ABSTRACT BOOK AND PROCEEDINGS OF
ONE DAY NATIONAL SEMINAR

CURRENT TRENDS IN BIOLOGICAL SCIENCES, 2026

7TH APRIL, 2026

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DEPARTMENT OF BIOSCIENCES,
JIS UNIVERSITY

IN COLLABORATION WITH

MICROBIOLOGISTS SOCIETY,
INDIA

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Editor's Desk

Scientific progress is driven not only by discovery but also by meaningful dialogue and collaboration. The *One Day National Seminar on Current Trends in Biological Sciences*, held on 7th April 2026 at JIS University and organized by the Department of Biosciences in association with the Microbiologists Society, India, exemplified this collective spirit. The event brought together researchers, scholars, and students from across the country to deliberate on emerging trends and recent advances in the biological sciences. The seminar provided a dynamic platform for the exchange of innovative ideas and fostered interdisciplinary discussions across diverse domains of life sciences. The contributions presented reflect the evolving landscape of biological research, encompassing novel approaches, integrative perspectives, and contemporary scientific challenges. These interactions encouraged critical thinking and enabled participants to engage constructively with ongoing developments in the field. Beyond academic discourse, the seminar facilitated meaningful networking and collaboration, reinforcing the importance of collective inquiry in advancing scientific knowledge. The exchange of ideas and perspectives during the event is expected to inspire future research initiatives and strengthen the broader scientific community. This collaborative effort underscores the shared commitment of JIS University and the Microbiologists Society, India, to promoting research, innovation, and knowledge dissemination in the biological sciences.

- Editor

Dr. Avik Acharya Chowdhury

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NANOTECHNOLOGY:
A NOVEL APPROACH TO COMBAT ANTIBIOTIC RESISTANCE

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Abstract
Global public health is seriously threatened by the upsurge of drug-resistant microorganisms, which significantly limits the therapeutic options in infectious diseases. The antibiotic resistance is primarily influenced by overuse and misuse of antibiotics, although other factors like environmental stress (such as the build-up of heavy metals), unsanitary surroundings, unawareness, and ignorance also play major roles. The standard and conventional treatment options are lagged behind the rapid emergence of antibiotic-resistant bacteria, leading to infection persistence and spreading, novel strategies are fundamentally necessary in order to avoid critical health issues. There are several ongoing studies exploring the alternatives to combat AMR, such as bacteriophages, antimicrobial peptides, nanotechnology etc. The cutting-edge technology of utilising nanoparticles, focused on manipulating materials at the nanoscale, has emerged in the medical field by offering new approach to combating infectious diseases. Nanoparticles can be engineered to cause membrane disruption and induce cell death. Also, their encapsulation properties protect antimicrobial agents from degradation and allow for controlled drug release. The subcellular size of nanoparticles enables higher intracellular uptake of the drug which results in the reduction of the concentration of free drugs, reducing their toxic effect. Additionally, their small size and distinctive physical traits enable them to effectively target and dismantle biofilms, which are commonly associated to resistance development. Nanoparticles have demonstrated the ability to inhibit biofilm formation and disruption of established biofilms, leading to membrane damage and reduced viability of the bacteria. Further understanding of this technology is vital for developing effective treatments and regulatory policies to mitigate critical health concerns due to antibiotic resistance.

Keywords: *Antibiotic Resistance; Nanotechnology; Nanoparticles; Encapsulation.*

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COMPARATIVE MULTI-TARGET MOLECULAR DOCKING ANALYSIS OF NATURAL PHYTOCHEMICALS AGAINST SALIVARY BIOMARKERS IN ORAL SQUAMOUS CELL CARCINOMA (OSCC)

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Abstract

Oral squamous cell carcinoma (OSCC) poses a significant public health issue worldwide due to its widespread occurrence, late-stage diagnosis, and the involvement of numerous intricate molecular pathways that lead to unfavorable outcomes. Several proteins found in saliva and cells, including interleukin-6 (IL-6), matrix metalloproteinase-9 (MMP-9), cluster of differentiation-44 (CD44), p53, epidermal growth factor receptor (EGFR), and vascular endothelial growth factor (VEGF), are essential in tumor advancement through mechanisms such as inflammation, invasion, cell growth, and angiogenesis. This research utilized a multi-target computational strategy to explore the potential interactions of selected bioactive compounds derived from plants with these important OSCC-related proteins. A molecular docking analysis was carried out using the CB-Dock2 platform, assessing phytochemicals like curcumin, resveratrol, quercetin, epigallocatechin gallate, genistein, luteolin, and apigenin, alongside cisplatin as a reference. The binding efficiency was assessed using Vina scores, focusing on interaction stability and binding conformations. The findings revealed that all tested compounds demonstrated appreciable binding affinities across multiple targets, with energy values generally ranging between -6.0 and -9.1 kcal/mol. Among them, curcumin exhibited the most favorable interaction profile, suggesting strong and stable binding characteristics, while quercetin, luteolin, and apigenin also showed consistent multi-target engagement. The docking behavior of cisplatin aligned with expected patterns, supporting the reliability of the analysis. Overall, these results indicate that naturally occurring phytochemicals may act as promising multi-target agents capable of modulating various signaling pathways involved in OSCC progression. However, further validation through advanced computational simulations and experimental studies is essential to confirm their therapeutic applicability.

Keywords: *OSCC; Molecular Docking; Phytochemicals; Multi-target Therapy; IL-6; MMP-9; EGFR; VEGF.*

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SUCCESSION IN WETLANDS AND IT'S CHALLENGES

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Abstract

Hydrosere succession is a zestful ecological exercise sometimes called wetland succession through which functional transformation of aquatic habitat occurs. Natural inland wetlands mainly constitute of closed floodplain area. It ordinarily instigates in unsecured water systems dominated by plankton (phyto) and macrophytes. Unhurried sedimentation, helps production of inconsistent vegetation like, Typha, Phragmites. Agriculture and urban effluents help eutrophication of aquatic structure and disintegrate species interaction. Hydrological disengagement, caused by drainage and water rerouting, interrupts the periodic flood that is essential for successional progression. Planted wetlands become more diverse after few days of planting while unplanted wetland is more allowing to stress. During the successional stage of wetlands, invasive species further unsettle native species, inflict competitive exclusion and altering ecosystem. Sometimes different external factors affect the wetlands succession. Preserving the wetlands (that act as home of different animal) may increase species interaction and diversity.

Keywords: *Inland; Sedimentation; Disintegrate; Unplanted; Competitive exclusion.*

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ECOLOGICAL STATUS AND MAGNITUDE OF DISTINCT WETLANDS IN WEST BENGAL

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Abstract
The transitional zone of land and water comprises the Nature's Kidney. This Nature's Kidney not only act as filtration but also home of different micro and macro-organisms. Agricultural runoff, domestic sewage, industrial effluents are the major pollutants in wetlands. In West Bengal, Santragachi, Patlakhawa- Rasomati, Rasik beel, Ahiron beel, Sundarban, East Kolkata Wetland are the crucial wetlands and provides ecosystem stability. Wetlands contains most fecund diverse animals like, mammals, fishes, amphibia. East Kolkata Wetland (8100 ha) are used to treat Kolkata's sewage and this wastewater also used for aquaculture. The Ahiron lake of Murshidabad district is the homeland of different birds, like Red creasted pochard, Gadwall, White eyed pochard, etc. and its water is mainly polluted by soil transferring for the brick field. The species composition of Sundarban includes different species of fishes, amphibians, birds, planktons, fungi, bacteria, reptiles, invertebrates, plants. Pollution of wetlands have negative impact on ecosystem as it reduces number of species. So, wetland conservation is essential for stabilizing ecosystem.
Keywords: *Filtration; Effluents; Sewage; Aquaculture; Ecosystem.*

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BIOREMEDIATION OF HEAVY METALS AND HAZARDOUS WASTE

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Abstract
Bioremediation succours removal of heavy metals, hazardous waste and it's an innovative method. Bioremediation presuppose using living organisms (bacteria, plants) to remove wastes in a sustainable way. The countless heavy metals like Pb, Hg, Cd, etc. are produced from mining, industrial processes, agriculture. Precarious wastes toxicity and reactivity strike human immune system. The T cell and B cell of immune system cannot identify these hazardous wastes. The In-situ method and Ex-situ method are the two major component in bioremediation. In situ method is straightforward and lucrative method as compared to Ex-situ method. Bioremediation objectives include, control of heavy metals, hazardous waste and remove toxic pollutants from polluted sites. Beside this, some common methods are phytoremediation, bioleaching, biopiles, bioventing, biostimulation. Biosorption, Bioaccumulation and Bio- transformation are the three basic principle for bioremediation. In recent time, metagenomics and metatranscriptomics are used to enhance the efficiency of the microorganisms.

Keywords: *Heavy Metals; Reactivity; Biosorption; Bioaccumulation; Metatranscriptomics.*

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DIVERSITY OF DINOFLAGELLATES, TOXICITY, AND HUMAN IMPACT IN THE COASTAL REGION OF WEST BENGAL

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Abstract
This study describes several dinoflagellate species from the coastal region of South 24 Parganas, West Bengal. Microscopic analyses, along with suitable staining techniques, were performed to examine their morphology. Some of the recorded species are known to cause allergic reactions, homeostatic imbalance in humans, and may contribute to biomagnification and bioaccumulation through the food chain. This study may help in identifying harmful dinoflagellate species, along with their density and availability within the photic zone. Several species, including *Tripos* sp., *Protoperidinium* sp., and *Ceratium* sp., were found in the Matla-Hooghly delta region under semi-high to medium salinity conditions, during high tide, in turbid water environments. Samples were collected from both surface water and bottom sediments. This study may contribute to our understanding of estuarine and marine dinoflagellate diversity, population distribution, and toxicity in the coastal and estuarine regions of the Bengal delta.
Keywords: *Dinoflagellates; Coastal Region; Phycotoxins; Human Impact; Biodiversity.*

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CURCUMIN FROM *CURCUMA LONGA*: A NATURAL ANTIMICROBIAL AND ANTIOXIDANT AGENT AGAINST MULTIDRUG-RESISTANT PATHOGENIC BACTERIA

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Abstract

Curcuma longa (turmeric) is a widely recognized medicinal plant rich in curcumin, a bioactive polyphenolic compound known for its significant antimicrobial and antioxidant properties. With the increasing threat of multidrug-resistant pathogens, there is a growing need to explore plant-based alternatives for effective and sustainable therapeutic applications. This study aimed to evaluate the antimicrobial potential of turmeric extracts and to characterize selected pathogenic bacteria using standard biochemical assays. Crude extracts were prepared from dried rhizome powder using methanol, chloroform, and toluene through Soxhlet extraction and ultrasound-assisted extraction techniques. The presence of curcumin was initially confirmed by Thin Layer Chromatography (TLC) and further quantified using High Performance Thin Layer Chromatography (HPTLC), which yielded an Rf value of approximately 0.528, indicating the presence of the target compound. Biochemical characterization of seven pathogenic bacteria was carried out using IMViC tests, Triple Sugar Iron (TSI) test, catalase, oxidase, and amylase assays to confirm their identity and metabolic properties. The antimicrobial activity of the extracts was evaluated using the agar cup method, where significant zones of inhibition were observed against multiple pathogens. The highest inhibition was recorded against *Bacillus subtilis* (30.6 mm) using Soxhlet methanol extract, while notable inhibitory effects were also observed against *Escherichia coli* and other tested organisms. Furthermore, total phenolic and flavonoid contents were estimated, and antioxidant activity was assessed using the DPPH free radical scavenging assay, confirming strong antioxidant potential of the extracts. The findings demonstrate that *Curcuma longa* extracts possess potent antimicrobial and antioxidant activities, suggesting their potential as eco-friendly, cost-effective alternatives to conventional antibiotics, particularly against multidrug-resistant bacteria. This study highlights the importance of plant-derived bioactive compounds in advancing human health and combating emerging microbial resistance.

