insights from Dental Professionals on Re -emerging Threat

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INTRODUCTION

Tuberculosis (TB) remains a global health concern, with oral manifestations often overlooked in dental settings. Dental professionals play a crucial role in early TB detection and infection control. This study assesses the awareness, knowledge, and management strategies of dental practitioners regarding TB.

AIM & OBJECTIVE

The aim of this study is to assess the knowledge, attitude, and practices of dental professionals regarding tuberculosis, recognizing its significance as a public health concern. The objectives include evaluating awareness related to TB transmission, clinical symptoms, and oral manifestations, assessing infection control measures such as sterilization, understanding of multidrug-resistant TB (MDR-TB), accessibility of treatment, and involvement in TB-related awareness programs. This study seeks to identify existing gaps and promote the integration of TB-related education within the dental field .

MATERIAL AND METHODS

This cross sectional study includes structured questionnaire to collect data from Dental professionals recruited via online platforms . Ethical approval was priorly obtained .Informed consent was obtained from those who were enrolled in the study .

RESULTS

The study revealed a generally encouraging level of awareness among dental professionals regarding tuberculosis, particularly in terms of transmission (85%) and symptoms (78%). However, knowledge related to oral manifestations (38%) and multidrug-resistant TB (45%) was found to be limited. While 64% adhered to appropriate sterilization protocols, only 30% had participated in TB-related awareness programs. Awareness of treatment accessibility stood at 70%. These findings suggest that although the foundational understanding of TB is present, there is a need for more targeted training, especially in recognizing oral signs and managing MDR-TB, to strengthen the role of dental professionals in TB control.

CONCLUSION

To conclude, this study emphasizes the vital role of dental professionals in combating tuberculosis, reflecting a promising level of awareness while also highlighting opportunities for further enhancement—particularly in areas such as oral manifestations and MDR-TB. With continued support through updated guidelines and focused training, the dental community can play an even more impactful role in TB detection and prevention.

Case Series of Mucormycosis, An institutional study

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Mucormycosis is a fungal infection characterized by angioinvasion, caused by the species Mucorales. The use of emerging immunomodulatory drugs in treating malignancies and autoimmune conditions has led to notable changes in the occurrence of mucormycosis. Mucorales have emerged as the second most frequent cause of invasive fungal infections, following *Aspergillus*. These pathogens are particularly significant in individuals with diabetic ketoacidosis, immunocompromised individuals, patients undergoing chemotherapy for malignancies or recipients of organ or hematopoietic stem cell transplants.

AIM AND OBJECTIVE:

To assess the prevalence, clinical manifestations and outcomes of mucormycosis in patients who reported during and post COVID times.

MATERIALS AND METHODS:

A retrospective case series was conducted in the Department of Oral and Maxillofacial Pathology & Oral Microbiology, from the period of 2021 to 2025. Patients with a confirmed diagnosis of mucormycosis following recovery from COVID-19 form the part of the study.

RESULTS AND CONCLUSION:

The relationship between mucormycosis and distinct patient characteristics including age, gender, anatomical site of fungal involvement, and underlying predisposing factors were

analysed. The predisposing factors included uncontrolled diabetes mellitus, recent COVID-19 infection, immunosuppressive therapy, and prolonged corticosteroid use. These findings reinforce the need for early diagnosis, and prompt antifungal therapy.

Molecular Identification and Genotyping of Bacterial Species in Saliva and Amniotic Fluid from Women in Preterm Labour

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Fusobacterium nucleatum is a key pathogen implicated in 25-40% of preterm births linked to intrauterine infections, having been detected in the placenta, amniotic fluid, and fetal tissues. While its oral-gut associations are well studied, the genetic link between oral and intra-amniotic *F. nucleatum* remains underexplored. This study explores the Molecular identification, sequence based genotyping and genetic diversity of *Fusobacterium nucleatum* from the salivary sample and amniotic fluid of preterm delivered mothers using 16S rRNA sequencing

and phylogeny, suggesting a possible hematogenous route of microbial translocation. Saliva and amniotic fluid samples were collected from 18 preterm cases. DNA was extracted and subjected to 16S rRNA-based PCR amplification and Sanger sequencing. *Fusobacterium* was detected in 100% of saliva samples and 66.7% of amniotic samples. Phylogenetic analysis revealed a high genetic similarity of *F. nucleatum*, *F. pseudoperiodonticum*, and *F. periodonticum* across paired specimens. Notably, vaginal deliveries showed higher amniotic positivity than C-sections ($p = 0.034$). This is the first study to report the detection of *Fusobacterium pseudoperiodonticum* in both saliva and amniotic fluid of preterm labour cases, suggesting its potential role in intrauterine microbial translocation and adverse pregnancy outcomes, emphasize the need for integrated oral health screening in pregnancy.

Key Words: Preterm birth, Saliva, Amniotic fluid, *Fusobacterium*, 16S rRNA, DNA sequencing, Genetic Diversity

Unveiling Hidden Halophiles: The Role of Metagenomics in Discovering Halophile Diversity from Salt Evaporation Tank sample

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Conventional microbiological methods have long been employed to study halophilic microorganisms, but these approaches often fall short in detecting unculturable or low-

abundance species. Metagenomics, a culture-independent technique, has revolutionized the field by enabling the analysis of microbial communities directly from environmental samples. This study compares the efficacy of metagenomics and conventional methods in detecting halophiles in diverse environments. In the present study, soil samples from salt evaporation tank of tannery industry, Ranipet, Tamilnadu, India was utilized to isolate and study halophiles. Part of the sample was utilized for isolating halophiles by conventional method while part of the sample was studied by metagenomics. By using conventional method, halophilic bacterial species *Halomonas halophila* (GAD1), *Halomonas aidingensis* (GAD2), *Chromohalobacter salexigens* (GAD4) and *Halomonas salina* (GAD8). But metagenomics study revealed the existence of halophiles of different clades such as bacteria, fungi and also actinomyces. Our results demonstrate that metagenomics can identify a broader range of halophilic microorganisms, including previously undetectable species. The presence of undetectable halophiles was revealed through metagenomic analysis of DNA sequences, highlighting the power of this approach in uncovering hidden microbial diversity. In contrast, conventional methods relying on culturing and isolation failed to capture the full extent of halophilic diversity. By leveraging metagenomics, researchers can explore the uncharted territory of microbial diversity, unlocking new opportunities for biotechnological innovation and environmental monitoring. This study underscores the superiority of metagenomics in detecting halophiles, paving the way for future research in extreme environments.

