

ABSTRACT BOOK AND PROCEEDINGS OF
ONE DAY NATIONAL SEMINAR

CHALLENGES IN MICROBIOLOGY: DETECTION, PREVENTION & BENEFICIAL UTILIZATION 2026

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Hosted by

**Department of Microbiology,
West Bengal State University**

In Collaboration with

Microbiologists Society, India

10th April, 2026



Editor

Dr. Sibani Sen Chakraborty

Co-Editor

Mr. Arghyadeep Bhattacharjee

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MESSAGE FROM THE ORGANIZING SECRETARY

It gives me pleasure to present the Proceedings of the Seminar on “Challenges in Microbiology: Prevention, Detection and Beneficial Utilisation. The volume reflects the enthusiasm, innovation, and scientific excellence of researchers, academicians, and students who have contributed their valuable work to this seminar. The proceedings bring together wide range of topics presenting recent advancement in the field of microbiological research encompassing antimicrobial resistance, microbial biotechnology, environmental microbiology, advancement in diagnostic methodologies and its significant role in improving human health, industrial applications and beneficial utilisation in environmental sustainability. The seminar provided a rich platform for exchange of scientific ideas and research findings. This proceedings volume is not only a record of the scientific contributions presented during the seminar but will serve as a valuable reference for students, researchers and academicians for inspiring future scientific inquiry and innovation.

I extend my sincere appreciation to all the authors who have contributed for the proceedings volume, the reviewers for their careful evaluation of the submissions, and the members of the organizing committee for their unwavering dedication. I also express my gratitude to our distinguished speakers and participants for their support and active involvement in making this seminar a success.

I trust that the proceedings book will inspire new ideas contributing meaningfully to the advancement of microbiology addressing emerging challenges through innovative and sustainable approaches.

I extend my best wishes to all readers and look forward to the continued scientific growth encouraged through this seminar.

With warm regards,



Sibani Sen Chakraborty

Convener & Organising Secretary

***National Seminar on “Challenges in Microbiology:
Prevention, Detection and Beneficial Utilisation”.***

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ABSTRACTS

COMBINATION AGAINST UTI PATHOGEN AS GENOTOXIC AS WELL AS CYTOTOXIC WITH EMPHASIS ON COMPUTATIONAL SIMULATION

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Abstract

Urinary Tract Infections (UTIs) are among the most prevalent bacterial infections worldwide and are increasingly associated with multidrug-resistant (MDR) uropathogens such as *Escherichia coli* and *Klebsiella pneumoniae*. The growing emergence of antibiotic resistance against conventional aminoglycosides necessitates the exploration of alternative and combinatorial therapeutic strategies. The present study aimed to comparatively evaluate the antimicrobial efficacy, genotoxicity, and cytotoxicity of aminoglycosides and selected phytoextracts, both individually and in synergistic combinations, against common UTI pathogens. Aminoglycosides including doxycycline and streptomycin were investigated alongside phytoextract-derived compounds such as plumbagin and allicin. Experimental analyses involved antimicrobial susceptibility testing, minimum inhibitory concentration (MIC) determination, thin-layer chromatography (TLC), gel electrophoresis, UV spectroscopy, cup-plate assay, and biofilm inhibition studies. To complement the experimental findings, computational approaches including molecular docking and molecular dynamics (MD) simulations were employed to evaluate the binding affinity and interaction stability of phytocompounds with bacterial ribosomal RNA and membrane-associated proteins in comparison with standard aminoglycosides. The computational predictions were further correlated with in vitro observations to assess synergistic or antagonistic interactions. The findings indicated that certain phytoextracts enhanced aminoglycoside activity by improving membrane permeability and target binding efficiency while simultaneously reducing genotoxic and cytotoxic effects observed with antibiotics alone. The study highlights the therapeutic potential of phyto-antibiotic combinations as sustainable alternatives for combating recurrent and drug-resistant UTIs. Furthermore, the integration of computational simulation with experimental microbiology provides a predictive platform for optimizing antimicrobial combinations prior to in vivo validation. Overall, this multidisciplinary strategy offers promising prospects for the development of safer, more effective, and resistance-limiting antimicrobial therapies.

**TERMITE - THE TERMINATOR OF LIGNOCELLULOSE: AN ALTERNATIVE
APPROACH FOR FUEL TO HAVE A CARBON-NEUTRAL FUTURE**

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Abstract

Termites are the ultimate "terminators" of wood. They are capable of destroying lignocellulose they consume. But rather than focusing on the damage they do, this poster highlights how their digestive systems could be the game changer to the next generation of green energy. The termite gut is a masterpiece of biological engineering, where a rapid-fire hydrogen exchange takes place. And it allows microbes to convert plant fibers into energy with nearly perfect efficiency. By extracting and stabilizing these microbial communities, we can design industrial bioreactors that can transform raw wheat straw or even raw lignocellulosic contents into biofuel without the need for harsh chemical processing. This termite-inspired approach actually is a sustainable alternative approach to traditional fuel production. Ultimately, by studying these tiny "biorefineries," we can transform a notorious pest into a beneficial tool for a carbon-neutral future.