Keywords: *Curcuma longa; Curcumin; Antimicrobial Activity; Multidrug-Resistant Bacteria; Antioxidant Activity; HPTLC Analysis.*

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GENOME ANALYSIS OF *THERMOANAEROBACTERIUM VIRENDRII* TO VALIDATE ITS CONSOLIDATED BIO-PROCESSING (CBP) CHARACTERISTICS AS A BIOBUTANOL PRODUCING STRAIN

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Abstract

Consolidated bio-processing (CBP) is a promising method for biofuel production from lignocellulosic biomass (LCB) which combines the hydrolysis and fermentation processes in a single step. It thus reduces cost, improves yield and productivity as opposed to conventional methods. Microbes with CBP characteristics can be suitable as industrial strains and can be identified by genome database using various in silico methods. In our research, we studied the genome of *Thermoanaerobacterium virendrii* (*Thermoanaerobacterium* sp. RBIITD) for its CBP characteristics for application in butanol production. This strain was capable of utilizing LCB to produce butyrate and n-butanol with no detectable acetone or ethanol, by following a non-Acetone-Butanol-Ethanol (non-ABE) pathway. The CBP characteristic of a strain can be justified by its surface attachment onto the LCB which will facilitate the hydrolysis process. A complete genome analysis of the organism revealed that cellulosome-like substrate attachment may be possible due to the presence of proteins like dockerin type I repeat protein, S-layer protein, BIg-1 protein, as well as DOMON-like superfamily domain and several carbohydrate binding modules (CBMs). It has a wide range of cellulolytic, xylanolytic, starch-pectin hydrolysing, and oligosaccharide hydrolysing enzymes that are required for hydrolysis of LCB into pentose and hexose sugars. It also has two monofunctional alcohol dehydrogenase, and one bifunctional alcohol/acetaldehyde dehydrogenase enzymes that ferment the hydrolysed sugars to butyrate and butanol. Phylogenetic tree analysis of these enzymes revealed a close relationship with similar butanol producers. Molecular docking analysis showed lower binding energy for complex formation with butyraldehyde than with acetaldehyde, higher number of bonds displayed with butyraldehyde as compared to that with acetaldehyde, and lesser bond lengths during butyraldehyde binding compared to those during binding of acetaldehyde. Therefore, the CBP characteristics of a strain can be predicted by genome analysis for the presence of surface-adhesion proteins, hydrolytic enzyme clusters, and solventogenic enzymes.

Keywords: *Consolidated Bioprocessing (CBP); Lignocellulosic Biomass (LCB); Thermoanaerobacterium Virendrii; Butanol Production; Cellulosome-Like Complexes; In Silico Genome Analysis.*

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GREEN APPROACH FOR DYE REMOVAL: BIOSORPTION POTENTIAL OF *CITRUS LIMETTA* PEEL AND *SACCHARUM OFFICINARUM* BAGASSE

Tuhin Ganguli[#1], Bishal Ghosh[1], Abhishek Pal[2], Chandan Rai[2], Dr. Abhishek Das[3], Dr. Suparna Ghosh[*2]

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Abstract

The increasing discharge of synthetic dyes from textile, leather, paper and pharmaceutical industries has become a major environmental concern due to the toxicity, chemical stability and persistence of these pollutants. Among these, Crystal Violet (CV) and Malachite Green (MG) are cationic dyes known for their mutagenic, carcinogenic, and bioaccumulative properties, posing serious risks to aquatic ecosystems as well as human health. Conventional wastewater treatment methods, including coagulation, chemical oxidation and membrane filtration, are often limited by high operational costs, incomplete dye removal and the generation of secondary sludge. Although adsorption using activated carbon is highly effective, its widespread application is restricted due to high material and regeneration costs. In this context, there is a growing interest in developing low cost and sustainable alternatives derived from agricultural waste. The present study explores the biosorption potential of sweet lime (*Citrus limetta*) peel and sugarcane (*Saccharum officinarum*) bagasse, both of which are abundantly available agro-wastes rich in cellulose, hemicellulose, lignin, and functional groups such as hydroxyl and carboxyl, that facilitate dye binding. Furthermore, a microbially modified adsorbent will be developed to enhance adsorption efficiency, mechanical stability and reusability. The study aims to systematically evaluate and compare the removal efficiencies of these biosorbents for CV and MG under varying conditions, including pH, contact time, adsorbent dosage and initial dye concentration. In addition, adsorption kinetics, isotherm models and thermodynamic parameters will be analyzed to elucidate the underlying mechanisms. The outcomes of this research are expected to contribute to the development of an eco-friendly and cost effective biosorbent for sustainable dye wastewater treatment.

Keywords: *Citrus Limetta Peel; Saccharum officinarum Bagasse; Biosorption; Crystal Violet; Malachite Green; Agro-Waste Adsorbents.*

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PHYSICOCHEMICAL DRIVERS OF SOMATIC INVESTMENT IN FISHES WITH OBSERVATIONS ON LIGHT-INDUCED BEHAVIORAL RESPONSES IN *CLARIAS SP.*

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Abstract

Environmental conditions play a critical role in regulating physiological performance, behavioral responses, and growth patterns in fishes. Physicochemical factors such as salinity, pH, light regime, and water hardness influence metabolic activity and energy allocation. As fishes remain in constant interaction with their surrounding aquatic environment, these factors significantly affect internal homeostasis and somatic investment, defined as the allocation of energy toward growth, tissue maintenance, and structural development. These environmental parameters influence feeding behavior, respiration, osmoregulation, and overall metabolic processes, thereby determining how energy is distributed between maintenance and growth. Among these factors, light regime acts as an important behavioral and physiological regulator, affecting locomotor activity, social interaction, and circadian rhythms in fishes. A short-term observational study was conducted on Clarias under controlled laboratory conditions to examine behavioral responses under different light conditions. Fish were exposed sequentially to normal LED, blue, yellow, and red light over a fifteen-day period. Behavioral parameters including swimming activity, resting behavior, air-breathing frequency, escape response, and social interaction were systematically observed and recorded. Observations revealed stable and controlled activity under blue light, increased locomotor activity and interaction under yellow light, and initial hyperactivity followed by gradual adaptation under red light. Aggressive biting behavior resulting in visible skin lesions was recorded during the yellow light phase, indicating heightened stimulation. These findings demonstrate that light spectrum influences behavioral energy expenditure and interaction patterns in fishes. Understanding the relationship between physicochemical conditions and behavioral responses provides valuable insight into physiological efficiency and supports the development of improved aquaculture management strategies.

Keywords: *Physicochemical Factors; Somatic Investment; Behavioral Responses; Light-Induced Activity; Aggression; Clarias Species; Aquaculture Management; Environmental Regulation of Growth.*

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ECOLOGICAL RESTORATION OF WETLANDS AND ECOTOURISM

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Abstract
Ecological restoration and sustainable ecotourism have powerful approach to environmental conservation. Ecotourism ensures the economic development of a particular area. Wetlands, helps carbon sequestration, and act as homeland of different flora and fauna. Flood mitigation is another part of wetlands. Unplanned urbanization, industrial effluents, agricultural wastes mainly create pollution in wetlands. Revegetation of native plant species and improve water quality are the two basic components of ecological restoration. Low dissolved oxygen, high amount of phosphate, sulphate, ammonia affects wetland ecosystem. Sometimes, invasive alien species may introduce new diseases, changing genetic variation that directly affects native species. Restored natural landscape ecosystems are well-suited for ecotourism, that helps to environmental awareness. In the restored wetlands ecotourism involves hiking, nature enjoyment, birdwatching. Ecotourism creates increasement of livelihood for local communities. Ecotourism and restoration depend on local people's and awareness and participation. The revenue of the tourism helps wetlands for self-sustaining cycle. The active and continuous monitoring of the wetland's ecological health helps to ensure restoration of wetlands.
Keywords: *Particular; Mitigation; Landscape; Participation; Monitoring.*

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EXPLORING KINASE DEPENDENT MUCIN EXPRESSION IN COLORECTAL CANCER

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Abstract

Colorectal cancer (CRC) stands as the third most common cancer and ranks second in terms of morbidity. In CRC, all signaling pathways are controlled by different kinases (EGFR-MAPK, GSK-3β, PI3K/AKT, and TGF-β, etc.), and remain key targets to overcome CRC. Mucin proteins form the protective layer of the normal epithelial cell layers, but in CRC their expression may be altered and contribute to chemoresistance. A few previous studies suggested that mucin expression may be controlled by the kinases and provides more complexities to the CRC treatment. But the overall interplay between kinases and mucins in CRC remains poorly understood and must be explored further to develop some natural modulators and overcoming CRC. In the current study, KinMap tool was used first to select top kinases that may play crucial role in CRC development and the impact of differential expression of mucins on CRC patients' survival were further investigated by different bioinformatics tools (UALCAN, KM-plotter, etc.). Next, the PPI network between kinases and mucins was developed by employing STRING. Eight kinases (GSK-3β, EGFR, JAK1, etc.), were found to be directly and indirectly linked with mucin proteins. In order to validate the importance of identified kinases in mucin expression, one of the kinases, namely GSK3β, were targeted by known inhibitors (LiCl and CHIR99021) in HT-29 colon cancer cells and the expression of different mucins were checked at RNA and protein levels. Inhibition of GSK3β resulted in alteration of different mucins expression (MUC4, MUC5AC, MUC17, MUC20, etc.), both at RNA and protein level. So further investigation is needed in order to understand the role of GSK3β and other kinases in mucin expression, which could lead to the identification of natural and synthetic compounds and further development of therapeutic agents capable of mitigating CRC pathology.

Keywords: *Colorectal Cancer (CRC); Kinase Signaling Pathways; Mucin Proteins; GSK-3β Inhibition; Protein-Protein Interaction (PPI) Network; Chemoresistance.*

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LEAF EXTRACT OF *SEMECARPUS ANACARDIUM*: A POTENTIAL SOURCE OF BIOACTIVE COMPOUNDS CAPABLE OF TARGETING INFLAMMATION-EMT AXIS IN COLON CANCER

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Abstract

Colorectal cancer (CRC) is a multifactorial disease. It is the second most common cause of cancer-related deaths (9.4%) worldwide. Studies have revealed that the cyclooxygenase-2 (COX-2) pathway plays a central role in the development of inflammation-mediated CRC. Inflammatory microenvironment may impact tumour development as it promotes epithelial-mesenchymal transition (EMT), which is a crucial step towards metastasis. So, inflammation and EMT are a complex, interconnected network and targeting this axis might present a new avenue for anti-inflammatory therapeutic strategies in colon cancer. Our primary goal is to target the EMT-inflammation axis with natural compounds (whole leaf extract) derived from Indian medicinal plants due to the failure of conventional treatment strategies and their side effects. Based on the literature review, we shortlisted *Semecarpus anacardium* (commonly known as Marking Nut tree) plant with reported anti-inflammatory and anti-cancer properties. Fresh leaves were collected from the Western Ghats region of Maharashtra. The leaves are air-dried for 14 days and ground into a fine powder. Then, the ethanolic extract of the leaves was prepared. Colon cancer cells (HT-29) were treated with various doses of the leaf extract. MTT assay was performed to assess the cell survivability of colon cancer cells (HT-29) in response to the treatment. Later on, gene expression analysis of different components of EMT pathway (E-cadherin, N-cadherin, Vimentin, Snail, Slug, Twist) and inflammatory markers (COX-2, NF-κB p65) were done via qPCR to check whether our leaf extract is able to inhibit the inflammation-EMT axis. Also, wound healing assay and colony formation assay were performed to check the anti-proliferative and anti-migratory activity of the extract with respect to the control group. Our extract significantly modulated the inflammatory and EMT markers and worked effectively in other functional assays, thereby inhibiting the inflammation-EMT axis. However, further characterisation of plant extract, identification of bioactive compounds presents and their effects on cellular and molecular level in colon cancer cells are very much crucial for comprehensive understanding of inflammation-EMT crosstalk. This approach may help the development of novel therapeutic agents capable of modulating inflammation-EMT axis in Colon cancer.

Keywords: *Colorectal Cancer (CRC); Inflammation-EMT Axis; Semecarpus Anacardium; NF-Kb Signaling; HT-29 Cells; Anti-Proliferative Activity.*

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EXPLORING THE ANTIMICROBIAL AND ANTIBIOFILM POTENTIAL OF INDIGENOUS PLANT *TINOSPORA CORDIFOLIA* AGAINST NOSOCOMIAL *ENTEROBACTER CLOACAE*

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Abstract

The increasing prevalence of antimicrobial resistance and biofilm-associated infections has intensified interest in natural bioactive compounds as alternative antimicrobial agents. Phytoextracts are one of the major sources of bioactive compounds which show antimicrobial, antibiofilm and anti-inflammatory properties. *Tinospora cordifolia*, an indigenous medicinal plant has long been used as anti-inflammatory and antimicrobial agent in ayurveda also shows antibiofilm activity against Gram-negative bacteria. In the present study, the antimicrobial and antibiofilm activity of *T. cordifolia* against a nosocomial pathogenic bacteria *Enterobacter cloaca* has been observed through different assays including biofilm reduction, cell viability, EPS disruption. Different microscopic analyses further validated the obtained results. *T. cordifolia* extract showed significant inhibition of bacterial growth along with marked reduction in biofilm formation, indicating its potential role in disrupting microbial adhesion and reduction of extracellular polymeric matrix. These findings suggest that *T. cordifolia* could serve as a promising plant-based therapeutic alternative for managing drug-resistant infections, thereby contributing to improved public health, reduced antibiotic dependency, and enhanced human welfare.