Keywords: Bacteria, Halomonas, Halophiles, Metagenomics, Soil.

Larvicidal activity of *Bacillus thuringiensis israelensis* (Bti) and its enhanced activities with selected aqueous plant extracts

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Mosquitoes adversely affect human health because they act as vectors for a wide variety of dreadful diseases. Now-a-days mosquito control is facing a threat due to the emergence of resistance to synthetic insecticides. The present study is a preliminary work to control mosquito larvae with the use of bio-pesticides in combination with easily available plant extracts. *Bacillus thuringiensis israelensis* (Bti) is a natural biological enemy of mosquito larvae that is safe for humans and all creatures except fungal gnats, black flies and a few very closely related insects. Bti is only activated in the gut of insect but it's not as effective for all kinds of mosquito. *Culex* and *Anopheles* larvae are most susceptible while *Aedes* are less susceptible. There is also a greater chance that mosquito may build resistance to it, and resistance has already been reported in some areas through scientist are already working on ways of preventing the problem. Hence in this study we have used integrated pest management control of Bti in combination with selected plant extracts (*Ocimum basilicum*, *Vitex negundo*, *Azadirachta indica* and *Mentha piperita*). The efficacy was determined through bioassay method as per WHO guidelines with slight modifications. Mortality percentage and

LC50 were calculated after monitoring the treatment sets for a period of 96 hours. *Vitex negundo* showed high mortality rate with 2.5 LD50 and LC50 of 0.77

Index Terms: *Bacillus thuringiensis israelensis*, Larvae, Bio assay, Mortality, LC₅₀, LD₅₀

An In-Silico Analysis of Amantadine: Potential Inhibitor of HIV Nef Protein

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Human Immunodeficiency Virus (HIV) infection remains a major global health concern, with approximately 39.9 million people currently affected. The global prevalence among adults aged 15–49 is 0.6%, while African nations bear a significantly higher rate of 3.4%, representing two-thirds of global cases. HIV's high mutation rate and ability to establish latency complicate the development of effective treatments. The HIV Nef protein, a small multifunctional factor, is pivotal in viral replication, pathogenesis, and disease progression. Notably, it shares sequence similarity with the Influenza A M2 protein, which is targeted by the antiviral drug amantadine. This study investigates the potential anti-HIV activity of amantadine through PyRx-based molecular docking with the Nef protein, identifying chain A as a preferred binding site, with binding energies of -5.5 kcal/mol. Interaction profiles, including bond types and key residues, were visualized via Biovia Discovery Studio. A 100 ns molecular dynamics simulation confirmed the complex's stability, with average RMSD of 0.5510 nm, RMSF of 0.2157 nm, SASA of 85.3 nm², and a radius of gyration of 1.6 nm. Additionally, 3D QSAR, ADME evaluations, and normal mode analysis (NMA) via the iMOD server identified key flexible and

deformable regions, supporting amantadine's therapeutic potential against HIV.

Keywords: HIV, Nef Protein, Amantadine drug, Molecular Docking & MD simulation

Periapical Pathologies in the background of Actinomycotic infection: A Retrospective Study

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INTRODUCTION

Periapical actinomycosis is a rare subtype of actinomycosis—a chronic infection caused by *Actinomyces* species—that affects the periapical region of teeth. It is often linked to persistent or recurrent periapical lesions, particularly in teeth that have undergone endodontic treatment. Although *Actinomyces* are part of the normal oral flora, disruption of the mucosal or epithelial barrier due to dental procedures, trauma, or infection can enable these bacteria to penetrate deeper tissues and initiate a chronic inflammatory response.

AIM & OBJECTIVE

This study aims to investigate the role of periapical actinomycosis in persistent or recurrent periapical lesions following endodontic treatment from the clinical data of the patients at the department in the past 5 years (2021-2025).

MATERIALS AND METHODS

This retrospective study was conducted using cases from the Department of Oral Pathology between January 2021 and June 2025. Clinical records and histopathological reports of patients with persistent or recurrent periapical lesions were reviewed. Cases with confirmed histological evidence of *Actinomyces* colonies in the periapical region were included.

RESULTS

This is an ongoing retrospective study. Preliminary findings have identified a subset of periapical lesions showing histopathological features consistent with actinomycosis. Most of these cases are associated with previously endodontically treated teeth presenting with persistent symptoms such as swelling, pain, or sinus tract formation. Histological examination has revealed characteristic *Actinomyces* colonies surrounded by chronic inflammatory infiltrates.

CONCLUSION

Periapical actinomycosis, though rare, is an important and often overlooked cause of persistent periapical lesions, particularly in endodontically treated teeth. Early recognition, supported by histopathological confirmation, is essential for appropriate management. Increased clinical awareness can help prevent misdiagnosis and ensure timely treatment.