DECODING THE INVISIBLE:

AI AND MACHINE LEARNING IN MICROBIAL IDENTIFICATION

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Abstract

Traditional microbial diagnostic approaches remain constrained by challenges in specimen collection and transport, labour intensive culture requirements, low sensitivity for fastidious organisms, misidentification, and prolonged turnaround time for antimicrobial susceptibility testing. These limitations can delay clinical decision-making and adversely affect patient outcomes. The integration of artificial intelligence AI, particularly machine learning or ML and deep learning, is rapidly transforming diagnostic microbiology by enabling high-throughput, rapid, and accurate analysis of complex datasets. This poster highlights the transition from conventional methods to AI-assisted diagnostics, emphasizing the importance of standardized sample processing to ensure reliable outputs. Advanced ML models, including convolutional neural networks or CNNs, have demonstrated remarkable efficiency in image-based microbial identification, automated colony counting, and enhancement of microscopic resolution. AI also facilitates rapid pathogen detection, prediction of antimicrobial resistance patterns, and optimization of treatment strategies. Case-based insights from diseases such as COVID-19, Malaria, and Tuberculosis illustrate the potential of AI in achieving timely and precise diagnosis. Furthermore, AI-driven platforms contribute to real-time disease surveillance, outbreak prediction, and epidemiological monitoring, strengthening public health responses. Despite its advantages, AI implementation requires careful consideration of ethical issues, including data privacy, algorithmic bias, and validation across diverse populations. Overall, the integration of AI into microbial diagnostics represents a paradigm shift, offering scalable, cost-effective, and user-friendly solutions that enhance diagnostic accuracy and support improved healthcare delivery.

**MECHANISTIC INSIGHTS INTO GASTRIC MICROBIOME DYSBIOSIS:
RICHNESS, DIVERSITY AND HOST MODULATORS**

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Abstract

Background: Gastric cancer (GC) pathogenesis is increasingly associated with complex alterations in the gastric microbiome extending beyond *Helicobacter pylori* infection. Dysbiosis within the gastric ecosystem contributes to mucosal inflammation, genotoxic stress, and tumorigenesis. This study aimed to delineate microbial richness, diversity, and taxonomic transitions across healthy, gastritis, and GC cohorts, while evaluating the effects of demographic and metabolic factors.

Methods: Publicly available 16S rRNA sequencing datasets (n = 164) were retrieved from the NCBI Sequence Read Archive and processed through a standardized bioinformatics pipeline. High-quality reads were aligned to the SILVA v138 database, clustered into operational taxonomic units (OTUs) at 97% similarity, and taxonomically classified using the RDP classifier. Alpha (Chao1, Shannon, observed OTUs) and beta diversity (Bray–Curtis, PCoA) indices were computed, with statistical significance assessed via PERMANOVA.

Results: A total of 31,450 sequences generated 320 OTUs in healthy controls, 380 in gastritis, and 460 in GC samples, indicating progressive richness along the disease continuum. GC samples exhibited the highest richness but heterogeneous diversity. Elderly and male cancer patients showed increased richness, whereas obesity correlated with decreased richness. Taxonomic profiling revealed enrichment of *Proteobacteria*, *Fusobacteria*, and *Clostridium* species in

gastritis and GC, with depletion of commensal *Clostridia* and *Bacteroidia*. *Fusobacterium nucleatum* and *Escherichia-Shigella* predominated in GC. Beta diversity confirmed distinct compositional separation (PERMANOVA: $F = 1.41$, $R^2 = 0.016$, $p = 0.002$).

Conclusions: Gastric disease progression involves stepwise dysbiosis with pathogen enrichment and commensal loss modulated by host factors. The identified microbial signatures may serve as diagnostic and prognostic biomarkers for GC. natural landscape ecosystems are well-suited for ecotourism, that helps to environmental awareness.

Keywords: *Helicobacter pylori*, Gastric Microbiome, 16S rRNA Analysis, Microbial Diversity.

**IN-VITRO AND IN-SILICO ASSESSMENT OF VAISHVANARA CHURNA FOR
ANTIMICROBIAL DRUG REPURPOSING**

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Abstract

Traditional medicine has been used for several years to treat diseases in India, but their mechanism of action has been unknown. On the other hand, development of alternative to antibiotics is urgently needed to combat global problem of drug-resistance. The aim of this study is to evaluate the efficacy of the alcoholic extracts of Vaishvanara churna (VC), a drug widely used for gastrointestinal diseases, against pathogenic bacteria. Alcoholic extracts of VC were tested to evaluate their antibacterial potential against six bacterial strains- *E. faecalis*, *S. aureus*, *B. cereus*, *E. coli*, *P. aeruginosa* and *K. pneumoniae*, by agar well diffusion and microbroth dilution assay, followed by membrane depolarization through flow cytometry. The minimal biofilm inhibition concentration and minimal biofilm eradication of extracts were determined by inverted & confocal microscopy. LC-MS/MS (QTOF) was used to reveal the phytochemical array and in silico study to incorporated virtual screening utilizing bioinformatics tools. Both extracts of VC showed MBC in the range of 0.94 to 62.5 mg/ml, which also raised fluorescence of DiBaC4 showing membrane depolarization. Moreover, the drug ruptured the biofilm network in *S. aureus* and *P. aeruginosa*. The methanolic extract of the drug showed the presence of more prominent bio-active molecules. High throughput virtual screening of selected phytocompounds along with identified target receptors of corresponding strains, illustrated primarily two phytocompounds Irinotecan and Retronecine showing high binding affinity for the receptors. Bacterial genes from *Klebsiella*, *E. coli*, *Staphylococcus* showed good interaction with the phyto-compounds. The alcoholic extracts of VC have potent antibacterial activity which has been further corroborated by in silico analysis.