Keywords: *Enterobacter Cloacae; Tinospora Cordifolia; Antibiofilm Activity; Extracellular Polymeric Matrix.*

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ISOLATION AND PHYSICOCHEMICAL PROFILING OF A LYTIC *E. COLI* BACTERIOPHAGE FROM ENVIRONMENTAL WATER SAMPLES

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Abstract

Bacteriophages have re-emerged as powerful biological agents capable of targeting multidrug-resistant (MDR) bacteria with high specificity. In this study, a lytic Escherichia coli bacteriophage was isolated and characterized from environmental water samples collected from the Durgapur region. Preliminary screening through drop assays confirmed clear lysis zones exclusively in the Durgapur Barrage sample, indicating the presence of active phages. The phage was further purified using plaque isolation, high-titer propagation through broth and plate lysis methods, followed by cesium chloride (CsCl) density gradient ultracentrifugation to obtain a concentrated and contaminant-free preparation. Physicochemical profiling revealed that the phage retained optimal stability and lytic efficiency at neutral pH 7, while maintaining moderate activity under mildly acidic and alkaline conditions. Temperature stability assays showed that the phage remained active between 4°C and 50°C, with a decline in infectivity at extreme temperatures. One-step growth curve analysis demonstrated a short latent period and high burst size, indicating strong replication dynamics. Phage DNA was successfully isolated and subjected to restriction digestion to determine its genomic pattern. SDS-PAGE followed by silver staining confirmed the presence of distinct structural proteins characteristic of the phage particles. Importantly, preliminary observations suggested the phage's ability to disrupt *E. coli* biofilm layers, as indicated by reduced turbidity and visible clearance in phage-treated cultures. This highlights its potential application not only in targeting planktonic MDR *E. coli* but also in degrading biofilm-associated infections.

Keywords: *Bacteriophage; E. coli; Phage Therapy; Biofilm Degradation; Plaque Assay; CsCl Purification; One-Step Growth Curve.*

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FROM INFECTION TO CANCER: TRAF6 AS THE MOLECULAR BRIDGE IN *H. PYLORI*-DRIVEN CHRONIC DISEASE

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Abstract

Helicobacter pylori remains the primary etiological agent for gastric adenocarcinoma, affecting nearly half the global population. While the bacteria's virulence factors, such as CagA and VacA, are well-characterized, the intracellular mechanisms that translate these bacterial signals into chronic, oncogenic inflammation remain a critical area of study. TNF Receptor Associated Factor 6 (TRAF6), a unique E3 ubiquitin ligase, emerges as a central scaffold in this transition. This study explores the signaling hierarchy wherein *H. pylori* activates host Toll-like Receptors (TLR2/4). This recruitment triggers the MyD88-dependent pathway, centering on the activation of TRAF6. As a pivotal signaling hub, TRAF6 facilitates the ubiquitination of the IKK complex, leading to the constitutive activation of NF-κB. This results in a sustained "cytokine storm" of IL-6, TNF-α, and IL-1β, creating a microenvironment conducive to cellular transformation. We map the "Correa Pathway" of gastric carcinogenesis-from chronic gastritis to intestinal metaplasia and dysplasia-demonstrating that TRAF6 acts as the molecular bridge sustaining the "smoldering" inflammation required for these phenotypic shifts. The persistent activation of TRAF6-mediated pathways not only drives inflammation but also promotes cell survival and genomic instability. Given its role at the intersection of innate immunity and oncogenesis, TRAF6 represents a high-value therapeutic target. Current and emerging strategies focusing on small-molecule TRAF6 inhibitors offer a promising shift from traditional antibiotic-heavy regimens to precision "immuno-interruption" of the gastric cancer cascade. Future research must determine the efficacy of targeting this bridge to arrest disease progression in high-risk populations.

Keywords: *Helicobacter pylori; TRAF6 Signaling; NF-κB Activation; Toll-Like Receptors (TLR2/4); Gastric Carcinogenesis (Correa Pathway); Pro-Inflammatory Cytokines*

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BEYOND AMYLOID: THE SHIFT FROM BACE1 TO TAU IN ALZHEIMER'S DISEASE

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Abstract

Over the last 20 years, research into AD has changed significantly in its focus, shifting from primarily investigating Aβ production, to focusing more on Tau pathogenesis. The initial therapeutic strategies that were developed, were based on a BACE1 (β-site amyloid precursor protein cleaving enzyme 1) (the enzyme that initiates the cleavage of APP and the generation of Aβ). Preclinically, there were strong indications of the potential of BACE1 inhibitors as a therapy. However, BACE1 inhibitors that have been tested in clinical trials have all failed due to a lack of cognitive benefits and a high incidence of adverse effects, with significant levels of synaptic dysfunction and neurodegeneration occurring following BACE1 inhibition. This demonstrates the limitations of inhibiting BACE1 globally, given that BACE1 has essential physiological roles in neuronal development, synaptic plasticity, and myelination. In addition to the BACE1 findings, many studies have demonstrated a greater correlation between tau pathology and neurodegeneration/cognitive decline than Aβ pathology. While the degree of amyloid accumulation generally does not demonstrate strong correlations with disease severity, the aggregation/propagation of tau demonstrates strong spatio-temporal correlations with neuronal loss and clinical progression. Molecular imaging and biomarker development have helped to clarify the importance of tau in the pathogenesis of AD, and have also provided powerful tools for monitoring disease progression. This analysis explores the underlying mechanistic and translational components of our transition from BACE1-based therapies towards tau-centric strategies. This includes synthesizing data from unsuccessful BACE1 clinical trials, new data related to tau propagation, and the changing perspective of Alzheimer's disease (AD) from a purely pathological condition to one that encompasses multiple contributing factors. Additionally, we provide an overview of current tau-focused therapeutic approaches, including but not limited to aggregation inhibitors, immunotherapy, and modifications of post-translational modifications. Taken together, this transition highlights the need for more selective, staged and disease phenotype-based therapies that can be matched with the underlying biology of the disease in order to improve patient outcomes.

Keywords: *Alzheimer's Disease (AD); Tau Pathology; BACE1 Inhibitors; Amyloid-B (Aβ); Neurodegeneration; Tau-Targeted Therapeutics*

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ADAPTIVE BIOFILM FORMATION AND EPS OVERPRODUCTION IN MICROBIAL CONSORTIA UNDER HEAVY METAL STRESS

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Abstract

Heavy metal contamination in aquatic and terrestrial ecosystems poses a significant environmental challenge, necessitating the development of efficient and sustainable remediation strategies. In this study, a metal-tolerant, extracellular polymeric substance (EPS)-producing microbial community was enriched from contaminated dumping grounds of East Kolkata and evaluated for its biofilm-forming and metal sequestration potential under single and multi-metal stress conditions. Enrichment and screening based on culture viscosity identified a robust EPS-producing consortium, with optimized production observed under mildly alkaline conditions and sucrose supplementation. Comparative analysis revealed that exposure to multi-metal stress (Hg, Pb, Ni, Co at MIC levels) significantly enhanced EPS production, as evidenced by increased viscosity and biomass accumulation relative to individual metal stress. Growth kinetics demonstrated differential toxicity, with nickel exerting the highest inhibitory effect, whereas lead and mercury showed comparatively lower impact on microbial proliferation. Quantitative analysis using atomic absorption spectroscopy indicated substantial metal sequestration by both microbial cells and purified EPS. Notably, under individual metal stress, nickel exhibited the highest sequestration efficiency (up to ~72%), whereas in multi-metal systems, cobalt showed enhanced uptake (~36%), suggesting competitive interactions among metals. Furthermore, biofilm quantification assays demonstrated maximal biofilm formation under multi-metal stress, corroborated by increased crystal violet retention (OD_{570}). Scanning electron microscopy (SEM) analysis confirmed dense and structured biofilm architecture under mixed metal conditions, while energy-dispersive X-ray (EDX) spectroscopy validated the co-adsorption of metals, particularly nickel and cobalt, within the biofilm matrix. These findings collectively indicate that environmental stress from multiple heavy metals triggers adaptive responses in microbial communities, leading to enhanced EPS production and stable biofilm formation. The study highlights the potential application of such naturally enriched microbial consortia in bioremediation systems for efficient removal of heavy metals from complex contaminated environments.

Keywords: *Heavy Metal Biosorption; EPS, Biofilm; Microbial Consortia.*

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PATH TOWARDS A GREENER SILVER: SYNTHESIS AND APPLICATION

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Abstract

The development of metal nanoparticles with tailored physicochemical properties compared to bulk metals has expanded their applications in biomedical studies. In particular, silver nanoparticles (AgNPs) have showed significant promise in antimicrobial, anti-inflammatory and wound healing capabilities. Unfortunately, the more common synthesis strategies are restricted by toxic chemicals and energy-intensive protocols, limiting their potential for translation to clinical applications. The green synthesis through plant extracts is being a sustainable alternative method where phytochemicals extracted from different plant parts act as reducers and stabilizing agents, providing biocompatible and stable nanoparticles. This review focuses on plant-mediated synthesis of AgNPs and their functional advantages, including enhanced stability, reduced aggregation, and high surface area-to-volume ratio which is central to unique behaviour of nanomaterial compared to its bulk counterpart. One of its major highlights is an elucidation of the mechanistic basis of AgNP mediated antimicrobial action, an aspect that is often overlooked in reports limited to synthesis protocol and antimicrobial assays. Mechanisms by which AgNPs induce microbial cell death include loss of membrane integrity, generation of reactive oxygen species, interference with DNA and protein synthesis, and Ag^{+} ions released by AgNPs that bind thiol-containing biomolecules. They exert these multimodal effects specifically against multidrug-resistant (MDR) pathogens, a key public health challenge worldwide. The role of AgNPs in wound healing is also highlighted, including their ability to control inflammation, promote cell proliferation, and enhance tissue regeneration. Despite these advantages, concerns regarding toxicity and non-specific interactions persist. Future research should prioritize the development of low-toxicity, functionally targeted AgNPs exhibiting synergistic biological functions. A mechanistically informed green synthesis approach will be critical for addressing safer and effective clinical translation.

Keywords: *Silver Nanoparticles (AgNPs); Green Synthesis; Plant-Mediated Nanomaterials; Antimicrobial Mechanisms; Multidrug-Resistant (MDR) Pathogens; Wound Healing.*

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ANTIMICROBIAL, ANTI-BIOFILM, AND ANTICANCER ACTIVITIES OF GREEN-SYNTHESIZED SILVER NANOPARTICLES USING *ARTEMISIA INDICA* LEAF EXTRACT

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Abstract

The green synthesis of metallic nanoparticles using plant-derived phytochemicals has emerged as a sustainable and environmentally friendly alternative to traditional chemical methods. In this study, we report for the first time the synthesis of silver nanoparticles (AgNPs) using an aqueous leaf extract of *Artemisia indica* (Indian wormwood), a medicinal plant with well-known therapeutic value but previously unexplored potential in nanobiotechnology. Phytochemical profiling through LC-MS analysis identified 62 metabolites, including flavonoids, phenolics, and terpenoids, which play a crucial role in reducing and stabilizing the nanoparticles. The formation of *A. indica*-derived AgNPs (AI-AgNPs) was confirmed by UV-Vis spectroscopy, while FTIR analysis revealed that functional groups such as hydroxyl, carbonyl, and amine groups were involved in nanoparticle capping and stabilization. Further characterization using TGA, XRD, DLS, FE-SEM, TEM, and EDX demonstrated that the nanoparticles are thermally stable, crystalline, and predominantly spherical, with sizes ranging from 20 to 80 nm, and confirmed the presence of elemental silver. Functionally, the AI-AgNPs exhibited strong broad-spectrum antimicrobial activity, showing the highest effectiveness against *Bacillus subtilis* and *Pseudomonas aeruginosa*, with a minimum inhibitory concentration (MIC) of 0.006 µg/µL. They also displayed remarkable anti-biofilm activity, achieving up to 92% inhibition against *B. subtilis* at 0.012 µg/µL. FE-SEM analysis further revealed significant disruption of bacterial cell membranes following treatment. In addition, the nanoparticles demonstrated notable anticancer activity against human breast adenocarcinoma (MCF-7) cells, with an IC_{50} value of 14.2 ± 1.6 µg/mL, while showing no cytotoxic effects on normal Vero cells. Overall, this study highlights how nanoparticle surface chemistry and nano-bio interactions play a critical role in shaping their antimicrobial, antibiofilm, and anticancer properties.