Decoding Cross-Species Immune Signatures: An Integrated One Health Approach Reveals Novel Targets for Pan-Pathogen Defense

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Emerging and re-emerging infectious diseases often originate at the animal–human–environment interface, demanding a unified One Health strategy. This study explores the immunological convergence across humans, domestic animals, and wildlife to identify conserved immune signatures critical for pan-pathogen defense. By integrating multi-omics datasets (transcriptomics, proteomics, and epigenomics) and immunological profiling from representative species, we reveal shared molecular pathways—including Toll-like receptor signaling, inflammasome activation, and interferon-stimulated gene networks—that are consistently mobilized in response to viral and bacterial threats. Notably, key mediators such as IRF7, MX1, and cGAS-STING were recurrently enriched across species, highlighting potential universal immune checkpoints. Environmental factors like microbiome diversity and pollutant exposure modulated these responses, underscoring the ecological complexity of immune regulation. Functional validation in cross-species cell models confirmed the broad-spectrum protective potential of select targets. These findings establish a blueprint for pan-pathogen immunological resilience and offer a foundation for next-generation vaccines and therapeutics that transcend species boundaries. This work reinforces the value of One Health-informed immunology as a transformative lens in global infectious disease preparedness.

Keywords: Cross-species immunology, Pan-pathogen resistance, One Health paradigm, Immune signaling pathways, Comparative omics analysis, Zoonotic disease defense, etc.

A Review on Pharmaceutical & Nutraceutical Applications of Algae

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Algae as a diverse lineage of photosynthetic organisms has experienced unprecedented attention over the past few decades. As a sustainable, multifunctional bioresource for the pharma and nutraceutical industries this diverse lineage from macroalgae, microalgae and cyanobacteria boasts a variety of bioactive metabolites like polysaccharides, pigments, peptides, and polyunsaturated fatty acids that exhibit approximately potent antiviral, anticancer, antioxidant, antimicrobial and anti-inflammatory activities. For example, specific polysaccharides from brown algae like fucoidan, alginate and laminarin characterized and evaluated for biosafety profile concern their immunomodulatory, wound healing and drug delivery abilities. The well-established arsenal of pharmacological efficacy for cyanobacterial derived bioactive compounds, particularly from *Spirulina* and *Nostoc* conferred protection against oxidative stress, inflammatory responses and microbe-associated pathogen infections. In particular, the pharmaceutical potential for algal-derived β -glucans and nanoparticles has gathered interest in synthetic biology and nanomedicine for novel

development of smart delivery systems with enhanced bioavailability and targeted specificity. Microalgae's qualitative statuses as a functional food additive render observed biodistribution advantages in cardiovascular systems, metabolic stability, and gut microbiome. The Rhodophyta are a dominant contributor which renders fiber-rich compositions, antioxidants, and specialized phyco-compounds to the nutraceutical landscape. As evolving extraction techniques occurs with a biorefinery approach, scalable and sustainable development of high-value algal derivatives increasingly feasible. This all includes how derivatives from algae are changing the antiquated notions between food and medicine and science. When combining therapeutic advantages with sustainable possibilities, algae are a transformative solution for the future of human wellness.

Keywords: Bioactive Metabolites, Sustainability, Nutraceuticals, Drug Delivery

SEM analysis of *Passiflora incarnata* leaf

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Passiflora incarnata, commonly known as passionflower, is a fast-growing perennial vine with climbing or trailing stems. It has large, intricate flowers with prominent styles and stamens. Extrafloral glands in *Passifloraceae* species have aroused the interest of many researchers because of their wide morphological diversity. Hence this present work analysed the foliar trichomes on *Passiflora incarnata*. Scanning electron microscopy analysis was carried out. Phytochemical screening was also studied which are of taxonomic significance. Rich

source of saponins, glycosides and proteins. The major phytoconstituents of this plant is Passicol, a polyacetylenic compound. Keywords: Epidermal, Glandular, Passiflora, Stomata, Trichome, SEM.

Key words: passiflora, SEM, Analysis

Metagenomic approaches in advancing Microbiology research

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Metagenomics is the study of the structure and function of entire nucleotide sequences isolated from all organisms within a bulk environmental sample. This emerging field recognizes the need for advanced computational tools to understand the genetic composition and activity of microbial communities, many of which cannot be cultured in isolation. With the vast amount of data generated through next-generation sequencing, analysing microbial genomes requires both biological insight and computational expertise. As microbiology enthusiasts, understanding microbial genomes is crucial to manipulating them for human benefit. Traditionally, most microbial knowledge has come from artificial lab conditions, limiting ecological relevance. The accidental discovery of the antimicrobial activity of *Staphylococcus* illustrates the hidden potential of microbes—but such breakthroughs shouldn't be left to chance. Metagenomics enables deliberate exploration of microbial capabilities, offering possibilities in medicine, biotechnology, and environmental sustainability. Microbes influence digestion, vitamin production, immune development, and enzyme synthesis, and their genomic data can help us

replicate and deliver beneficial strains to those in need. Additionally, microbes have historically shaped Earth's biosphere and continue to play a vital role in ecological balance. Metagenomics offers a transformative lens through which to view biology—one that embraces the complexity and collective function of microbial communities.

Keyword – Metagenomics, microbial genome

Cervical cancer metabolomics: a systematic review of biomarker identification, validation, and clinical translation

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Cervical cancer (CC) affects approximately 604,127 women worldwide annually, with a staggering 341,831 deaths, accounting for 7.5% of all cancer deaths in women. In India alone, CC is the second most common cancer among women, with an estimated 123,907 new cases and 77,348 deaths each year. Given the global burden, there is an urgent need for novel, non-invasive biomarkers for early detection, prognosis, and treatment monitoring.

The review aims to elucidate the potential of metabolomics in identifying and validating biomarkers for cervical cancer. By synthesizing existing literature on metabolomic approaches, we provide a comprehensive overview of the current landscape, highlighting the promise and challenges of translating metabolomics biomarkers into clinical practice.

A rigorous analysis of existing studies can reveal the diagnostic and prognostic potential of metabolomics, while also

underscoring the need for standardized protocols and larger validation cohorts. This review sets the stage for future research, emphasizing the importance of advancing multi-omics in cervical cancer diagnosis, prognosis, and treatment monitoring. By exploring the metabolic landscape of cervical cancer, we can unlock new avenues for improving patient care and outcomes.