**EXPRESSION, PURIFICATION OF PHAGE DERIVED PROTEIN ENDOLYSIN AND
DEPOLYMERASE AGAINST MDR *SALMONELLA* SPP. AND ITS
APPLICATION *IN-VITRO* AND *IN-VIVO* IN MICE**

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Abstract

Salmonella infections are becoming a significant public health concern globally as well as in India. It causes foodborne illnesses, enteric fever, gastroenteritis, and invasive systemic infections. Salmonella species that are multidrug-resistant (MDR) are a rising public health issue because they reduce the efficacy of traditional medications. The normal gut microbiota can potentially be disrupted by antibiotic treatment. Bacteriophage derived proteins offer a promising alternative due to their inherent ability to penetrate and disrupt bacterial biofilms through enzymatic degradation of extracellular polymeric substances and targeted bacterial lysis. Alternative and focused treatments are therefore required. MDR bacteria can be precisely eliminated by bacteriophages without harming helpful microorganisms. Endolysins and Depolymerase shows antibacterial and antibiofilm activity. Bacteriophages were isolated using plaque assay and characterized for its host range, lytic activity, and genomic safety. Genes encoding endolysin and depolymerase will be identified from phage genomes, amplified by PCR, digested with appropriate restriction enzymes, and cloned into similarly digested pET-28a vector. Recombinant plasmids will be transformed into *E. coli* BL21, followed by protein expression. BALB/c mice infected with MDR Salmonella will receive bacteria, antibiotics and phage-derived proteins. Therapeutic efficacy will be assessed by stool bacterial load using microbiological and qPCR assays. The inflammatory responses will be studied from intestinal tissue and serum. The study aims to develop a potent, phage derived proteins against MDR Salmonella infections and assess their impact on gut microbiome diversity in comparison to antibiotics.

Keywords: Multidrug-Resistant (MDR), Microbiota, Biofilm, Bacteriophage, Endolysin, Depolymerase.

**ISOLATION, CHARACTERIZATION AND APPLICATION OF
A LYTIC PHAGE SALFIN-1 AGAINST SALMONELLA SPP.**

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Abstract

Salmonella is a globally distributed zoonotic pathogen. It is one of the most frequent causes of bacterial gastroenteritis-related morbidity and mortality in older people and children under the age of five via consuming contaminated animal products. Several serovars of the genus Salmonella have lately been shown to be multidrug resistant. So, it's become important to isolate lytic Salmonella bacteriophages for bactericidal efficacy. In our present study, Salmonella phage Salfin-1 was isolated from Ganga, as a lytic phage with good potential lytic activity against *Salmonella enterica* serovar *typhi* BCR62. Phage has broad host range and able to infect *S. paratyphi*, *S. typhimurium*, and *Escherichia coli*. It is relatively stable under a wide range of pH (5-9), temperatures (4°C–50°C). The latent period and burst size of Salfin-1 against *Salmonella enterica* serovar *typhi* BCR62 are 30-35 min and 1748 PFU/cell respectively. This phage can able to lyse almost all bacterial cells within 5 hours of infection at 37°C, with different MOI. A significant reduction was observed in bacterial population of *Salmonella enterica* serovar *typhi* BCR62 biofilm. Efficiency of Phage was checked for reducing Salmonella in pasteurized milk and chicken eggs. Overall, the current work shows that Salfin-1 has a promising role for usage as biocontrol agent and proposes its application in food industries. Whole Genome Sequencing was done by Illumina sequencing, revealed the genomic size ~39 kbp.

Keywords: Salmonella, Bacteriophage, Morbidity, Biofilm, Whole Genome Sequencing.

**NANOSCALE ANTIMICROBIALS FOR A POST-ANTIBIOTIC ERA:
NANOBIOTICS IN ACTION**

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Abstract

The rapid escalation of antimicrobial resistance (AMR) has emerged as a major global health challenge of the 21st century. Conventional antibiotics are increasingly ineffective against multidrug-resistant (MDR) bacteria, particularly the ESKAPE group, which are the leading causes of nosocomial infections. These pathogens have developed multiple resistance mechanisms that collectively render conventional antibiotics ineffective. In addition to MDR, persister cells pose a growing concern by causing chronic and recurrent infections, further complicating treatment outcomes. Addressing this crisis demands fundamentally novel therapeutic strategies. The need for more durable antimicrobial therapies can be met through the integration of nanotechnology into next-generation antimicrobial platforms. Recent advances in nanotechnology have introduced nanobiotics as a promising alternative strategy to combat MDR pathogens. Nanoscale materials, including metallic nanoparticles, polymeric nanocarriers, liposomes, and quantum dots, attack bacteria through multiple mechanisms such as disruption of cell walls, generation of reactive oxygen species, release of bactericidal metal ions via a “Trojan horse” mechanism, and photothermal or photodynamic destruction. These multifaceted mechanisms differ significantly from conventional antibiotics, reducing the likelihood of resistance development. Emerging nanosystems, such as ATP-functionalised gold nanoclusters, ROS-generating hydrogel microspheres and MXene-based photothermal platforms, are specifically engineered to target persister cells and prevent their resuscitation in a synergistic manner. Despite these promises - cytotoxicity, dose optimization, regulatory approval challenges the clinical translation. This review poster discusses the potential, promises and future prospects of nanobiotics to combat AMR.

FORMULATION AND EVALUATION OF A BACTERIOPHAGE COCKTAIL TARGETING MULTIDRUG-RESISTANT SHIGELLA SPP. IN A MICE MODEL

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Abstract

Shigellosis, a major cause of diarrheal morbidity and mortality, is difficult to treat due to rise of multidrug-resistant (MDR) *Shigella* strains. Bacteriophage therapy can be a reliable alternative of antibiotics. To address this, a lytic phage cocktail named ShigaphageIN was developed, containing six *Shigella*-specific phages (*Sfin-1*, *Sfin-2*, *Sfin-3*, *Sfin-4*, *Sfin-5* and *Sfin-6*). In vitro, the cocktail completely lysed 16 MDR *Shigella* strains within four hours. In vivo studies using BALB/c mice showed that phage treatment reduced bacterial CFUs by 60%, compared to only 25% with antibiotics, and prevented weight loss seen in antibiotic-treated mice. qPCR of stool samples revealed higher Ct values in phage-treated groups, confirming reduced bacterial loads. Phage therapy also significantly lowered pro-inflammatory cytokines (IL-6, IFN- γ , TNF- α) and LPS-specific IgG and IgA levels, indicating reduced inflammation. Histological analysis showed that phage-treated mice had normal colon structure with minimal inflammation, while infected and antibiotic-treated mice exhibited severe damage. Additionally, spectroscopic and microscopic analyses confirmed biofilm disruption by the phage cocktail. Overall, ShigaphageIN demonstrates strong antibacterial, anti-inflammatory, and antibiofilm activity, highlighting its promise as an alternative therapeutic approach against MDR *Shigella* infections.