Keywords: *Artemisia indica; Silver Nanoparticles; Green Synthesis; Antibacterial; Antibiofilm; Anticancer.*

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WHISPERS FROM THE SOIL: HARNESSING *LYSINIBACILLUS* SP. AND *OSCILLATORIA* SP. FOR SUSTAINABLE AGRICULTURE

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Abstract

The overuse of chemical fertilizers has led to declining soil health and environmental imbalances. In response, microbial inoculants and biofertilizers have gained attention as sustainable alternatives, enhancing crop productivity and soil fertility. Central to this are Plant Growth Promoting Rhizobacteria (PGPR) with traits such as hormone production, nutrient solubilization, and stress modulation. In this study soil derived *Lysinibacillus* sp. and *Oscillatoria* sp., were isolated from Kotulpur, Bankura, West Bengal, India, was evaluated for their plant growth promoting activity. The *Lysinibacillus* sp. is a mesophilic multidisciplinary soil microbe. It produces a good amount of Indole-3-acetic acid (IAA), both in the presence and absence of L-tryptophan, a key plant growth promoting hormone confirmed by Spectrophotometric analysis. *Oscillatoria* sp. also is source of biologically active component which produces a huge amount of flavonoid and phenolic compounds. Gas chromatography–mass spectrometry (GC-MS) analysis further confirmed the presence of diverse bioactive compounds in *Oscillatoria* sp. Its antioxidant potential was validated through DPPH radical scavenging and β-carotene bleaching assays. A pilot experiment with Bengal gram (*Cicer arietinum*) seeds showed enhanced seed germination and seedling growth following treatment with these two species, confirming its plant growth-promoting property. These findings indicate that the consortium of *Lysinibacillus* sp. and *Oscillatoria* sp. promotes plant growth, likely through the synergistic effects of phytohormone production and enhanced antioxidant activity, which are responsible for plant development and stress tolerance. This study establishes *Lysinibacillus* sp. and *Oscillatoria* sp. as promising biofertilizer candidates for sustainable enhancement of plant growth and soil health, offering an eco-friendly alternative to chemical fertilizers.

Keywords: *Lysinibacillus sp.; Oscillatoria sp.; Biofertilizer; Plant Growth Promotion.*

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DESIGNING AND CONSTRUCTION OF *TP53*-SPECIFIC CRISPR-CAS BASED GUIDE RNA SYSTEM FOR GENERATING A DEFINED GENOMIC MISSENSE MUTATION

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Abstract

TP53 is a frequently mutated tumor suppressor gene in human cancers, with many pathogenic alterations arising as missense mutations within its DNA-binding domain. Among these, R175H is a major hotspot mutation that disrupts Tp53 structural stability, abolishes DNA binding, exerting both loss-of-function and gain-of-function effects that drive tumor progression. CRISPR-Cas9 was chosen due to Its ability to induce targeted double-strand breaks which makes it ideal for introducing single-nucleotide substitutions via homology-directed repair (HDR) with high precision and efficiency. Here we intend to design R175H-Knock-In guide RNA using in-silico tools to ensure optimal on-target activity and minimal off-target potential. Selected gRNA is cloned into Cas9 plasmid and validated by restriction digestion and Sanger sequencing. In Future, we plan to generate single-stranded donor oligonucleotide carrying R175H variant to promote silent blocking mutations, which will be co-delivered to enhance HDR. Sequencing of edited cells will confirm successful knock-in. Then Isogenic *TP53* mutant cell panels will be used to evaluate mutation-specific drug responses.

Keywords: *TP53; R175H; CRISPR; Cas9; HDR; Missense Mutation.*

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VALORIZATION OF AGRICULTURAL RESIDUES FOR BIOSURFACTANT PRODUCTION: A GREENER ALTERNATIVE TO CONVENTIONAL SURFACTANTS

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Abstract

Agricultural waste management is crucial for agriculture-based economies like India, generating approximately 500 million tons of agricultural residue annually. These wastes are often managed through ecologically destructive practices such as open-field burning or haphazard discarding, contributing 13.72% of the nation's greenhouse gas emissions. This leads to significant environmental and public health challenges. The utilization of these agricultural residues (such as rice husks, sugarcane molasses, wheat straw) as low-cost substrates in solid-state fermentation and submerged bioprocessing offers a transformative approach to waste management. Biosurfactants are surface-active amphiphilic compounds that are biologically produced from bacteria, yeasts and fungi and are one such promising class of molecules that can be synthesized through these waste channels. In addition to their applications as food additives and preservatives, these biosurfactants have several uses in other industries, such as wastewater treatment, agriculture, pharmaceuticals, environmental protection, cosmetics, and the petroleum sector. While conventional chemical surfactants like Alkylphenol ethoxylates (APEOs) and Perfluoroalkyl substances (PFAS), derived from non-renewable petrochemicals, are economically viable, their long-term use causes irreversible ecological damage. Biosurfactants outperform these chemical surfactants by offering biodegradability, low toxicity and high efficacy but have a high cost of production, which severely restricts their use. This review evaluates a transformative 'waste-to-wealth' approach: utilizing agro-residues as low-cost substrates for the production of biosurfactants via solid-state and submerged fermentation. We compare the yield and performance, specifically Critical Micelle Concentration (CMC) and surface tension reduction of biosurfactants produced by different microbes like *Bacillus sp.* and *Pseudomonas sp.* By repurposing agricultural wastes, this integrated bioprocess mitigates the environmental burden of incineration while facilitating a transition towards 'green chemistry' and sustainable industrial surfactants.

Keywords: *Agricultural Residues; Waste-To-Wealth; Biosurfactants; Solid-State Fermentation; Submerged Fermentation; Low-Cost Substrates; APEOs; PFAS; Critical Micelle Concentration (CMC); Surface Tension Reduction; Green Chemistry; Sustainable Bioprocessing.*

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RAPID ENVIRONMENTAL SURVEILLANCE OF WHO PRIORITY PATHOGEN USING CRISPR DIAGNOSTICS

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Abstract

Environmental sources like water and soil play a crucial role in disease persistence and transmission, making them a critical target in disease surveillance. WHO critical pathogen list includes *Acinetobacter baumannii*, *Mycobacterium tuberculosis*, and *Klebsiella pneumoniae,* which contribute to the global mortality rate. *A. baumannii* leads to 40-60% mortality, *M. tuberculosis* causes 10+ million cases and 1.3+ million deaths annually, with 3-4% of new and 18-21% previously treated cases classified as MDR/RR-TB, and 6-8% of MDR cases progressing to XDR-TB, Meanwhile *K. pneumoniae* shows >50% resistance to 3rd-generation cephalosporins and ~8% to >50% carbapenem resistance, resulting in urgent requirement of environmental source surveillance. In this study, we propose a CRISPR-based diagnostic platform for detecting WHO-enlisted pathogens from environmental samples, targeting conserved and virulence-significant genes such as outO in *A. baumannii*, Rv1509 in *M. tuberculosis*, and KvgS in *K. pneumoniae*. Water and soil samples were collected aseptically, followed by nucleic acid extraction. Initial bacterial identification was done with PCR using universal 16S rRNA primers. An integrated in-silico and experimental workflow will be employed. Gene sequences were retrieved from NCBI, analysed using BLAST to select strains with 99-100% identity, and aligned using MEGA to identify conserved regions. These regions will be cloned. Pathogen-specific crRNAs (3-4 per target) were designed using CHOPCHOP. IVT was done to prepare crRNA. In case of environmental samples, the template was amplified using RPA assay. A lateral flow assay was proposed using labelled ssDNA probes like biotin-FITC, FAM-DIG, His-DNP, with collateral cleavage mediated by Cas12a. Cleaved probes inhibit antibody binding, hence no bands, while intact probes show bands. Gold nanoparticles will be used for detection, allowing for rapid, sensitive, and simultaneous detection.

Keywords: *CRISPR-Cas12a Diagnostics; Multidrug-Resistant Pathogens (MDR/XDR); Environmental Surveillance; Rapid Pathogen Detection.*

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CRISPR-BASED DETECTION OF AMR GENES IN CLINICAL SAMPLES FOR RAPID POINT-OF-CARE DIAGNOSTICS

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Abstract

Antimicrobial resistance (AMR) has been recognized as one of the major threats in present era, causing 1.27 million deaths worldwide annually, as per World Health Organization. Methicillin-resistant *Staphylococcus aureus* (MRSA) is one of the most important antimicrobial-resistant microbes, accounting for 8-10% of deaths associated with antimicrobial resistance annually. The urgent need for the rapid detection of MRSA resistance determinants cannot be overstated. In this study, we examined the *mecA* gene and the *mec* right extreme junction (MREJ) region for MRSA detection. We screened 23 clinical MRSA strains for *mecA* gene, while 35 clinical strains were examined for MREJ region for conserved domain selection. For developmental purpose, *mecA* gene was cloned and subjected to PCR screening and DNA sequencing, for confirmation. The same approach was used in cloning and validating the MREJ region. The recombinase polymerase amplification (RPA) method was employed in amplifying target DNA from clinical samples. To enable rapid and sensitive detection, we used CRISPR-Cas12a-based system. Sequence-specific CRISPR RNAs (crRNAs) were designed using CHOPCHOP, and synthesized via in vitro transcription. Cas12a nuclease guided by crRNA, binds to the complementary target DNA forming an RNP complex, leads to double-stranded breaks along with collateral cleavage of a nearby Fluorophore-quencher labelled ssDNA, separating the quencher and generating a measurable signal. This approach allows detection at extremely low concentrations (~10 copies per reaction), whereas conventional PCR methods require 10^2-10^3 copies offering a rapid, sensitive, and scalable strategy for AMR genes detection, with strong potential for point-of-care diagnostics.

Keywords: *CRISPR-Cas12a Diagnostics; Methicillin-Resistant Staphylococcus Aureus (MRSA); Meca Gene Detection; Antimicrobial Resistance (AMR); Point-Of-Care Diagnostics.*

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REVIEW ON MORPHOLOGICAL TRAITS, BIOACTIVE POTENTIAL AND SALINITY TOLERANCE IN A UNIQUE MANGROVE FERN: *ACROSTICHUM AUREUM* L.

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Abstract

Acrostichum aureum L., commonly known as the golden leather fern, is a halophytic pteridophyte widely distributed in tropical and subtropical coastal ecosystems. It represents one of the few fern species naturally established within mangrove habitats along the Indian coastline and demonstrates remarkable structural and physiological adaptations that enable survival under saline and waterlogged conditions. The present review consolidates existing knowledge on the ethnobotanical significance, phytochemical composition, morphological adaptations of *A. aureum*. Special attention is given to the plant's distinctive root system, which contributes to its ability to persist in saline substrates and fluctuating tidal environments. Comparative observations of macro- and micromorphological characteristics of the frond lamina, including the length-to-width ratio, leaf area, and stomatal index, between populations growing in mangrove and nearby non-mangrove regions of West Bengal, India, reveal adaptive variations associated with environmental stress. Additionally, the species forms symbiotic associations with Arbuscular Mycorrhizal Fungi (AMF), which enhance nutrient uptake and improve tolerance to saline conditions. Physiologically, the fern exhibits two sequential responses to salinity: an initial osmotic phase that restricts the expansion of young leaves, followed by a later ionic phase that contributes to the progressive senescence of mature tissues. Salinity tolerance is mediated through multiple mechanisms, including osmotic adjustment, selective exclusion of excessive sodium and chloride ions, and the capacity of tissues to tolerate ion accumulation. Beyond its ecological adaptations, *A. aureum* is also recognized as a source of bioactive secondary metabolites, with contraceptive, cytotoxic, wound-healing, anti-inflammatory, antioxidant, and antimicrobial properties. Collectively, these findings underscore the ecological resilience and therapeutic potential of *A. aureum*, suggesting that further investigation of its physiological strategies and phytochemical constituents may encourage future pharmacological exploration and mangrove conservation.

Keywords: *Acrostichum aureum; Mangrove Fern; Salinity Adaptation; Osmotic Stress; Ionic Regulation; AMF; Secondary Metabolites; Pharmacological Potential.*

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CIRCULATING TUMOR CELLS IN CANCER MANAGEMENT: FROM METASTATIC DRIVERS TO REAL TIME BIOMARKERS

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Abstract
Circulating tumor cells (CTCs) are rare malignant cells shed from primary or metastatic tumors into the bloodstream or lymphatic system and are central mediators of metastasis, accounting for the majority of cancer related deaths. Their clinical relevance lies in their utility as minimally invasive biomarkers in liquid biopsy, enabling real time and longitudinal monitoring of disease progression and therapeutic response, unlike conventional tissue biopsies. After intravasation, CTCs can disseminate and persist as disseminated tumor cells (DTCs), eventually forming micrometastases under favorable conditions. CTCs are recognized as independent negative prognostic indicators across multiple cancers and reflect the molecular and phenotypic heterogeneity of the primary tumor, including states of proliferation, dormancy and senescence. A defining feature of CTCs is their ability to undergo epithelial mesenchymal transition (EMT), characterized by loss of epithelial markers (e.g., E-cadherin) and gain of mesenchymal traits (e.g., vimentin), promoting motility, invasiveness and stemness. Clinically, CTC enumeration and molecular profiling offer significant potential for early detection, prognosis and personalized therapy. However, their low abundance, heterogeneity and technical challenges limit widespread clinical application. Emerging approaches integrating single cell sequencing, artificial intelligence and multi-omics are improving detection accuracy and advancing CTC based precision oncology.
Keywords: *Circulating Tumor Cells (CTCs); Metastasis; Biomarkers; Multi-Omics.*

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

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Abstract

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. 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. 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: $F = 1.41$, $R^2 = 0.016$, $p = 0.002$). 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.