Keywords: Cervical Cancer, Metabolomics, Biomarkers Identification, Clinical Translation, Cancer Metabolome, Diagnostic Biomarkers & Prognostic Biomarkers

Designing of a multi-epitope vaccine against hepatitis A virus

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Hepatitis A virus (HAV) is one of the significant public health risks in resource limited surroundings. Though it does not cause serious liver disease like hepatitis B or C, in rare cases it can lead to liver failure. Despite the availability of effective vaccines, various factors impose development of alternative strategies. This study employed a comprehensive immunoinformatics driven reverse vaccinology approach to design a multi-epitope vaccine targeting HAV. A total of 1529 cytotoxic T lymphocyte (CTL) and 1063 B-cell epitopes were predicted from HAV proteome. A reverse vaccinology approach was used to reduce the predicted CTL epitopes by adjusting MHC class I processing,

immunogenicity, and other parameters. Finally, epitopes that are non-toxic, antigenic and non-allergenic were chosen. Among these 40 CTL and 3 B-cell epitopes were identified. Molecular docking confirmed stable interactions between epitopes and selected HLA alleles. A final construct comprising nine CTL and three B-cell epitopes was designed, resulting in a 133-amino-acid sequence. The secondary and tertiary structures of the vaccine construct were predicted, refined, and validated. The vaccine construct's codons were then optimized for maximum protein expression. *In silico* cloning was used to insert the gene construct into the pcDNA 3.1 (+) vector. This final construct can be used to develop an effective epitope-based HAV vaccine candidate.

Keywords: hepatitis, hepatitis A virus, multi-epitope vaccine, CTL epitopes

Pharmacoinformatics-Based Screening of *Punica granatum* Phytochemicals Against STAT3

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Breast cancer is the most prevalent malignancy among women worldwide, posing a significant healthcare burden, especially in developing nations like India. Although conventional therapies such as chemotherapy and radiotherapy remain central to treatment, limitations including systemic toxicity and drug resistance continue to challenge their efficacy. This research

project explores the therapeutic promise of phytochemicals derived from *Punica granatum* (pomegranate), a medicinal plant renowned for its antioxidant and anti-inflammatory properties. Using pharmacoinformatics tools, we identified potential bioactive compounds and investigated their interactions with STAT3, a key oncogenic target involved in breast cancer progression. Molecular docking revealed Punicalagin as the most promising ligand, exhibiting superior binding affinity (-9.2 kcal/mol) compared to standard drugs like Doxorubicin and Tamoxifen. Comprehensive ADMET and QSAR profiling affirmed the drug-likeness, safety, and pharmacokinetic suitability of the screened compounds, highlighting Punicalagin's potential as a safe and natural candidate for breast cancer therapy. These results highlight the potential of phytocompounds for targeted breast cancer therapy and emphasize the need for experimental validation to confirm their clinical efficacy.

Anti Phytoviral Activities of Gunapaselam, on Tobacco Necrotic Virus (TNV) Affecting *Cyamopsis Tetragonoloba* L (Taub)

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Tobacco Necrotic Virus (TNV) is a plant disease affecting most of the legumes and other vegetable crops. The primary symptom being abnormal colouring or necrotic tissue in the leaves. Currently only chemical control of the virus is possible. There are, however, cultural management options to reduce the risk of the virus. The 'ABC' of TNV is (A) refers to dark brown raised patches, (B) dark sunken lesions (C) light brown cracked patches.

Gunapaselam is a plant tonic made with fish extracts along with jaggery. Serial dilutions of the Fish Tonic ranging from 1, 10, 100 to 1000 µl were applied to the host plant *Cyamopsis tetragonoloba* (Cluster Bean). The promising levels being 100 µl. Gunapaselam was applied as a liquid foliar spray.

Keywords: Antiviral, Cluster bean, Cyamopsis, Fish Tonic, Gunapaselam

**Pharmacoinformatics-Based Screening of *Punica granatum*
Phytochemicals Against Breast Cancer**

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Breast cancer is the most prevalent malignancy among women worldwide, posing a significant healthcare burden, especially in developing nations like India. Although conventional therapies such as chemotherapy and radiotherapy remain central to treatment, limitations including systemic toxicity and drug resistance continue to challenge their efficacy. This research project explores the therapeutic promise of phytochemicals derived from *Punica granatum* (pomegranate), a medicinal plant renowned for its antioxidant and anti-inflammatory properties. Using pharmacoinformatics tools, we identified potential bioactive compounds and investigated their interactions with

STAT3, a key oncogenic target involved in breast cancer progression. Molecular docking revealed Punicalagin as the most promising ligand, exhibiting superior binding affinity (-9.2 kcal/mol) compared to standard drugs like Doxorubicin and Tamoxifen. Comprehensive ADMET and QSAR profiling affirmed the drug-likeness, safety, and pharmacokinetic suitability of the screened compounds, highlighting Punicalagin's potential as a safe and natural candidate for breast cancer therapy. These results highlight the potential of phytochemicals for targeted breast cancer therapy and emphasize the need for experimental validation to confirm their clinical efficacy.

Keywords: Cancer, *Punica granatum*, STAT3, ADMET, QSAR

Antiviral activity of a marine seaweed *Tubularia ornata* (turner) j. agardh (phaeophyceae) against Herpes Simplex Virus ii (HSV-II)

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Tubularia ornata marine brown seaweed found along the coastal areas of Rameswaram, Tamil Nadu, India was screened in vitro for antiviral activity against Herpes Simplex Virus-II. Two extracts one aqueous and the other ethanolic (95%) were screened for activity. The extracts were subjected to Pretreatment assay and post treatment assay. On the other hand dextran sulphate was used a positive control and the bioactive compounds efficacy was compared with it.