Keywords: Shigaphage^{IN}, Multidrug Resistant (MDR), Quantitative PCR (qPCR), Histological Analysis, Serum Cytokines.

**THE GUT-BRAIN AXIS: DECODING THE CONNECTION BETWEEN GUT
MICROBES AND NEUROLOGICAL DISORDERS**

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Abstract

The gut brain axis plays a dynamic role in current research trends. The gut brain axis links the central nervous system to the gut using a bidirectional communication -system. The communication between the gut and the CNS are regulated through various pathways like the neuroendocrine, humoral and immune pathways. The brain function is directly or indirectly influenced by the gut microbiome through the production of neurotransmitters like GABA, dopamine, etc. or through the regulation of immune responses via the blood-brain barrier (BBB) or directly through the vagus nerve. The bacterial Short Chain Fatty Acids (SCFAs) plays an important and a major role in this communication system. In this presentation we will discuss about major role of the gut microbiome in various neurological conditions like Alzheimer's Disease, Parkinson's Diseases, Autism spectrum disorders and depression. This presentation also emphasizes on the importance of probiotics and prebiotics in the diet to maintain the health of the gut microbiome. Research says that the symptoms of various neurological disorders are influenced by the gut microbiome. Thus, it is important to maintain good gut microbiome health. Probiotics and prebiotics are proven to be healthy and nutritional for gut health. Various therapeutic approaches are been studied based on an individual's gut microbiome and immune characteristics. Further study in this will help facilitating innovative technologies of prevention and treatment of various diseases.

Keywords: Gut Brain Axis, Vagus Nerve, Neurological Disorders, Probiotics, Prebiotics.

FROM CHALLENGES TO SOLUTIONS: MICROBIOLOGICAL PERSPECTIVES IN JUTE RETTING

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Abstract

Jute retting is a crucial biological process that directly affects the quality of fibre, as it helps separate the fibres from the plant stem by breaking down the natural binding materials. This process is largely driven by microorganisms present in water bodies. However, traditional retting methods often face several challenges related to detection, prevention, and effective use of these microbes. One of the key difficulties is identifying the right microorganisms responsible for efficient retting. Natural retting environments contain a wide variety of microbes, but not all of them contribute positively. This makes it hard to pinpoint and monitor the beneficial ones. Modern techniques such as metagenomics and enzyme analysis can help in better understanding and identifying these useful microbial communities. Another important issue is preventing problems like over-retting. When jute is left in water for too long, excessive microbial activity can weaken the fibres and reduce their quality. Since traditional retting is not well controlled, maintaining the right balance of environmental conditions like pH, temperature, and oxygen level is often challenging. Despite these problems, microbes also offer great potential when used properly. By isolating and applying selected beneficial bacteria that produce fibre-degrading enzymes, retting can be made faster, more uniform, and more efficient. Such approaches can also reduce dependency on large volumes of water and minimize environmental pollution. Overall, improving how we detect, control, and utilize microbes can make jute retting more reliable, sustainable, and environmentally friendly, benefiting both farmers and the jute industry.

**DECODING PARKINSON'S DISEASE: NGS-BASED SNCA MUTATION PROFILING
AND IN SILICO STRATEGIES TO TARGET A-SYNUCLEIN AGGREGATION**

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Abstract

Parkinson's disease (PD) is a common age-related neurodegenerative condition that characterized by the gradual loss of dopamine-producing neurons in the substantia nigra and the accumulation of Lewy bodies composed of aggregated α -synuclein. The most common causes of neuronal degeneration in PD are oxidative stress, mitochondrial dysfunction, impaired protein degradation, and toxic aggregation of misfolded α -synuclein. Mutations in the SNCA gene play a central role in this process. Missense variants in the coding exon 2-4 of the highly conserved SNCA gene are responsible for affecting the N-terminal region of α -synuclein which is critical for membrane binding and protein folding. Variants such as A53T, A30P and E46K and G51D alter the protein structure and significantly increase aggregation propensity, which accelerates disease progression. In this study, an integrative approach combining Next-Generation Sequencing (NGS) and in silico analysis was used to investigate SNCA variants and identify potential therapeutics. High-depth NGS enabled detection of rare and low-frequency mutations, while computational methods—including molecular docking, virtual screening, molecular dynamics simulations, and pharmacophore modelling—were employed to assess small-molecule interactions with α -synuclein and their ability to inhibit aggregation. Several compounds, including dopamine analogues and natural molecules such as honokiol and punicalagin, were identified as promising inhibitors capable of stabilizing α -synuclein and preventing misfolding, with some predicted to cross the blood–brain barrier. Overall, this study highlights the potential of integrating genomic profiling with computational drug discovery to accelerate the development of mutation-specific, brain-penetrant therapies for Parkinson's disease.

Keywords: Parkinson's Disease, SNCA Mutations, Next-Generation Sequencing, In Silico Modeling, alpha -Synuclein Aggregation.