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

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GREEN SYNTHESIS OF SILVER NANOPARTICLES FROM *SARCOCHLAMYS PULCHERRIMA*: ENHANCED ANTIMICROBIAL AND ANTI-BIOFILM ACTIVITY

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Abstract

Sarcochlamys pulcherrima (Roxb.) Gaud., a small evergreen tree belonging to the Urticaceae family, is widely distributed in the hilly regions of northeastern India. The plant possesses significant ethnomedicinal importance and is traditionally used by tribal communities in Assam for both therapeutic purposes and as a food source. The present study investigates the potential of *S. pulcherrima* leaf extracts in the green synthesis of silver nanoparticles (AgNPs) and evaluates their antimicrobial and antibiofilm activities. The synthesis of AgNPs was achieved using leaf extracts under controlled heating conditions to enhance biological activity. Characterization of the synthesized nanoparticles was carried out using UV-Visible and FT-IR spectroscopy. The UV-Visible spectra exhibited characteristic surface plasmon resonance (SPR) bands in the range of 403-431 nm, confirming nanoparticle formation in agreement with existing literature. Further characterization studies are currently in progress. The antimicrobial activity of the synthesized AgNPs was evaluated against both Gram-positive and Gram-negative bacteria, including *Bacillus*, *Escherichia coli*, *Staphylococcus aureus*, and *Pseudomonas aeruginosa*. The results demonstrated notable antibacterial efficacy, with zones of inhibition comparable to the standard antibiotic penicillin at varying concentrations. Additionally, the antibiofilm potential of the AgNPs was assessed against the same pathogens. The findings revealed significant inhibition of biofilm formation, indicating the effectiveness of AgNPs in combating persistent infections. In conclusion, *S. pulcherrima* leaf extract serves as an effective bioresource for the synthesis of silver nanoparticles with enhanced antimicrobial and antibiofilm properties. These findings highlight their promising potential for future applications in antibacterial therapies and biomedical fields.

Keywords: *Traditional Medicine; Silver Nanoparticles; Antimicrobial Activity, Zone of Inhibition, Antibiofilm Activity*

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COMPUTATIONAL STRATEGY TO SCREEN FOR POTENTIAL PHYTOCHEMICALS AGAINST VIRAL RDRP: A PROPHYLACTIC APPROACH FOR RESPIRATORY DISEASES

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Abstract

RNA viruses like SARC CoV 2 Virus, Rhino Virus, HMPV Virus, HIPV Virus, Influenza A Virus, RSV Virus, Nipah Virus are prevalent causes of respiratory illness in India. These viruses are highly infectious and are responsible for asymptomatic human -to- human transmission. Some of them shows high prevalence in children (less than 5 years) and some severe in comorbid adults. All these viruses can replicate and transcribe the RNA on basis of RNA template with the help of RNA dependent RNA polymerase (RDRP) inside host cell. Therefore, targeting RDRP with specific phytochemicals to avert their growth inside host cell, can be a novel approach in the prevention of respiratory disease. Three phytochemical Sarsasapogenin, Tormentic Acid and Ginsenosides were selected from Pubchem on the basis of their drug likeness and molecular docking strategy was adopted to evaluate their binding affinity for the target protein. Molecular docking analysis between target RDRP proteins and phytochemicals revealed various bond interactions (like-Hydrogen bond, Hydrophobic bond and Salt Bridges bond) between the target and the ligands, highlighting strong binding energy. The negative binding energy between the phytochemicals and RDRP protein of specific viruses indicates the inhibition of protein expression and the bond interaction also emphasized rigid binding between the ligand and target RDRP. Hence, this can be a novel therapeutic approach to prevent virus mediated respiratory illness.

Keywords: *RNA Viruses, Respiratory Infections, RNA-Dependent RNA Polymerase (RDRP), Phytochemicals, Molecular Docking, In Silico Study, Binding Affinity, Antiviral Activity, Drug Discovery.*

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TISSUE BIOPSY VS LIQUID BIOPSY: IMPACT OF BIOENGINEERING IN MODERN DIAGNOSTICS

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Abstract

Bioengineering has greatly improved in the field of medical diagnostics by introducing advanced and reliable techniques for disease detection and monitoring. One of its major applications is biopsy, which is commonly used for diagnosing various diseases, particularly cancer. Traditionally, tissue biopsy has been considered as the standard method, where a small portion of tissue is surgically removed from the affected area for examination. Although this method offers precise insights into tumor structure and characteristics, it is invasive and may cause complications such as infection and bleeding. With rapid progress in bioengineering, liquid biopsy has developed as a modern and less invasive alternative. It involves analyzing circulating tumor DNA, tumor cells, and other biomarkers found in body fluids like blood. This method eliminates the need for surgical procedures and offers a safer, quicker, and more convenient diagnostic option. Liquid biopsy also allows continuous monitoring of disease progression making it very useful in clinical settings. This study highlights the role of bioengineering by comparing tissue and liquid biopsy based on their methods, advantages, and applications. Tissue biopsy provides localized and direct information from the tumor site but is often limited by sampling bias and challenges associated with repeated procedures. In contrast, liquid biopsy enables a more comprehensive analysis of tumor-derived components circulating in body fluids, offering improved insight into tumor heterogeneity and facilitating continuous disease monitoring. Modern bioengineering techniques such as polymerase chain reaction and next-generation sequencing have increased the accuracy and efficiency of liquid biopsy. In conclusion, bioengineering has revolutionized diagnostic methods, and liquid biopsy shows great potential in supporting personalized medicine and improving patient care in the future healthcare system. This approach also supports early diagnosis, better treatment planning, and improved patient outcomes in systems.

Keywords: *Bioengineering, Tissue Biopsy, Liquid Biopsy, Circulating Tumor DNA, Cancer Detection, Personalized Medicine.*

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MOLECULAR ORCHESTRATION OF BIOLUMINESCENCE: QUORUM SENSING SIGNALING AS A NOVEL TARGET FOR ANTI-VIRULENCE THERAPY

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Abstract

Bioluminescence in marine bacteria like Vibrio fischeri is known for population-reliant microbial communication, regulated by quorum sensing (QS). Here, the bacterial cells synthesize and release small signaling molecules called autoinducers (AIs). As there is a rise in bacterial populations, the concentration of AIs also increases, and once it reaches the threshold, autoinducer molecules bind to transcriptional regulators (e.g., LuxR) to turn on the lux operon, resulting in the emission of light (bioluminescence). Interestingly, many human pathogens, including Pseudomonas aeruginosa, perform similar QS mechanisms to manage the expression of virulence factors such as toxins, enzymes, and biofilms. In P. aeruginosa, there are two receptors, LasR and RhlR, in the Las and Rhl systems, respectively, to detect autoinducers (3-oxo-C12-HSL and C4-HSL, respectively) and control gene interaction networks by controlling pathogenicity. This whole process allows bacterial populations to create coordination among them and infections only after reaching a sufficient number. Recent research studies reported some quorum quenching (QQ) strategies, which break and create interruptions in QS without killing bacteria. QQ acts by inhibiting autoinducer production, degrading autoinducers via enzymes such as lactonases or acylases, or blocking receptor binding. These interruptions prevent bacteria from understanding population concentration and coordination ability among them, thus suppressing virulence factor expression and allowing the host immune system to clear the infection naturally. Unlike traditional antibiotics, quorum quenching decreases particular pressure of resistance and thus also provides a novel anti-virulence therapeutic approach. Understanding the molecular orchestration of quorum sensing in both bioluminescent and pathogenic bacteria serve as a bridge between marine microbiology and clinical science and highlights promising strategies for managing infectious diseases through targeted communication interference.

Keywords: *Quorum Sensing, Quorum Quenching, Bioluminescence, Vibrio fischeri, Pseudomonas aeruginosa, Lux Operon, LasR/RhlR Receptors, Lactonases & Acylases, Biofilm.*

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PRIME EDITING: THE NEXT GENERATION OF CRISPR TECHNOLOGY

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Abstract

In modern medicine, the development of precise gene-editing tools has become essential for designing effective therapies to correct pathogenic mutations in the human genome. Many genetic disorders are now known to arise from small changes in DNA, particularly single base pair mutations. Therefore, advanced genome-editing technologies are being developed to accurately modify these mutations and improve treatment strategies. Among the available techniques, the CRISPR-Cas9 system is the most widely used genome-editing tool. It was first applied for genome editing in 2012 and has since transformed research in medicine, genetics, and agriculture. This technology consists of two main components: a single guide RNA (sgRNA), which directs the system to a specific target gene, and the Cas9 enzyme, an endonuclease that cuts DNA. The sgRNA binds with Cas9 to form a complex that recognizes a specific DNA sequence near a protospacer adjacent motif (PAM) site in the genome. Once the target site is identified, Cas9 creates a double-strand break in the DNA, which is then repaired by the cell's natural DNA repair mechanisms. Although CRISPR-Cas9 is powerful, it relies on double-strand break repair pathways that may not always be ideal for precise gene correction in therapeutic applications. To overcome these limitations, newer technologies such as base editing and prime editing have been developed. These advanced methods allow more accurate and efficient editing without causing double-strand DNA breaks, making them promising tools for rectifying genetic mutations. Overall, CRISPR-based technologies, including base and prime editing, have significantly expanded the possibilities of genome engineering and continue to play a crucial role in advancing gene therapy, biological research, and crop improvement.

Keywords: *Base Editing; CRISPR /Cas9; Primer Editing; Prime Editing Derived Techniques*

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ROLE OF ARTIFICIAL INTELLIGENCE AND POINT-OF-CARE DIAGNOSTICS IN IMPROVING DIABETES MANAGEMENT

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Abstract

Diabetes mellitus is a long-term metabolic disorder that affects millions of people across the world. If not managed properly, it can lead to serious complications such as cardiovascular disease, kidney damage, stroke, and diabetic foot ulcers. Although diabetes cannot yet be completely cured, early detection and regular monitoring play a crucial role in controlling the disease and improving patients' quality of life. In recent years, the integration of Artificial Intelligence (AI) with point-of-care (POC) diagnostics has begun to transform the way diabetes is managed. These technologies allow healthcare providers to obtain quick and reliable information, helping them make timely and personalized treatment decisions. AI systems can analyze real-time data collected from glucose meters, continuous glucose monitoring devices, wearable sensors, and electronic health records. By identifying patterns in this data, AI can help predict fluctuations in blood glucose levels and assess the risk of potential complications. Machine learning models also assist clinicians in the early detection of diabetes, selecting appropriate treatment strategies, and adjusting insulin doses more accurately, thereby reducing the chances of human error. At the same time, AI-enabled POC diagnostic devices provide immediate test results, which is particularly useful in primary healthcare centers and remote or resource-limited settings where rapid decision-making is essential. In addition, AI-based mobile applications and smart wearable devices support patients in managing their daily routines by tracking diet, physical activity, and medication adherence. This encourages greater patient involvement in their own care. Overall, combining AI with POC diagnostics supports more precise, accessible, and patient-centered diabetes management while strengthening preventive healthcare strategies.

Keywords*: Artificial Intelligence; Diabetes mellitus; Insulin; Machine Learning; Point-of-Care.*

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PLANT-BASED DIET: A SUSTAINABLE APPROACH TO HEALTHY LIVING

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Abstract

A plant-based diet is a dietary pattern that emphasizes foods derived mainly from plants, such as fruits, vegetables, whole grains, legumes, nuts, and seeds. These foods provide several essential nutrients, fiber, vitamins, minerals, and antioxidants that contribute to overall well-being and is thus suitable for supporting a healthy lifestyle. Furthermore, numerous plant-derived compounds have traditionally been used for the management of various health conditions, including inflammation, metabolic disorders, viral infections, and other diseases. Adopting a plant-based diet promotes balanced nutrition by encouraging the consumption of whole, nutrient-rich foods thereby reducing the intake of processed and pro-inflammatory foods. This approach can ameliorate energy levels, mental clarity, and overall quality of life. It also plays significant role in weight management, blood glucose regulation, other chronic diseases, and immunomodulation. A properly planned plant-based diet can supply important nutrients such as protein, calcium, and vitamin D that are necessary for maintaining healthy bones and body functions. However, individuals following this diet should pay attention to nutrients like iron and zinc, which can be obtained from foods such as whole grains, beans, lentils, and other legumes. Many people who follow a strict plant-based diet choose to avoid red meat, poultry, and sometimes dairy products. Common forms of plant-based diets include vegan, vegetarian, and whole-food plant-based diets. Despite its many health benefits, a plant-based diet may have some challenges if not carefully managed, such as the risk of certain nutrient deficiencies or digestive concerns. Therefore, maintaining a well-planned diet and limiting fast foods and highly processed items is essential. Overall, a balanced plant-based diet can effectively promote health and help reduce the risk of chronic diseases.