Keywords: Antiviral; Dextran Sulphate; Herpes Simplex Virus; In Vitro; Seaweed; Tubularia

Trinity: A herbal candy for common cold

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In today's era, common cold being one of the most common illness for both adult and children. Medicated candy is the best drug delivery system for there are no side effects and its from edible day to day ingredients. This herbal candy is made from three plants viz. *Coleus amboinicus* Lour. (Mexican mint), *Ocimum tenuiflorum* Linn. (Tulsi) leaves and *Borassus flabellifer* Linn. (Palm candy powder). Optimisation of the organoleptic characters and the phytochemical screening was done to prove the utility of the product. In addition the antioxidant property of the candy was carried out.

Key words: herbal candy, phytochemicals, antioxidant property and Vitamin C

**Efficacy of Dasagavya on tTNV-tobacco necrotic virus affected
green gram (*Phaseolus radiatus*)**

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ABSTRACT

Dasagavya a formulation made of ten components was investigated to check the efficacy on TNV affected green gram. The parameters observed were sprouting percentage, sprout number, sprout length and sprout mass. The experiment consists of ten different concentrations in a completely

randomized design. The highest sprout number was recorded at 10µl. A strong correlation was obtained between sprout length and sprout number. A positive control was also maintained simultaneously.

Keywords: Green Gram, Dasagavya, Sprout, Concentrations, TNV

Antiviral Potential of Indian Medicinal Plants Against Influenza and SARS-CoV: A Systematic Review

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This systematic review explores the antiviral potential of Indian medicinal plants against influenza and SARS-CoV. Various plants, including Tulsi (*Ocimum sanctum*), Neem (*Azadirachta indica*), Ashwagandha (*Withania somnifera*), and Giloy (*Tinospora cordifolia*), Yashtimadhu (*Glycyrrhiza glabra*), Bhunimba (*Andrographis paniculata*), and Haridra (*Curcuma longa*), exhibit promising antiviral activity through bioactive compounds that inhibit viral replication and modulate host immune responses. The initial research revealed 1304 studies, but on subsequent screening, 115 eligible studies were reported. A total of twenty research articles focused on the extracts and metabolites derived from traditional medicinal plants, specifically targeting SARS-CoV and influenza. Active phytochemicals like andrographolide, azadirachtin, glycyrrhizin, eugenol, withanone, tinocordiside, and ursolic acid have been found to inhibit viral entry, disrupt replication enzymes like neuraminidase and SARS-CoV main protease.

(Mpro), and modulate the host immune response. These compounds also offer anti-inflammatory and antioxidant benefits, supporting host defense during infection. While the findings are largely based on in vitro, in vivo, and in silico data, they suggest strong potential for the development of plant-derived antiviral therapies. This review underscores the value of integrating traditional medicinal knowledge with modern research approaches to discover effective, affordable, and accessible antiviral agents. However, further pharmacological validation and clinical studies are necessary to confirm efficacy and safety in humans. Indian medicinal plants may thus serve as a complementary resource in the global fight against viral infections and emerging pandemics.

Keywords: Antiviral activity, Bioactive compounds, COVID -19, Immunomodulatory effects, Influenza.

***Spirulina platensis*: From NASA's Space Nutrition Program to
Terrestrial Pharmaceutical Applications**

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Spirulina platensis (*Arthrospira platensis*), a filamentous cyanobacterium, represents the most commercially successful microalga in pharmaceutical and nutraceutical applications, officially adopted by NASA since the 1970s as a critical nutritional supplement for astronauts and utilized in Controlled Ecological Life Support Systems for dual nutrition and oxygen production functions. This blue-green algae contains 55-70% complete protein and C-phycocyanin (10-20% dry weight), demonstrating

potent anti-inflammatory, antioxidant, and immunomodulatory properties alongside essential vitamins, carotenoids, and specialized polysaccharides. Clinical investigations validate *S. platensis* efficacy in cardiovascular health through 10-15% LDL cholesterol reduction, enhanced insulin sensitivity in diabetes management, and significant anti-inflammatory effects in recent COVID-19 trials, while neuroprotective and hepatoprotective properties support brain and liver health with anticancer activities against multiple tumor cell lines. The global nutraceutical market for *S. platensis* exceeds \$400 million annually, with products marketed as powders, tablets, and functional foods targeting athletic performance and nutritional supplementation, maintaining FDA GRAS status and established safety profiles. Current production utilizes optimized cultivation systems (pH 8.0-11.0, 30-37°C) while future research emphasizes nanoencapsulation technologies and targeted delivery systems, positioning *S. platensis* as the gold standard for microalgae-derived therapeutics bridging traditional nutrition with evidence-based pharmaceutical applications from terrestrial health management to advanced space exploration.

Keywords: *Spirulina platensis*, microalga, cyanobacteria, C-phycocyanin, nutraceuticals, anti-inflammatory, antioxidant, cardiovascular health, diabetes, clinical trials, NASA, space nutrition, GRAS status, therapeutic applications

Exploring the antidiabetic and anticancer potential of silver nanoparticles synthesized from *Macrocystis pyrifera*

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Macrocystis pyrifera, commonly known as giant kelp, is a brown seaweed with significant potential in pharmaceutical and biomedical applications due to its bioactive compounds. Recent studies have focused on enhancing its properties through nanotechnology, specifically the use of silver nanoparticles (AgNPs). The synthesis of AgNPs using *M. pyrifera* extracts has demonstrated promising anti-inflammatory, antioxidant, anti-diabetic, anticancer, and antimicrobial activities. Silver nanoparticles exhibit superior therapeutic properties due to their small size, high surface area, and ability to interact with biological systems at a molecular level. The extraction process typically involves the use of solvents to obtain bio-active compounds from *M. pyrifera*, which can then serve as a reducing agent for silver ions to form AgNPs. In vitro and in vivo studies have shown that AgNPs synthesized from *M. pyrifera* possess significant biological effects, including the inhibition of inflammatory cytokines, scavenging of free radicals, regulation of glucose metabolism, induction of apoptosis in cancer cells, and antimicrobial activity against a wide range of pathogens. These findings suggest that *M. pyrifera*-derived silver nanoparticles hold promise as a multifunctional therapeutic agent, offering a sustainable approach to addressing various health challenges. Further research is required to optimize the synthesis methods and evaluate the long-term safety and efficacy of these nanoparticles in clinical applications.