**CRISPR-CAS(CLUSTERED REGULARLY INTERSPACED SHORT PALINDROMIC
REPEATS) SYSTEMS IN MICROBIOLOGY FROM BACTERIAL ADAPTIVE
IMMUNITY TO GENOME EDITING AND FUTURE APPLICATIONS**

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Abstract

CRISPR–Cas systems represent a powerful adaptive immune mechanism naturally present in bacteria and archaea, enabling protection against invading bacteriophages and foreign genetic elements. These systems function through three coordinated stages: spacer acquisition, CRISPR RNA (crRNA) biogenesis, and interference, where Cas nucleases recognize and cleave complementary target sequences. Among the diverse CRISPR types, the Type II CRISPR–Cas9 system has gained exceptional importance due to its simplicity and programmability, making it the most widely used tool for genome editing. In microbiology, CRISPR-based genome engineering has accelerated functional genomics by enabling precise gene knockout, knock-in, and multiplex modifications for studying virulence factors, metabolic pathways, quorum sensing, and stress response genes. Beyond research applications, CRISPR technology has significant industrial relevance, allowing strain optimization for fermentation, enzyme production, and biosynthesis of valuable biomolecules. Furthermore, CRISPR-based antimicrobials provide a promising strategy to combat antibiotic resistance by selectively targeting resistance determinants and plasmids, thereby reducing the spread of multidrug-resistant pathogens. Recent developments in Cas12 and Cas13 systems have also expanded CRISPR utility in rapid molecular diagnostics, enabling sensitive detection of microbial DNA or RNA for clinical and environmental monitoring. Despite challenges such as off-target effects and delivery limitations, ongoing advancements in high-fidelity nucleases and phage-mediated delivery platforms continue to enhance safety and precision. Overall, CRISPR–Cas systems have transformed modern microbiology and hold strong potential for next-generation therapeutics, diagnostics, and synthetic biology innovations.

**INTEGRATED OPTIMIZATION OF NUTRITIONAL AND PHYSICOCHEMICAL
PARAMETERS FOR THERMOSTABLE LIPASE PRODUCTION BY
SERRATIA MARCESCENS SCL1**

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Abstract

Thermostable lipases are among the most valuable industrial biocatalysts due to their broad applications in the food, pharmaceutical, detergent, biodiesel, leather, and oleochemical industries. In the present investigation, a thermostable lipase-producing bacterium, *Serratia marcescens* scl1, previously isolated and identified from pharmaceutical waste, was evaluated for enhanced extracellular lipase production through the optimization of culture conditions. A one-factor-at-a-time (OFAT) strategy was employed to systematically assess the influence of different physicochemical and nutritional parameters on enzyme production. The effects of incubation temperature, initial medium pH, agitation speed, incubation period, inoculum size, carbon and nitrogen sources, substrate concentration, metal ions, and surfactants were individually examined to determine the optimum conditions for maximal lipase synthesis. Among the tested variables, the highest lipase production was obtained at 35°C and pH 7.0, indicating the mesophilic and near-neutral growth preference of the isolate for efficient enzyme secretion. Olive oil at a concentration of 2.0% (v/v) served as the most suitable lipidic carbon source, whereas 1.0% (w/v) starch was identified as the most effective non-lipidic carbon source. Among the nitrogen supplements evaluated, 1.0% (w/v) yeast extract significantly enhanced lipase production, while lysine and ammonium nitrate also promoted substantial enzyme yields. Further optimization revealed that an agitation speed of 150 rpm, an incubation period of 24 h, and an inoculum size of 4.0% were optimal for extracellular lipase production. In addition, supplementation of the production medium with MgCl₂ and the non-ionic surfactant Tween 80 markedly stimulated enzyme synthesis, suggesting their positive role in maintaining membrane permeability and enzyme stability. Lipase activity was quantitatively determined by a spectrophotometric assay using p-nitrophenyl

palmitate (p-NPP) as the substrate. Statistical validation of the experimental data was performed using one-way analysis of variance (ANOVA) followed by Tukey's multiple comparison test, which demonstrated that the observed differences in lipase production under various optimization conditions were statistically significant ($p < 0.005$). Overall, the study establishes the optimal nutritional and environmental conditions for enhanced production of thermostable lipase by *Serratia marcescens* sc11. The optimized process provides a valuable foundation for large-scale fermentation, downstream processing, and the potential industrial exploitation of this robust biocatalyst in diverse biotechnological applications.

Keywords: Thermostable Lipase, Para-Nitrophenyl Palmitate, ANOVA, *Serratia Marcescens* sc11.

**ISOLATION, MORPHOLOGICAL, AND MOLECULAR CHARACTERIZATION OF
BACTERIAL ENDOPHYTES FROM JUSTICIA ADHATODA (VASAKA)**

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Abstract

Medicinal plants are potential hosts to beneficial microorganisms termed endophytes and they include bacteria, fungi and yeast. Though bacterial endophytes are the most prospective source and reservoir of bioactive compounds, there are a very few studies on bacterial endophytes of medicinal plants. *Justicia adhatoda* (Vasaka) is a medicinal plant used in Ayurveda to treat respiratory disorders such as cough, bronchitis. In the present study, leaves of Vasaka from two locations of Kolkata, India were collected. From plants of two locations, six and seven types of bacterial endophytes were isolated and screened. This revealed that isolates of both locations were majorly Gram-positive cocci and many of them were endospore forming. They invariably utilize glucose and mannose as their carbon source, but did not use lactose or citrate at all. None of them were sulphur reducing in nature. Few of them were capable of producing phosphatase and few produces urease. The isolates were stress tolerant as they withstood up to 7.5% NaCl and produced catalase to neutralize the oxidative stress. Few of them were indicative of aerobic respiration as they were oxidase+. These strains were phylogenetically identified by 16S rRNA gene sequencing and found that *Staphylococcus arlettae*, *Bacillus licheniformis*, *Staphylococcus hominis*, *Cytobacillus depressus*, *Bacillus thuringiensis*, *Exiguobacterium profundum* & *Bacillus oleronius*. Collectively this study showed that the leaves of Vasaka harbour bacterial endophytes which are similar in pattern in different locations and their stress tolerance and phosphate solubilization nature suggest application of them as potential source of novel bioactive compounds having medicinal importance.