Keywords: *Plant-Based Diet; Nutritional Health; Disease Prevention; Balanced Nutrition; Chronic Disease Management.*

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DESIGN OF PEPTIDE NANOPORES FOR ANTIMICROBIAL APPLICATIONS

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Abstract
The rapid rise of antibiotic resistance poses a critical threat to global health and economic stability, significantly diminishing the efficacy of existing therapeutics. This challenge necessitates the development of innovative strategies, including nanotechnology-driven approaches. Among these, small antimicrobial peptides capable of forming transmembrane nanopores have emerged as promising candidates for next-generation antibiotics. These peptides self-assemble within lipid membranes to form barrel-shaped, cylindrical nanopores containing central water-filled ion channels with diameters of a few nanometers. Such structures disrupt membrane integrity, enabling rapid leakage of intracellular contents and leading to swift bacterial cell death. Importantly, as these peptides target the bacterial membrane-an essential and conserved cellular component-the likelihood of resistance development is considerably reduced. Despite their potential, naturally occurring nanopore-forming peptides are rare. De novo peptide design therefore represents a powerful strategy to expand this class of antimicrobial agents. However, experimental characterization of these metastable and dynamic membrane assemblies remains challenging at high resolution. In this context, computer simulations provide critical atomic-level insights into peptide-membrane interactions, self-assembly mechanisms, and pore stability. Such computational approaches can guide the rational design of peptide nanopores with optimized structural and functional properties. Overall, peptide nanopores offer a promising alternative to conventional antibiotics, with significant potential for combating multidrug-resistant infections and improving global health outcomes.

Keywords: *Antibiotic Resistance; Antimicrobial Peptides; Peptide Nanopores; Peptide Design; Computer Simulation.*

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EFFECTS OF NATURAL PRODUCTS ON HUMAN HEALTH

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Abstract
Natural products obtained from plants, animals, and mineral sources have long been utilized for supporting human health and managing diseases. They are an integral part of traditional healthcare systems such as Ayurveda and other indigenous practices. These substances include herbs, fruits, vegetables, and spices that contain various bioactive compounds contributing to their health-promoting effects. A key benefit of natural products lies in their nutritional importance. They supply essential nutrients like vitamins, minerals, proteins, and dietary fiber required for proper body functioning. Anti-inflammatory, antimicrobial, antiviral, and antioxidant activities are effects help in strengthening the immune system on human body. the risk of chronic illnesses such as heart disease, diabetes, and certain types of cancer by reducing oxidative damage in cells. Another advantage is that natural products are often perceived as safer alternatives to synthetic drugs when used appropriately, as they generally produce fewer side effects. They also contribute to improving digestion, enhancing immunity, and maintaining overall health. Common natural remedies such as turmeric, ginger, garlic, and honey are widely used in daily life for their healing benefits.
Keywords: *Natural Product; Human Health; Immunity; Herbal Medicine; Bioactive Compounds*.

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INTEGRATION OF ARTIFICIAL INTELLIGENCE IN MODERN CYTOPATHOLOGY FOR CERVICAL CANCER DETECTION

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Abstract
Cervical cancer remains one of the most common cancers affecting women worldwide, particularly in low- and middle-income countries where access to regular screening is limited. Cytopathology, especially the Papanicolaou (Pap) smear test, plays a crucial role in the early detection of precancerous and cancerous cervical lesions. However, manual screening of cytology slides can be time-consuming and subject to human error due to large sample volumes and variability in interpretation. The integration of Artificial Intelligence (AI) into modern cytopathology has emerged as a promising approach to improve the accuracy, efficiency, and consistency of cervical cancer detection. AI-based systems use machine learning and deep learning algorithms to automatically analyze digital Pap smear images, identify abnormal cellular features, and assist cytopathologists in diagnosis. Advanced technologies such as convolutional neural networks (CNNs) enable rapid detection of atypical squamous cells and high-grade lesions with high sensitivity and specificity. Additionally, AI-assisted screening platforms can prioritize high-risk cases, reduce workload, and support large-scale population screening programs. The integration of AI with digital cytology therefore represents an important advancement toward more reliable, cost-effective, and accessible cervical cancer screening and early diagnosis.
Keywords*: Artificial Intelligence, Cervical cancer screening, Papanicolaou smear cytology, Deep Learning, Convolutional Neural Networks.*

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ANTIOXIDANT AND ANTI-INFLAMMATORY EFFECTS OF NATURAL PRODUCTS ON HUMAN HEALTH

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Abstract

Natural products have long been used to support health and well-being. Many plant-based foods and herbs contain compounds with strong antioxidant and anti-inflammatory properties that help protect the body. When harmful molecules known as free radicals accumulate in excess, they can damage cells and contribute to the development of diseases such as cancer, cardiovascular disorders, and certain neurological conditions. Natural compounds found in plants and foods can help neutralize these free radicals and maintain cellular health. Among these beneficial compounds are polyphenols, flavonoids, vitamins, and bioactive molecules such as curcumin. Curcumin, a major component of turmeric, is widely recognized for its antioxidant and anti-inflammatory effects. It helps reduce oxidative stress by neutralizing reactive oxygen species and supporting the body's own defense mechanisms. In addition, curcumin can regulate inflammatory responses by inhibiting specific pathways involved in inflammation. As a result, it may help lower inflammatory markers, including C-reactive protein, and strengthen the body's ability to manage inflammatory conditions. Other natural sources, such as tea, ginger, garlic, and foods rich in resveratrol, also contribute to reducing oxidative stress and inflammation. These natural compounds can support the immune system and help regulate biological signals that trigger inflammation, thereby promoting overall health and potentially lowering the risk of chronic diseases. Overall, natural products play an important role in maintaining health because of their antioxidant and anti-inflammatory activities. They may help protect cells, reduce damage caused by oxidative stress, and control inflammation. However, further research is needed to better understand the appropriate dosages, bioavailability, and long-term safety of these natural compounds in human health.

Keywords*: Natural Product; Antioxidants; Anti-Inflammatory; Phytochemicals; Curcumin; Oxidative Stress; Human Health.*

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ROLE OF NATURAL PRODUCTS IN REDUCING OXIDATIVE STRESS ASSOCIATED WITH ALZHEIMER'S DISEASE

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Abstract

Alzheimer's disease, the most common form of dementia worldwide, significantly impairs a patient's capacity to perform daily tasks. The most recent WHO data estimates that 35.6 million individuals worldwide suffered from dementia in 2010; by 2050, that number could have tripled. Plant products are known to provide a wide range of unique and creative secondary metabolites. From ancient times, various continents have used plant-based natural products as a treatment for Alzheimer's disease. Certain Plants produce novel bioactive substances with distinctive structures, including quinones, lactones, phenols, alkaloids, steroids, terpenoids, and other compounds. Among other things, these separated metabolites exhibit antibacterial, antioxidant, anti-inflammatory, antiviral, and anti-Alzheimer's characteristics. The primary focus of this review is the published research articles regarding the anti-Alzheimer's effects of natural plant products, such as seeds, fruits, roots, etc. Among the naturally occurring substances that are analysed based on their structure and classification are alkaloids, peptides, terpenoids, and steroids. The classification, occurrence, and bioactivities of these natural chemicals from various natural sources.

Keywords: *Alzheimer's Disease; Phytochemicals; Neuroprotective Natural Products; Plant Secondary Metabolites; Anti-Alzheimer's Activity; Bioactive Compounds.*

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NATURAL PRODUCTS AND THEIR ROLE IN COLON DISEASES AND COLORECTAL CANCER: A THERAPEUTIC REVIEW

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Abstract

Natural products obtained from plants, herbs, and other biological sources play an important role in maintaining human health. They are widely used due to their safety, affordability, and effectiveness in preventing and managing chronic diseases, especially those related to the digestive system. Colorectal cancer (CRC) is one of the most commonly occurring cancers and is often linked to inflammation of the colon and early undetected tumors growth. Inflammatory bowel diseases, IBD, such as Crohn's disease and ulcerative colitis (UC), increase the risk of CRC, which is caused by gut-brain axis imbalance, stress, and changes in gut microbiota. UC is an immune-mediated inflammatory disease, while colon cancer develops due to genetic mutations, chronic inflammation, unhealthy lifestyle, and family history. Although treatments like chemotherapy and immunotherapy are available, a complete cure for CRC is still lacking. Flaxseed, which contain major amount of Omega-3 fatty acid serves as a good option to control inflammation. Mucilage along with soluble fiber in flaxseeds together acts as a protective layer over the intestinal lining which may help with irritation and healing. It contains lignans which is a rich source of antioxidant, has strong anti-inflammatory and bioactive properties that soothes the gut health in diseases like ulcerative colitis and most importantly may slow down the abnormal cell growth. Micronutrients present in it such as - magnesium, phosphorus, selenium helps tone down certain enzymes and cytokines which stay overactive during flare-ups and helps in maintaining a healthy gut microbiome. It promotes the growth of beneficial bacteria, improve digestion, reduce infections, and nurture the colon cells. Natural products provide a safe, cost-effective, and beneficial approach to maintaining colon health and preventing diseases. Therefore, this review emphasizes its potential as a good functional food in IBD management.

Keywords: *Colorectal Cancer; Ulcerative Colitis; Natural Products; Anti-Inflammatory Activity; Inflammatory Bowel Disease.*

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ADVANCING SUSTAINABLE AGRICULTURE WITH NANOFERTILIZERS

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Abstract

Nano-fertilizers (NFs) are nutrient fertilizers encapsulated within a nanomaterial of organic or metallic components utilized for the purpose of controlled and stable release of fertilizers for enhanced and sustainable plant growth. Considered as an emerging field of agricultural research to boost up food grain production, it provides suitable alternative to negate the harmful effects of chemical fertilizers. Though crop productivity is increased, extensive application of chemicals doesn't provide viable long-term strategy, disturbs soil mineral balance, diminishes soil fertility and affects food chains. Nano-fertilizers are eco-friendly and can improve nutrient use efficiency by targeted delivery through plant root systems. Nano-materials can be synthesized from metals, metal oxides, organic polymers or carbon-based materials, with characteristic size of 1-100 nm, high surface area and high availability for absorption. NFs fit the model of enhanced Nutrient Use Efficiency (NUE) with maximum absorption leaving behind minimal environment footprint. Furthermore, integration of nanotechnology with soilless hydroponics and aeroponics offers an environment friendly and productive substitute to traditional methods, speeding up crop yield, seed germination, plant metabolism, and protecting plant from diseases. NFs can be applied in powder or liquid form to alter crop tissue function and prolong microgreen shelf life by modulating immune system. Despite these advantages, a concern regarding their long-term environmental and food chain effects with economic feasibility foresees further investigation.

Keywords: *Nano-Fertilizers; Crop Yield; Sustainable; Nutrients; Efficiency.*

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ADVANCEMENTS IN NANOMEDICINE FOR CANCER THERAPY: INTEGRATING TARGETED DELIVERY, STIMULI-RESPONSIVITY, AND PRECISION ONCOLOGY

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Abstract

The field of oncological nanomedicine has evolved from a theoretical concept into precision medicine, altering the prospect of cancer diagnosis and therapy. Typical chemotherapy is often limited by its non-specific distribution, which, eventually results in significant toxicity and therapeutic concentrations within the tumor. Nanomedicines (typically defined as materials that engineered at the 1-100 nanometer scale), report these challenges by capitalizing the unique physiology of the tumor microenvironment. Essential to this model, is the Enhanced Permeability and Retention (EPR) effect. Where, the disorganized and vasculature malignant tissue allows the passive buildup of nanoparticles, while impaired lymphatic drainage guarantees their continuous presence at the site. Recent research has shifted focus towards active targeting and responsive systems to overcome the biological barriers that limit the passive diffusion. By functionalizing nanoparticle surfaces with various ligands such as antibodies, peptides, these platforms can achieve high-affinity binding to receptors on cancer cell membranes, by enabling receptor-mediated endocytosis and reducing "off-target" accumulation in healthy tissues. The development of stimuli-responsive nanocarriers allows controlled drug release triggered by internal factors, such as the acidic pH of the tumor and external stimuli like near-infrared light or magnetic fields. In 2026, the integration of nanomedicine with immunotherapy has emerged as a potent frontier; lipid nanoparticles (LNPs) and biomimetic carriers are now being used to deliver mRNA vaccines and modulators that reprogram the immunosuppressive tumor microenvironment and effectively converting "cold" tumors into "hot" tumors that are susceptible to the host's immune system. Despite of various challenges of large-scale manufacturing and the heterogeneity of the EPR effect in human patients, nanomedicine continues to bridge the gap between innovation and clinical efficacy while offering a pathway towards highly personalized, less toxic, and more effective cancer management strategies.