Key words: *Macrocystis pyrifera*, Silver nanoparticles, Therapeutic agent, bioactive compounds.

Screening of natural plant extracts for antioxidant, anti-inflammatory and anti microbial properties

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This study aimed to evaluate the bioprospecting of different solvent extracts of medicinal plants *Euphorbia hirta* Linn. inflorescence. The phytochemical, total phenolic, DPPH (2, 2-Diphenyl-1-picrylhydrazyl) free radical scavenging activity, antimicrobial contents of the extract were evaluated using in-vitro assays. Results revealed that aqueous and ethanol extracts contained more phenolic compounds. Aqueous extract showed highest scavenging activity followed by ethyl acetate, ethanol and hexane. For antibacterial activities, best zone of inhibition (ZOI) was observed in case of the aqueous and ethanol extract as compared to other extracts against *Escherichia coli*, *Pseudomonas aeruginosa*, *Klebsiella pneumonia*. There is no inhibition activity against *Staphylococcus aureus* and *candida albicans*. Additionally, we have done anti-inflammatory activity where aqueous extract revealed promising result. . In conclusion, this study demonstrated the aqueous extracts of *Euphorbia hirta* Linn. has significant antioxidants, anti-inflammatory and anti-microbial activities.

Keywords: *Euphorbia hirta* Linn., Phytochemical, DPPH, *Escherichia coli*, *Pseudomonas aeruginosa*, *Klebsiella pneumonia*.

**GCMS and Molecular docking Analysis of Plant Extract for
Anticancer Properties**

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Plants are excellent sources of functionally bioactive compounds and essential nutrients. The phytochemical constituents have enormous potential in treating both plant and human diseases. *Euphorbia hirta* Linn is one of the most important plants known for its ethnobotanical and ethnomedicinal values. Gas chromatography-mass spectrometry (GC-MS) analyses of the aqueous extracts revealed the functional groups, and bioactive compounds present in inflorescence of the plant. Characteristic peaks were observed. The GC-MS analysis also revealed the occurrence of bioactive compounds that are known to possess a variety of pharmacological activities. Subsequently, in-silico molecular docking studies of the identified bioactive compounds predicted potential anticancer properties. To the best of our knowledge, this is the first-hand report on the bioactive compounds of inflorescence of *E. hirta* Linn extracts showing anticancer pharmacological significance. This study identifies *E. hirta* Linn. inflorescence as a promising candidate for cancer therapy,

supported by its significant cytotoxicity and strong molecular interactions. The findings provide a foundation for further research into these plant extracts as complementary agents in cancer treatment.

Key words: *Euphorbia hirta* Linn., GC-MS, Anti-cancer, Molecular Docking

Emerging and re-emerging infectious diseases

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Emerging and re-emerging viral infections represent a growing public health challenge, both globally and within India. The escalating threat of emerging and re-emerging diseases stems from a complex interplay of viral, human, and ecological factors. RNA viruses are particularly adept at adapting to new hosts and environments due to their rapid mutation & genetic recombination. Human factors like rapid urbanization, high population density, increased global travel, and technological advances significantly fuel the spread of infections. Ecological changes, including deforestation, agricultural expansion, and climate change, disrupt natural ecosystems and alter vector dynamics, creating ideal conditions for the rise and transmission of zoonotic diseases. A critical concern is the melting of glaciers, which can release ancient, dormant microbes and viruses into the environment, posing risks of new diseases to humans, animals, and plants, as seen with the 2016 Siberian anthrax outbreak.

India has identified over 30 novel infectious agents, with 60% being zoonotic. Outbreaks of diseases like Crimean-Congo

hemorrhagic fever, Nipah, JE, dengue, and chikungunya underscore the complex interplay of sociocultural, biological, and environmental factors driving these challenges.

India's fight against viral threats relies on strengthening the Integrated Disease Surveillance Programme (IDSP) and Viral Research and Diagnostic Laboratories (VRDLs). Effective control demands a multifaceted strategy: real-time surveillance, robust vector control, public health education, responsible antibiotic use, environmental conservation, and leveraging AI/genomics for early detection. Swift diagnostics, accessible treatments, and global collaboration are crucial to prevent future health crises.

Keywords: Genetic recombination , Zoonotic diseases , Dormant microbes

Waste to Fuel: Evaluating Agro-Waste Substrates and Yeast Immobilization for Sustainable Bio-ethanol Production
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As the requirement for vast sustainable global demand and eco-friendly energy sources has driven research into bioethanol production as an alternative to fossil fuels. This study focuses on Characterizing and Segregation yeast strains from grapes and sugarcane juice, evaluating their efficiency in bioethanol production using both free and immobilized cells. Four different agro-industrial waste substrates—banana peel, jaggery, sweet potato, and molasses—were employed to assess ethanol yield. The study employed morphological and physiological tests to

locate native *Saccharomyces cerevisiae* strains with thermo-tolerant and ethanol-tolerant characteristics. The fermentation efficiency of free versus immobilized yeast cells was compared, with immobilization achieve during sodium alginate yield, stability, and reusability. Analytical methods such as the DNS assay were used to determine sugar concentrations and ethanol production. This research underscores the potential of low-cost substrates and immobilized yeast technology for efficient and sustainable bioethanol production, with applying for renewable energy development and agricultural waste management.