**ALZHEIMER'S DISEASE: FROM PATHOGENESIS TO
POTENTIAL THERAPEUTIC STRATEGIES**

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Abstract

Alzheimer's disease is an insidious brain disorder that causes memory impairment, cognitive decline. Nowadays it is a critical neurodegenerative disease that mostly affects aged persons. It affects mainly the individuals aged 65 and older. The risk factors associated with AD are Genetics, Diabetes, Depression, Obesity, neuroinflammation etc. The main mechanism behind AD has two types of protein named Amyloid Precursor Protein (APP), Tau protein. APP is a transmembrane protein that is cleaved by secretase enzyme for proper function and amyloid beta plaque formed. This peptide accumulates in the brain and affects brain tissue, cerebral cortex, hippocampus adversely. The structure of tau protein disrupts by excessive amount of phosphate group and form neurofibrillary tangles. Significant mutation in the gene presenilin-1(PSEN1), presenilin-2(PSEN2) and APP also causes AD. Several therapeutic approaches are used to manage this type of brain disorder. Various kinds of medicine like aducanumab, cholinesterase inhibitor, NMDA, some monoclonal antibodies are used. Regardless of the various studies, there is no definite treatment for AD. Now some research studies aim to slow down or stop the progression of AD. Early diagnosis of AD can be possible through a better understanding its molecular mechanism and facilitate treatment using proper therapeutic strategies. The research on AD is still ongoing and researchers are developing many medicines and immunotherapies. In future we hope there will be improved outcomes in the diagnosis and treatment of AD.

Keywords: Alzheimer's Disease, Amyloid-Beta Plaque, Tau Protein, Neurodegeneration, Biomarkers, Cholinergic Hypothesis, APP, NMDA.

**FROM PATHOGEN TO POTENTIAL:
UNLOCKING THE POWER OF - *SERRATIA MARCESCENS***

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Abstract

Serratia marcescens is a Gram – negative opportunistic bacterium of growing clinical and biotechnological importance. It is a significant cause of nosocomial infections, particularly in immunocompromised individuals. Its pathogenicity is associated with multiple virulence factors including biofilm formation, hemolysins and the production of red pigment prodigiosin, which also contribute to antimicrobial resistance. Rapid detection remains challenging, although molecular methods have improved identification. Effective prevention relies on strict infection control practices including hand hygiene, sterilization and antimicrobial stewardship to limit the spread of multidrug resistant strains. Despite its pathogenic nature, *Serratia marcescens* exhibits significant biotechnological potential through the production of bioactive compound such as prodigiosin, lipopeptides and glycolipid biosurfactants, which possess antimicrobial, anticancer and emulsifying properties. These compounds have promising applications in medicine, agriculture, industry and environmental bioremediation. Thus understanding its dual role is essential for both clinical management and beneficial utilization.

Keywords: *Serratia marcescens*, Nosocomial Infection, Antimicrobial Resistance, Biofilm, Prodigiosin, Biosurfactants, Molecular Diagnostics, Infection Control, Antimicrobial Stewardship, Bioremediation.

**MYCOREMEDIATION OF CRYSTAL VIOLET DYE BY FUNGI *ASPERGILLUS*
TUBINGENSIS: A SUSTAINABLE “SELF-HEALING” SOLUTION FOR
ECOLOGICAL RESTORATION**

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Abstract

The discharge of textile dye wastewater can pose serious health risks to the ecosystem. Microbial degradation of dyes is vital to understanding the fate of dyes in the environment. *Aspergillus tubingensis* (NCBI accession no-PV639765) was isolated from rotten pomegranate. *Aspergillus tubingensis* dye discoloration properties had been observed (CV concentration 10mg/100ml, 50mg/100ml, 500mg/100 ml) in UV- visible spectroscopy at 590nm. It shows highest discoloration in 10mg/100ml, little decolorization in 50mg/100ml but it did not support growth and decolorization in 500mg/100ml. C-sources (dextrose, sucrose) and N-sources (sodium nitrate, peptone) and NaCl were used to observe their influence in dye discoloration in different concentrations i.e (0.5%, 1%, 2%, 5%, 8%, 10%), where it is observed good decolorization in interference of nutrient factors. In C-sources (mixed of 2% of dextrose and sucrose) and N-sources (2% of sodium nitrate and peptone) observed to decolorize CV in higher percentage. *Aspergillus tubingensis* did not support growth at 4°C but it support growth as well as dye discoloration at 38°C. It also grows very well with decolorize CV in pH, pH 1 it did not grow well and in pH 12 did not support fungal growth. Phytotoxicity tests revealed that CV discoloration products were less toxic than the parent compound. *Aspergillus tubingensis* was also found to decolorize safranin, methyl red, congo red but it did not decolorize malachite green, metanil yellow and tartrazine.

**FROM POLLUTION TO SOLUTION:
MICROBIAL DEGRADATION OF PLASTICS**

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Abstract

Plastic pollution is a major environmental problem due to the non-biodegradable nature of synthetic polymers like polyethylene and PET. Recent studies show that certain microorganisms, such as *Ideonella sakaiensis* and fungi like *Aspergillus*, can degrade plastics using enzymes like PETase. These enzymes break down complex polymers into simpler, eco-friendly products such as carbon dioxide, water, and biomass. Although microbial biodegradation is a promising and sustainable solution, its efficiency is limited and requires further research for large-scale application.