Keywords: *Nanomedicine; Targeted Drug Delivery; Precision Oncology; EPR Effect; Nanotherapy; Immunotherapy; Toxicity.*

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SMART NANOCARRIERS FOR SUSTAINABLE AGRICULTURE

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Abstract

The global distribution of plant pathogens is a major threat to agricultural sustainability. The existing agrochemical practices are obstructed by factors such as non-specific distribution, tissue penetration, environmental degradation, and lack of target site delivery, making it difficult to control plant pathogens, such as *Xanthomonas campestris*. Plant disease is being caused by climate change, but existing treatments don't work because they aren't site-specific. A new nanocarrier system called Surface Ligand-Engineered Nanoparticles for Targeted Delivery to Stomata (SENDS) was developed to address these issues. The SENDS system uses porous metal-organic frameworks (MOFs), in particular Zeolitic Imidazolate Framework-8 (ZIF-8) nanoparticles, that are functionalized with modularly assembled protein ligands in order to provide specificity to the delivery of antimicrobial compounds to the stomatal guard cells of plants (i.e., primary points of entry for plant pathogens). The ligands were rationally engineered such that they would provide optimal targeting of the stomata on diverse species, including *Arabidopsis thaliana* (mouse ear cress), *Brassica rapa* (Chinese cabbage), *Vicia faba* (broad bean), *Oryza sativa* (rice), and *Hordeum vulgare* (barley). The application of SENDS to plants resulted in a 20-fold reduction in *Xanthomonas campestris* (major crop pathogen) colonization compared to non-targeted foliar applications of SENDS containing an encapsulated antimicrobial plant alkaloid. Furthermore, quantitative measurements of the impact of SENDS on stomatal function indicated that SENDS enhance plant disease resistance by improving plant defence without compromising the normal functioning of stomatal cells, thereby supporting physiologically-correct stomatal aperture movement and photosynthetic function. This nanobiotechnology approach provides a targeted mechanism for enhancing plant disease resistance and contributes knowledge for future nanocarrier design to create more resilient and sustainable agricultural systems through disruption of colonization by plant pathogens in their earliest stages and establishing biocompatibility with minimal effect on the regulation of stomatal aperture.

Keywords: *Surface Ligand-Engineered Nanoparticles (SENDS); Precision Agrochemical Delivery; Plant-Pathogen Interactions; Nanobiotechnology in Agriculture; Antimicrobial Delivery Systems; Crop Disease Resistance.*

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COMPARATIVE ANALYSIS OF T3SS AND T6SS IN *VIBRIO PARAHAEMOLYTICUS* FOR CONTROLLING FOOD-BORNE DISEASES

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Abstract

Vibrio species are gram-negative bacteria that belong to the Vibrionaceae family. *Vibrio parahaemolyticus* one of the major foodborne pathogens among 12 pathogenic species. Pathogenicity of this species is mediated by two specialized secretion systems, such as Type III Secretion System (T3SS) and Type VI Secretion System (T6SS). These two secretion systems differentially mediate host-pathogen interactions, fitness, and disease progression. The T3SS Secretion System is a highly conserved injectisome that directly translocates effector proteins into host cells, affecting cytoskeletal architecture, signal transduction pathways, and other cellular processes, whereas, the T6SS Secretion System is a contractile nanomachine that mediates inter-bacterial antagonism in support of bacterial fitness establishment and maintenance in the host by injecting antibacterial effectors into target bacteria. T6SS also responsible for host-pathogen interactions mediations. We used different in-silico approaches for comparative analysis of genomic and transcriptomic data to understand the expression profiles, mechanisms, and outcomes of these two secretion systems in a simulated host environment. It has been found that the T3SS is directly associated with virulence because it is highly active in the early stages of infection. In contrast, T6SS is associated with virulence indirectly because it increases bacterial fitness and survival. T3SS and T6SS can be targeted to control infection quickly by reducing damage to host cells. T6SS can also be targeted to control infection by reducing persistence of infection. This study is likely to contribute to the understanding of the mechanisms of Type III and VI Secretion Systems. This approach can be utilized for understanding secretion systems by targeting for the development of new therapeutics for Vibrio species and other pathogenic bacteria.

Keywords: *Vibrio parahaemolyticus, T3SS, T6SS, Virulence Mechanisms, Host-Pathogen Interactions, Therapeutic Targets.*

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RATIONAL EVALUATION OF NANOPARTICLE-MEDIATED TARGETED DRUG DELIVERY IN CANCER THERAPY

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Abstract

Nanoparticle systems used for drug delivery provide advanced methods which improve cancer treatment results by increasing drug delivery to specific locations in the body and maintaining drug presence there. Nanocarriers which have a size between 1 and 100 nanometers enable longer blood circulation times while they deliver drugs directly to cancer cells and protect healthy tissues from harm. Some nanoparticles exhibit intrinsic tumor-targeting properties whereas other nanoparticles need surface functionalization with ligands such as antibodies or peptides in order to achieve selective recognition of cancer cells. Liposomes and polymeric nanoparticles and gold nanoparticles and dendrimers represent different nanocarrier systems which effectively lower treatment-related toxicity to patients. The successful development of nanoparticle-based therapeutics has reached the experimental stage but researchers still encounter challenges when introducing these treatments into clinical settings. The main obstacle exists because nanoparticles show different patterns of behavior in various tumor types and among different patient populations. Many nanocarriers depend on enhanced permeability and retention EPR effect to reach tumors but this mechanism behaves differently across cancer types so it cannot serve as a universal method for all tumors. The active targeting methods face performance issues which lead to biological effects that researchers did not want to see. The current challenges involve complex formulations which require difficulties in large-scale manufacturing and safety testing and potential internal accumulation of nanoparticles in human organs including the liver and spleen. Researchers aim to design nanomaterials which have better control and predictability through advanced manufacturing techniques and patient-specific tumor biology integration into their treatment design process. All nanoparticle-based drug delivery systems show high potential for future medical applications.

Keywords: *Nanoparticle-Based Drug Delivery; Targeted Cancer Therapy; Tumor Microenvironment; Enhanced Permeability and Retention (EPR) Effect; Surface-Functionalized Nanocarriers; Nanomedicine.*

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AI-DRIVEN NEOANTIGEN PRIORITIZATION FOR MRNA-BASED CANCER VACCINES IN TRIPLE-NEGATIVE BREAST CANCER (TNBC)

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Abstract

Triple-negative breast cancer (TNBC) is one of the most aggressive types of breast cancer, distinguished by lack of estrogen receptors (ER), progesterone receptors (PR) and human epidermal growth factor receptor 2 (HER2) expression. As a result, therapeutic options are restricted and patients frequently experience negative clinical results. Conventional treatments including chemotherapy can harm healthy tissues and have serious adverse effect due to their lack of selectivity. Furthermore, issues such as medication resistance and tumour heterogeneity diminish therapy efficacy and raise the risk of disease recurrence. The absence of robust personalized treatment strategies further constrains therapeutic success. Artificial intelligence (AI) and machine learning (ML) have recently emerged as essential tools in cancer immunotherapy. By evaluating huge amounts of genomic and transcriptomic data, these techniques aid in faster and more accurate identification of tumour-specific neoantigens. They also enhance immunogenicity assessment, HLA binding prediction and mutation detection which are critical for developing the design of personalized treatment strategies. mRNA vaccines emerged as a viable treatment option for TNBC due to their ability to deliver tumour-specific neoantigens and elicit tailored immune responses. This method enables rapid and more exact identification of important antigens, facilitating the creation of personalized immunotherapies. The integration of AI-driven neoantigen discovery with mRNA vaccine technology represents a compelling approach for TNBC, with the potential to enhance treatment precision, improve clinical outcomes, and achieve durable therapeutic responses.

Keywords: *Triple-Negative Breast Cancer, Tumour Neoantigens, Artificial Intelligence, mRNA Vaccines, Personalized Oncology, HLA Binding Prediction, Cancer Immunotherapy.*

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FROM FARM TO FOOD CHAIN: THE HIDDEN DANGERS OF CHEMICAL PESTICIDES

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Abstract

The widespread application of chemical pesticides in current agricultural practices has raised significant concerns regarding environmental safety and human health. Pesticides, particularly organochlorine compounds such as Endosulfan, Aldrin, Dieldrin, and DDT, are known for their long-term stability and tendency to bioaccumulate within the food chain. As a result, they adversely affect biodiversity, degrade water quality, and compromise food safety, ultimately impacting human populations at higher trophic levels. This review work examines such chemicals, including Metproxybicyclone, Goltrevo (a bio-insecticide), and BICOTA, to highlight their persistence in the environment and associated toxicological risks. Evidence from existing literature suggests that exposure to these pesticides is associated with a range of health issues, such as non-Hodgkin lymphoma, Parkinson's disease, dermatitis, chronic respiratory disorders, neuropathy, nausea, vomiting, and breathing difficulties. Furthermore, these compounds have been shown to contribute to the development of antibiotic resistance in microorganisms, posing additional public health challenges. This comprehensive review discusses the environmental and health impacts of these chemicals. In addition, various remediation strategies are discussed, including physicochemical approaches like photodegradation and advanced oxidation processes, as well as biological methods such as bioremediation. Overall, the study underscores the necessity for a paradigm shift toward safer and more sustainable pest management practices. Adoption of these strategies is essential to minimize ecological damage, safeguard human health, and promote sustainable agricultural development.

Keywords: *Organochlorine Pesticides; Bioaccumulation; Environmental Toxicology; Pesticide-Induced Health Effects; Bioremediation; Sustainable Agriculture.*

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TARGETING NEURODEGENERATIVE DISORDERS WITH PHYTOCHEMICALS: A MECHANISTIC APPROACH

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Abstract

Phytochemicals are bioactive compounds that have an extensive role in treating chronic diseases or noncommunicable diseases (NCD) like cardiovascular diseases, type-2-diabetes mellitus, cancer, kidney, bone and liver diseases and neurodegenerative disorders (NDDs). World Health Organization (WHO) recognizes that 70-75% of global death is caused due to NCD, mainly cancer, NDDs and cardiovascular diseases. This review highlights the role of phytochemicals in preventing neurodegeneration, with emphasis on their sources, therapeutic benefits, underlying mechanisms of action and associated limitations. Neurodegeneration is defined by the progressive loss of neuronal integrity and cognitive function, which is characterized by diseases like Alzheimer's Disease (AD), Parkinson's Disease (PD), Huntington Disease (HD), amyloid lateral sclerosis and multiple sclerosis. Neurodegeneration mainly occurs due to mitochondrial dysfunction, protein misfolding, apoptosis, and oxidative stress. Phytochemicals exhibit antioxidative, anti-inflammatory and anti-amyloidogenic properties which helps in treating these diseases to some extent. Flavonoids, carotenoids, terpenoids, phenolic derivatives, and alkaloids can prevent NDDs by targeting neurotrophins and enhancing cognitive function. These phytochemicals, obtained from medicinal herbs, trees, grains, leaves, fruits, flowers, and vegetables, exhibit therapeutic potential through antioxidative, anti-inflammatory, and anti-amyloidogenic activities. Compounds such as ladostigil (AD and PD), maslinic acid (reduces oxidative stress), curcumin (inhibits inflammation), rotigotine (advanced PD), epigallocatechin-3-gallate (reduces oxidative stress), and resveratrol, berberine, and quercetin (prevent plaque accumulation) contribute to neuroprotection. However, despite their promising therapeutic potential, the clinical translation of phytochemicals is often constrained by factors such as low bioavailability, limited target specificity, and insufficient data on long-term safety and toxicity.