Keywords-: *Saccharomyces cerevisiae*, immobilized yeast, Ethanol, DNS

Bacterial vampirism – targeting iron addiction in pseudomonas aeruginosa using plant-derived iron chelators

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Pseudomonas aeruginosa is a highly resilient, drug-resistant bacterium that relies heavily on iron stolen from its host to fuel its growth, virulence, and biofilm formation. This dependency—referred to as **bacterial vampirism**—opens a promising window for therapeutic intervention. As traditional antibiotics lose effectiveness, attention is shifting toward strategies that cut off bacterial access to essential nutrients like iron. Natural plant compounds, particularly curcumin, have shown potential as iron chelators that may suppress virulence without promoting

resistance. However, despite encouraging lab-based results, real- world application faces several barriers. These include curcumin's low bioavailability, the risk of unintentionally depleting the host's iron stores, and bacterial fallback mechanisms like alternative iron uptake pathways. This presentation highlights these critical challenges and explores targeted solutions such as nanoformulations to enhance delivery, precision targeting to protect host tissues, and combination therapies to minimize resistance. It also underscores the importance of long-term resistance monitoring and testing curcumin alongside antibiotics. By repositioning iron chelation as a viable antimicrobial approach, this work proposes a shift in focus—moving from killing bacteria to starving them—offering a safer, more sustainable path in the fight against *P. aeruginosa*.

Keywords: *Pseudomonas aeruginosa*, iron chelation, curcumin, bacterial vampirism, plant- derived therapy, antimicrobial resistance.

**Screening of Household Wastewater for Novel Protease-
Producing Bacteria and Process Optimization**
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Proteases are the key enzymes that break down proteins and are widely used in food, leather, detergent, and bioremediation industries. This study focused on isolating novel protease-producing bacteria from household wastewater. Among the isolates, the strain showing the highest proteolytic activity was identified as *Enterobacter ludwigii* using molecular techniques (BLAST). The culture was further refined for enhanced protease production using varied pH levels, carbon, and nitrogen sources. Optimal conditions were found at pH 9.0 with a 72 hour incubation period. Among the carbon tests, sucrose showed the highest enzyme activity of 26.4 U. These results highlight the potential of household wastewater as a source of industrially useful microorganisms and enzymes.

Keywords: Protease, *Enterobacter ludwigii*, Household wastewater, Optimization, Enzyme activity.

Rapid diagnostic tools for detecting emerging infectious diseases in clinical microbiology

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In today's fast-moving world, emerging infectious diseases are becoming more frequent and harder to control. Early detection is the key to saving lives, stopping the spread, and guiding the right treatment. Traditional diagnostic methods are often slow and can delay important medical decisions. That's where rapid diagnostic tools come into play.

This presentation explores modern diagnostic methods like RT-PCR, LAMP, CRISPR-based testing, Next-Generation Sequencing, and Point-of-Care (POC) tests. These tools provide fast, reliable results — sometimes in under an hour — and are used widely in hospitals, labs, and even in the field during outbreaks.

As future medical lab technologists, understanding these tools is essential. This presentation will help you learn how they work, where they're used, and why they are so important in today's healthcare system. Let's discover how rapid diagnostics are transforming clinical microbiology and our role in protecting public health.

Key words: Emerging Infectious Diseases, Rapid Diagnostic Tools, RT-PCR, Point-of-Care Testing (POCT), Clinical Microbiology

In silico* screening of *Nuphar lutea* phytochemicals as potential inhibitors of computationally-identified drug targets in *Francisella tularensis

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Tularemia or Rabbit fever is a highly contagious disease caused by the bacterial pathogen *Francisella tularensis*. It is a zoonotic disease with high infectivity and hence poses the threat of Bioterrorism. The symptoms of tularemia range from the skin ulcer to life threatening pneumonia. The limited availability of therapeutics and emergence of antibiotic resistance necessitates the discovery of novel druggable targets. This present study aims to identify the novel drug targets in the pathogen *F. tularensis* subsp. *tularensis* (Strain Schu S4) using subtractive proteomics pipeline. The complete proteome of *F. tularensis* subsp. *tularensis* (Strain Schu S4) comprising 1722 proteins was mined for potential drug targets using various computational tools. Finally, 6 target proteins that were non-redundant, essential, human non-homologous, and previously not reported as drug targets were selected. They were targeted with 163 phytochemicals from the plant, *Nuphar lutea*, using molecular docking analysis. Among the 163 compounds, notoamide I was found to be effective against selected target proteins and it proved to be a potential drug-like molecule in

ADMET analysis. These findings are the foundation for further *in vitro* studies and rational drug design for tularemia.

Keywords: Tularemia, *Francisella tularensis*, *Nuphar lutea*, Notoamide I, antimicrobial resistance, subtractive proteomics

THE FUTURE OF PHYTOCOMPOUNDS AS DRUGS IN THE ERA OF BIOINFORMATICS (PLANT TO PATIENT)

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The integration of herbal medicine and Bioinformatics is a revolutionary way of thinking for contemporary drug discovery. Medicinal plants have been the pillars of traditional medicine since the days of antiquity. They yield a rich array of bioactive compounds with diverse biological activities. Sequencing of medical plant genomes and transcriptomes further aids biosynthetic gene discovery as well as metabolite profiling. In the future, the intersection of AI-based drug screening, predictive toxicology and personalized Chinese herbal medicine provides new routes for evidence-based utilization. Bioinformatics tools such as ADMET investigations and ProTox-II, forecast pharmacokinetic behaviour and predict the risk of toxicity prior to animal or clinical experiments. Further, consistent information from various biological databases will facilitate the identification of new lead compounds with improved pharmacokinetics. Due to the unavailability of

conventional word-of-mouth knowledge, the global distribution of medicinal plants, and strict regulatory enforcement of safety profiles of herbal drugs; discovering, screening and identifying lead compounds from plants is very challenging. Cheminformatics and network pharmacology further explicated multi-target mechanisms and possible synergistic action of phytocompounds. Nevertheless, there has been little focus so far on the potential utilization of bioinformatics strategies that can tap into knowledge from plants.