UNVEILING THERMOSTABLE LIPASES FROM MEDICINAL WASTEWATER MICROBIOTA

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Abstract

Thermostable lipases are increasingly sought after because they retain their catalytic efficiency and structural integrity under harsh environmental conditions, including elevated temperatures and broad pH ranges. Although thermophilic microorganisms have traditionally been the primary source of such enzymes, mesophilic bacteria represent a promising yet comparatively less explored alternative. These organisms may produce enzymes with desirable industrial characteristics while offering the advantage of simpler and more economical cultivation. Therefore, the present study explores medicinal wastewater as a potential reservoir for isolating mesophilic bacteria capable of producing thermostable lipases. Out of the 19 bacterial isolates screened for lipase production, eight were confirmed to synthesize thermostable lipase through spectrophotometric analysis using pNPP (para-nitrophenyl palmitate) as the substrate. The enzymes exhibited their highest activity at 65°C. Among these, MWS6 (*Bacillus* sp.), MWS14 (*Enterococcus* sp.), and MWS18 (*Serratia* sp.) emerged as the most potent producers. However, *Enterococcus* sp. MWS14 also showed remarkable thermostability (6.45 ± 0.07 $\mu\text{mol/mL/min}$), a rare feature for this genus.

Whole-genome and bioinformatic analyses of *Enterococcus* sp. MWS14 unequivocally link genetic architecture to the thermostable lipase phenotype observed experimentally. The circular chromosome of MWS14 (2.79 Mbp) contained 2,612 coding sequences, 48 tRNA, 3 rRNA gene, and one CRISPR array. A circular plasmid of approximately 50 kb was identified, harboring genes for antibiotic resistance (erm, tet), metal homeostasis (copZ, cadA), and global transcriptional regulation (crp), along with IS3/IS6 and Tn3 transposases. Genome annotation via Prokka and RAST identified five lipase/esterase genes and robust stress-response systems. Physicochemical indices (Aliphatic Index > 80, Instability Index < 40) demonstrate that all identified lipases possess all hallmarks of thermostable α/β -hydrolases, and slightly negative GRAVY value

indicating stability. Bioinformatic indices and structural validation of Phospholipase/Carboxylesterase 2 (MolProbity 0.65) exhibiting the highest predicted thermal resistance (AI=100). Genomic redundancy and plasmid adaptations ensure metabolic resilience and ecological fitness in waste-rich habitats. Collectively, these findings provide the first comprehensive genotype-to-phenotype framework for a thermostable lipase-producing *Enterococcus sp.*, validating its potential as an industrial biocatalyst for high-temperature processes such as detergent, biodiesel, and polymer manufacture.

Keywords: Thermostable Lipase, Mesophilic Bacteria, *Enterococcus sp.* MWS14, Whole Genome Sequencing, Physicochemical Indices.

**ESTIMATION OF WITHDRAWAL PERIOD OF ANTIMICROBIAL
SULFADIMETHOXINE IN EDIBLE TISSUES OF STRIPED CATFISH
(PANGASIANODON HYPOPHthalmus) (SAUVAGE, 1878)**

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Nilemesh Das¹, Asit Kumar Bera¹, Ranjith Kumar Nadella³,
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Abstract

The rapid global expansion of the aquaculture industry has fuelled increased reliance on antimicrobials, chemicals, and pesticides for disease prevention and management. When such agents are deployed without adherence to established national and international regulatory frameworks, the consequences can include the emergence of drug-resistant pathogens, environmental perturbation, and measurable risks to consumer health. Against this backdrop, the study examined the tissue accumulation and clearance kinetics of sulfadimethoxine (SDM), a sulfonamide antimicrobial in widespread aquacultural use, in striped catfish (*Pangasianodon hypophthalmus*), a finfish of considerable and growing commercial importance. SDM holds USDA approval for the treatment of furunculosis in salmonids and enteric septicemia of catfish, and is among only three antimicrobial compounds currently sanctioned for use in food fish. Juvenile fish averaging 25 ± 1.8 g body weight were administered SDM via in-feed dosing at the therapeutic rate of 42 mg kg^{-1} body weight for 10 consecutive days, after which muscle and liver residues were quantified by LC-MS/MS across a 20-day post-treatment monitoring window. Muscle residue concentrations declined sharply from $2,440 \pm 243.5 \text{ } \mu\text{g kg}^{-1}$ on the first day after

drug cessation to $55.3 \pm 5.51 \mu\text{g kg}^{-1}$ by day 6—well below the EU MRL of $100 \mu\text{g kg}^{-1}$. Regression modelling yielded an estimated withdrawal period of 8 days, with a statistically projected value of 17 days at 95% tolerance and confidence levels. Given a mean water temperature of $28 \pm 1.7^\circ\text{C}$, a degree-day-based withdrawal recommendation of 476 degree-days is proposed for equivalent thermal conditions.

Keywords: Antimicrobial, Withdrawal, Sulfadimethoxine

**GUT HEALTH IS WEALTH:
THE ROLE OF MICROBIOTA IN HUMAN WELL-BEING**

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Abstract

Gut health plays a crucial role in maintaining overall human well-being. The human gastrointestinal tract hosts a diverse community of microorganisms, collectively known as the gut microbiota, which are essential for digestion, nutrient absorption, and immune function. A balanced microbiome contributes to metabolic health and even influences mental well-being through the gut-brain axis.

However, factors such as poor diet, stress, and antibiotic overuse can disrupt this balance, leading to various health issues. Understanding the importance of gut microbiota highlights the need for maintaining a healthy lifestyle and opens new possibilities for microbiome-based therapies.