Keywords: Herbal Medicine, Bioinformatics, Drug Discovery, Phytocompounds

Diagnostic latency associated with antimicrobial resistance mechanism

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Antimicrobial resistance (AMR) is a situation in which microorganisms evolve and survive despite being subjected to drugs that intend to kill them. Due to the delayed diagnosis, AMR is a giant global health problem that results in prolonged illnesses, increased healthcare expenditure, and less effective treatments. Most currently available tests are time-consuming and often fail to provide physicians with rapid results, leading them to sometimes resort to empirical therapy, which can contribute to antimicrobial resistance. More advanced technologies such as Whole Genome Sequencing (WGS) will detect resistant bacteria more and earlier on, but at

considerable cost, specialized manipulation, and in only more prosperous areas. Investment in new diagnostics, enhanced surveillance systems, and enhanced public awareness are necessary to fight antimicrobial resistance (AMR). Point-of-care tests like C-Reactive Protein (CRP) and molecular diagnostics are needed to reduce the clinical burden of AMR, direct proper use of antibiotics and avoid unnecessary prescriptions.

Keywords: Antimicrobial Resistance (AMR), Delayed diagnosis, Whole Genome Sequencing (WGS), C-Reactive Protein (CRPs), prescriptions.

Screening of novel, rare Probiotic strains from fermented grains, pulses and curd in villages of Virudhunagar district.

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Probiotic bacteria play a crucial role in the health of animals and human beings. More research is being carried out in this new field due to the new discoveries in health industry. Gut health, brain activity, immune system and many fields are connected to microbes living in the gut regions. Many Probiotic strains have been identified and documented. However, many

different strains are not yet explored on region specific. As bacterial strains could be slightly different in their DNA sequence and could provide better benefits. To screen the rare and unique bacterial strains, commonly used in fermented products such as rice, black gram, curd and millets were chosen. Serial dilution and plating was performed to confirm the presence of different species of bacteria in the resources. These samples were collected and pooled in a small volume to reduce the sequence cost and performed 16S rRNA sequencing. The data showed that there were many different bacteria from *Bacillus* to *Pseudomonas*. Although *Pseudomonas* genus has both pathogenic bacteria and some are beneficial for plants and humans. Moreover, we observed that there are quite a number of unique bacterial strains such as *Phascolarctobacterium wakonense*, *Alloprevotella tannerae*, *Mangrovibacterium marinum* and *Phascolarctobacterium faecium* were found in samples. More research is needed to confirm their identity and application in industries. Possible applications are discussed.

Keywords: Probiotic Bacteria, 16S rRNA sequencing, fermented foods, Unique bacterial strains, Region specific microbes

**Pharmacoinformatics-based investigation of phytocompounds
from *Camellia sinensis* in ethanol-induced lung injury**

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Prolonged alcohol consumption causes oxidative stress and damages the antioxidant defence system, leading to chronic inflammation and structural harm to lung tissues. This ongoing oxidative stress compromises epithelial barrier integrity, weakens the immune response, and heightens the risk of lung infections. These pathological changes contribute to the progression of ethanol-induced lung injury. In this study, 207 bioactive compounds from *Camellia sinensis* were obtained from the IMPPAT database and tested using molecular docking against NF- κ B, a key regulator of inflammation. A known NF- κ B inhibitor, parthenolide, was used as a standard drug, showing a binding affinity of -8.6 kcal/mol. Among the screened compounds, vanillin exhibited a stronger binding affinity of -8.8 kcal/mol, indicating its potential as a potent modulator of NF- κ B. Vanillin was further assessed for its ADME and toxicity profiles. ADME analysis, performed via Swiss-ADME, revealed that vanillin complies with Lipinski's rule of five, indicating its favourable drug-like properties, including high solubility, good gastrointestinal absorption, and ability to cross the blood-brain barrier. Toxicity predictions revealed no AMES toxicity, hepatotoxicity, or hERG inhibition, with an LD₅₀ of 1.937 g/kg, suggesting a safe profile. This study highlights vanillin as a

promising candidate for modulating NF- κ B-driven inflammation in ethanol-induced lung injury. Further experimental validation is needed to explore its therapeutic potential *in vivo*.

Keywords: *Camellia sinensis*, lung injury, alcohol, inflammation, oxidative stress, parthenolide

**ANTIOXIDANT POTENTIAL OF *GLYCYRRHIZA GLABRA* EXTRACT
AND ITS NANOPARTICLES AGAINST INFECTIOUS PATHOGENS**
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Glycyrrhiza glabra is one of the useful medicinal plants from the ancient days, which belongs to the Leguminosae family and is native to the Mediterranean and certain areas of Asia especially India. *G. glabra* is a typical herbaceous perennial, growing to 1 m in height, presenting pinnate leaves with a length of 7 to 15 cm. The flowers are purple to pale whitish blue, being arranged in a hermaphrodite inflorescence, whereas the fruit is an oblong legume with 2 to 3 cm of length and containing several seeds. *Glycyrrhiza glabra* is a plant with strong ethno-botanical history and the rhizome parts of this plant are used as a folk medicine. *G. glabra* is one of those ancient plants, which have been used in the traditional pharmacopoeias for its multifaceted activities against variety of systematic and nonsystematic ailments. *G. glabra* extracts have been shown to possess lot of medicinal properties like

antimicrobial, antioxidant, anti-inflammatory, antiulcer, anticancer properties due to presence of so many bioactive components, triterpene, saponins, flavonoids, alkaloids. The aim of the study was to analyze anti-microbial resistance of the microorganism against the extract and antioxidant potential of *Glycyrrhiza glabra* extract and its nanoparticles against infectious pathogens. Assay such as DPPH[•] radical, superoxide radical, phosphomolybdenum reduction and Fe³⁺ reducing power assays were carried out for antioxidant activity. The antibacterial and antifungal activity was tested by well diffusion method against pathogens such as *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Candida albicans*, *Candida tropicalis*, *Candida krusei* and the zone of inhibition was measured and compared with standards.

Keywords: Medicinal properties, Antimicrobial, pathogens, Antioxidant potential.

Wisdom is the reward of experience and should be shared



अनुसंधान नेशनल रिसर्च फाउंडेशन
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