THIRD-GENERATION BIOFUEL PRODUCTION FROM ALGAE

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Abstract

With the rising demand for clean and renewable energy, third generation biofuels from algae have emerged as a promising solution. Algae are fast-growing, photosynthetic organisms capable of producing high lipid content, making them an efficient source for biofuel production. Unlike conventional biofuel sources, algae do not compete with food crops and can be cultivated in wastewater or non-arable land. They also play a significant role in capturing carbon dioxide, thereby helping to reduce environmental pollution. Algal biofuels can be converted into biodiesel, bioethanol, and biogas, offering versatile energy applications. Although challenges such as high production costs and harvesting techniques exist, continuous advancements in biotechnology are making this approach more feasible. Thus, algal biofuels represent a sustainable and eco-friendly alternative for the future energy landscape.

**MICROBIAL SAFETY IN SEWAGE-FED
AQUACULTURE OF THE EAST KOLKATA WETLANDS**

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Abstract

East Kolkata Wetlands is the world's largest sewage-fed aquaculture ecosystem and is recognized as a Ramsar site, spreading approximately 125 km² is a vast stretch of lowlands. These wetlands are famous for Sewage-fed aquaculture. This unique system sustainably recycles urban wastewater through sewage-fed aquaculture. East Kolkata Wetlands happens to be the world largest sewage fed aquaculture system. While the nutrient-rich sewage enhances fish growth and supports sustainable production, it also introduces potential risks due to contamination from agricultural, industrial, and domestic sources, including pathogenic microorganisms. Microbial water quality is a major concern in the world because ingestion of contaminated water with microorganisms poses risks to human and animal health. In this present study thirteen samples were collected from four different sites within East Kolkata Wetland and sixty-nine isolates were isolated. Phylogenetic analysis using neighbor-joining methods revealed close evolutionary relationships with clinically and environmentally relevant reference strains such as *Bacillus* spp., coliforms such as *Escherichia* spp. and *Klebsiella* spp., along with opportunistic pathogens including *Pseudomonas* spp., *Shigella* spp., *Aeromonas* spp. and *Staphylococcus* spp. Sites receiving higher domestic and industrial sewage loads showed significantly elevated total bacterial and coliform counts, with a strong positive correlation between coliform density and overall microbial load, indicating increasing fecal contamination pressure. The integration of culture-based and molecular approaches highlights the persistence of potentially pathogenic bacteria in sewage-fed aquaculture systems. These findings emphasize the urgent need for continuous microbial monitoring and implementation of a One Health-oriented management strategy to safeguard environmental integrity, fish health, and public health in urban wetland ecosystems.

Keywords: East Kolkata Wetland, Sewage Fed Aquaculture, Microbial Contamination, Public Health, One Health Approach.

TRANSLATIONAL PHYSIOLOGY AND PRECISION MEDICINES

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Abstract

Translational Physiology and Precision Medicine have transformed the healthcare landscape and fundamentally changed the viewpoint of clinicians in the context of disease diagnosis, treatment, and understanding of many related areas. The paradigm shift is creating an opportunity for improving therapeutic options available to clinicians from the "Patient-Centered Perspective" that are enabling clinicians to identify and create Biomarkers for the purpose of decreasing the risk and improving the effectiveness of treatment. This paradigm shift focused primarily on the development of individualized treatment approaches based on an individual's molecular, physiological and environmental characteristics. The advancement of the technology from data-driven medicine to multi-omics biomarkers and digital profiling with the help of AI and Machine Learning (ML), which helps in the patient centric diagnostics. There are other crucial points like physiological integration to this system which eventually helps to check viewpoints on human metabolism and to compare with healthy individuals. Thus, developing metabolism based clinical test and metabolotherapies are used to gather data on cellular bioenergetics and metabolomics. Translation-omics goes further point on research of genomics to inclusive molecular profiling. AI and ML makes the quantitative study on approach on medicine helps us to learn certain aspects of each medicine for each individual by putting in the real-time data which facilitates the targeted and more precised works of medicine to each individual. Further applications may include real-time data to monitor and predictive interventions to give more comprehensive outlook on the health care system.

Keywords: Precision Medicine, Multi-omics Biomarker, AI and Machine Learning, Metabolotherapies.

PLASTIC-EATING BACTERIA: AN EMERGING MICROBIAL STRATEGY FOR SUSTAINABLE BIODEGRADATION OF SYNTHETIC POLYMERS

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Abstract

In modern life, plastic is widely used because of its durability, low cost, and versatility. However, this same durability has led to serious environmental problems, as plastics do not decompose easily and can remain in the environment for long periods. As a result, plastic waste accumulates in ecosystems, leading to several harmful effects such as soil and water contamination, formation of microplastics, harm to wildlife, and disruption of food chains. In many cases, toxic substances released from plastics further increase these risks. To address this issue, researchers have been exploring microbial biodegradation as a possible solution. One such bacterium, *Ideonella sakaiensis*, first reported by Yoshida *et al.* (2016), has shown the ability to break down polyethylene terephthalate (PET), a commonly used plastic. It produces enzymes like PETase and MHETase, which convert complex plastic polymers into simpler compounds. These products are relatively less harmful and can be used by the bacteria as a source of energy, helping to reduce plastic accumulation. The discovery of such plastic-degrading microorganisms offers a promising and eco-friendly alternative to conventional waste management methods. Researchers are also trying to improve their efficiency so that they can be applied on a larger scale. Although challenges such as slow degradation rates still remain, the potential of this approach is significant. Therefore, plastic-eating bacteria may play an important role in future strategies for sustainable environmental management and reduction of plastic pollution.

Keywords: Plastic biodegradation, *Ideonella sakaiensis*, PETase, Microplastics, Environmental sustainability.

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