Keywords: *Alzheimer's Disease, Parkinson's Disease, Oxidative Stress, Neurotrophins, Amyloid Lateral Sclerosis, Phytochemicals.*

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CESTRUM NOCTURNUM: PHYTOCHEMICAL COMPOSITION AND THERAPEUTIC POTENTIAL IN THE MANAGEMENT OF LIFESTYLE DISEASES

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Abstract

Cestrum nocturnum, a medicinal plant belonging to the family Solanaceae, is widely used in traditional medicinal systems due to its diverse therapeutic properties. The plant contains various phytochemical constituents such as alkaloids, flavonoids, glycosides, phenolic compounds, tannins, and essential oils, which are responsible for its biological and pharmacological activities. These bioactive compounds exhibit significant antioxidant activity through free radical scavenging activity as measured using DPPH and ABTS assays. They show significant anti- inflammatory activity by inhibiting cytokine mediators like TNF-α and IL-6, enzymes like COX-2 and 5-LOX and prostaglandin synthesis. The plant also shows antimicrobial activity against various bacterial and fungal pathogens and demonstrates immunomodulatory properties by enhancing immune response. Natural products play an important role in the prevention and management of lifestyle diseases such as diabetes mellitus, hypertension, cardiovascular diseases, obesity, and chronic inflammatory disorders. Studies have reported that *Cestrum nocturnum* exhibits antidiabetic activity by reducing blood glucose levels and inhibiting alpha-amylase activity, and also promotes wound healing by increasing collagen formation and accelerating tissue regeneration. The antioxidant and anti-inflammatory properties of the plant help in reducing oxidative stress and inflammation, which are major contributing factors in lifestyle-related diseases. This review highlights the phytochemical composition and therapeutic applications of *Cestrum nocturnum* and emphasizes its potential role as a natural therapeutic agent in the management of lifestyle-related diseases and the promotion of human health.

Keywords: *Phytochemicals, Antioxidant Activity, Anti-Inflammatory Activity, Lifestyle Diseases, Therapeutic Applications.*

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BACTERIAL HEAVY METAL RESISTANCE: A TOOL FOR SUSTAINABLE BIOREMEDIATION

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Abstract

Rising levels of toxic waste, particularly heavy metals from mining, are harming ecosystems, polluting water, and posing risks to human health. These heavy metals are also found in our surroundings due to both natural and anthropogenic activities, the natural activities include volcanic eruptions and rock weathering and the anthropogenic activities are mining and smelting, industrial waste water disposal, certain agricultural practices. Another major anthropogenic factor is the rising accumulation of e-waste, which has led to heavy metal pollution. Heavy metals are naturally occurring elements with high density and distinctive chemical properties that render them both essential and hazardous to living organisms. These heavy metals affect various environmental and biological systems. Lead impacts neurological health and brain development due to industrial pollution. Arsenic found in contaminated groundwater poses long term health risks like cancer. Even though copper and iron are essential in trace amounts, in critical concentrations they can cause cellular damage and oxidative stress in humans and plants. Mercury affects aquatic ecosystems and accumulates to cause neurological disorders in organisms. A bacterial strain named PRS01 was isolated from the soil samples collected at Durgapur oil refinery and was characterised to be best functional at high salinity, pH and temperature. The tolerance efficiency of the isolated strain was evaluated by examining its resistance to lead, arsenic, mercury, copper, and iron at concentrations known to be toxic to human health. Such microbial resistance can be applied in bioremediation strategies to clean contaminated environments. This approach is particularly useful for reclaiming polluted agricultural lands, improving soil quality, and supporting safe and sustainable crop production.

Keywords: *Heavy Metal Contamination, Bacterial Resistance, Bioremediation, Lead Toxicity, Arsenic Contamination, Mercury Bioaccumulation, Copper Toxicity, Sustainable Environmental Management.*

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ORIGINS OF BIOCHAR, APPLICATION & BENEFITS: REVIEW

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Abstract

Biochar is a specialized form of charcoal produced by heating organic waste like wood chips, agricultural residues, or manure in a high-temperature, low-oxygen environment. While it looks like ordinary charcoal, its purpose is very different: it is primarily used as a soil amendment to improve fertility and as a powerful tool for carbon sequestration. In modern times, biochar has gained attention due to its wide range of applications across agriculture, environmental science, and biotechnology. In agriculture, biochar improves soil structure, increases water retention, enhances nutrient availability, and promotes beneficial microbial activity. Its porous nature and large surface area make it an effective adsorbent for removing pollutants, including heavy metals and organic contaminants, from water and soil. Additionally, biochar is used in waste management, composting, and as a carrier material for enzymes and plant growth-promoting microorganisms. One of the most significant benefits of biochar lies in its potential for climate change mitigation. By converting biomass into a stable form of carbon, biochar contributes to long-term carbon sequestration, reducing the release of greenhouse gases into the atmosphere. It helps in recycling agricultural waste into a value-added product such as activated carbon, specialized organic fertilizers, soil potting mixes, animal feed additives for construction materials, supporting a circular bio-economy. Biochar also reduces soil acidity, minimizes nutrient leaching, and can decrease the need for chemical fertilizers. In conclusion, biochar represents a sustainable and multifunctional material with roots in ancient practices and relevance in modern environmental challenges. Its diverse applications and ecological benefits make it a promising tool for achieving sustainable agriculture, environmental remediation, and climate resilience.

Keywords: *Biochar; Carbon Sequestration; Soil Amendment; Environmental Remediation; Agricultural Sustainability; Adsorption of Pollutants.*

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BANACORE: *UPCYCLING BANANA WASTE BIOMASS FOR PAPER FABRICATION*

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Abstract

Bananas are considered one of the most important economic crops in the entire world. Bananas are cultivated in over 135 countries and consumed by everyone around the globe. During the process of banana harvesting and consumption, huge amounts of waste materials are generated, including the stem, leaves, flowers, and peels. A major portion of this waste is either disposed of in the fields or burned. Around 60% of the banana plant is considered waste after the bananas are collected. This waste is mostly not being utilized. This waste could be utilized for the production of biocomposite and biodegradable materials. Studies have also revealed that banana waste is considered a source of bioactive compounds that are beneficial for health due to antibacterial, anti-inflammatory, and antioxidant activities. Consequently, the biomass preferred especially banana pseudostem and banana peel rich in cellulose, lignin, hemicellulose, fibre, pectin can be implemented for biopolymer and biomaterial production. Banana pseudostem comprises significant cellulose content (20-44%), making it a sustainable raw material for extraction of high-purity cellulose using chemical and ultrasound-assisted treatments. Researches have shown that with the use of alkaline treatment with NaOH and sonication, cellulose purity of almost 99% is achievable. Moreover, the use of enzymatic and oxidation-based extraction techniques will further optimize the properties of cellulose. On the other hand, banana peel is also an important source of polysaccharide known as pectin. Pectin is used in the food and pharmaceutical industry. With regard to the use of extraction techniques, nowadays, the use of techniques known as ultrasound-assisted extraction and microwave-assisted extraction is being used due to faster results and efficiency. These techniques have shown an increase in the yield of pectin. Moreover, with regard to the optimization of the extraction process, factors such as the ripeness of the banana also play an important role. Therefore, the use of optimization techniques is also being done. Moreover, the valorization of banana waste is also an important factor in the production of cellulose and pectin-based materials, thus promoting the development of waste management.

Keywords: *Biocomposite, Biodegradable, Biopolymer, Anti-inflammatory, Antioxidant, Valorization, Sustainable Bioeconomy.*

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IMPLICATIONS OF COPD ONSET AND PROGRESSION ON MICROBIOME DYSBIOSIS: CURRENT STATE AND PROSPECTS

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Abstract

Rapid deterioration of air quality indices owing to the industrialization in the urban and peri-urban areas, vehicular emissions, and other voluntary exposures to toxicants such as tobacco smoking etc. has led to a spike in the oro-respiratory diseases such as Asthma, Chronic Obstructive Pulmonary Disease (COPD), various forms of oro-respiratory cancers amongst others. Among these, COPD is a major cause of mortality worldwide which impacts lungs, cardiovascular, gastrointestinal, and immune systems. While COPD is largely characterised by chronic bronchitis and emphysema, an altered microbiome has also been reported which may act as both biomarker as well as modulator of the disease. There is a diverse array of microbiomes in the airway which get altered as the disease progresses. In early stages, Firmicutes, actinobacteria and proteobacteria populate the microbiome. In patients with Acute Exacerbation Chronic Obstructive Pulmonary Disease (AECOPD), beneficial bacteria like *Prevotella* and *Veillonella* are replaced by harmful strains such as *Haemophilus influenzae*, *Moraxella catarrhalis* and *Pseudomonas aeruginosa.* Reports also indicate COPD outcomes are affected by the gut lung axis, a two-way communication. Bacteroides are abundant in the gut of healthy people compared to COPD patients. Experimental fecal microbiota transplantation has shown positive results in restoration of the gut microbiome balance and slowing emphysema. Lactic acid bacteria (LAB) like *Lactobaccilus rhamnosus* lowers pro-inflammatory cytokines which provides protection and improves airway passage. This primarily works by reduction of neutrophilic inflammation by indole-3-acetic acid (IAA) which inhibits or slows the process of lung function degradation by macrophage epithelial communication which is mediated by IL-22. These microbial patterns is important in prediction of types of diseases and clinical outcomes. Microbiome based therapies and optimization of effective delivery systems may be one of the promising approaches in the prevention of acute exacerbations (AECOPD) and improvement in long term outlook for COPD patients.

Keywords: *oro-Respiratory Disease, COPD, AECOPD, Microbiome, Inflammation, Emphysema, Gut Lung Axis.*

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FROM ELECTRONS TO MINERALS: THE FUTURE OF BIOREMEDIATION

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Abstract

Groundwater is an essential source of drinking water and irrigation for the entire planet, but widespread contamination of groundwater by Nitrate (NO_3^-) and Arsenic (As) poses serious health concerns, including methemoglobinemia and systemic cancers. Conventional physicochemical methods of remediation are environmentally unviable, thus making Electron Transport System (ETS) mediated bioremediation an innovative solution to groundwater pollution. The process of bioremediation of groundwater by Electron Transport System (ETS) relies on the metabolic diversity of microorganisms to link the nitrogen and iron cycles. In the Electron Transport System (ETS) process, microorganisms function as catalysts for redox reactions. Denitrifying microorganisms such as *Pseudomonas, Thiobacillus, Bacillus, Paracoccus*, etc., use nitrate as an electron acceptor. Through enzyme-mediated redox reactions, nitrate reductase, and nitrite reductase, nitrate (NO_3^-) is converted to harmless dinitrogen gas (N_2). Simultaneously, Nitrate-Dependent Fe(II) Oxidizing Bacteria (NDFO) such as *Acidovorax sp.* BoFeN1, besides catalysing denitrification, also oxidize Fe^{2+} to Fe^{3+} through enzyme-mediated redox reactions. This leads to the production of Hydrous Ferric Oxides (HFO) through biomineralization, which in turn acts as a geochemical curtain to immobilize arsenic. This structural integrity is maintained through the presence of Extracellular Polymeric Substances (EPS), which are secreted by *Gallionella* and *Leptothrix*. These EPS function as biological templates that stabilize iron nanoparticles to ensure that surface areas are maintained at levels that are effective for sequestering pollutants. Furthermore, Bio-electrochemical Systems (BES), which contain cathodic biofilms, ensure that there is always an electron flux. This eliminates the need for any external chemicals. By optimizing these microbial pathways, ETS-driven bioremediation offers a sustainable and efficient approach to restoring groundwater ecosystems.

Keywords*: ETS, Groundwater Contamination, Biomineralization, BES, HFO, NDFO, EPS, Iron Nanoparticles, Nitrogen and Iron Cycles, Denitrifying Microorganisms, Enzyme-mediated Catalysis, Geochemical Curtain, Sustainable Bioremediation.*

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THE IMPACT OF DIETARY POLYPHENOLS ON GUT MICROBIOTA AND CARDIOVASCULAR HEALTH

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Abstract

While chronic stress acts as a silent catalyst for cardiovascular disease, epidemiological studies suggest consumption of polyphenol rich foods play a crucial role in modulating gut microbiota and promoting cardiovascular health. Polyphenols act as prebiotics, fostering the growth of beneficial gut bacteria (*Bifidobacterium, Lactobacillus*) while inhibiting harmful pathogens (*Clostridium*). This modulation can improve gut barrier function and reduce metabolic endotoxemia. The degradation of polyphenols by the gut microbiota produces various beneficial metabolites, such as short-chain fatty acids (SCFAs), equine (from daidzein), and urolithins (from ellagic acid) which contributes in anti-inflammation, lipid reduction, and blood-pressure regulation. For example, Dietary anthocyanins from berries are fermented by gut bacteria (like Bifidobacterium) into phenolic acid metabolites, which significantly improve arterial flexibility and lower blood pressure. The ellagitannins rich foods promotes gut bacteria (*Roseburia faecis, Faecalibacterium prausnitzii* etc.) that produces Urolithin A, which enhances mitochondrial function in blood vessels and reduces arterial inflammation, effectively boosting cardiovascular health. Polyphenols also reduce systemic oxidative stress by neutralizing reactive oxygen species (ROS). By improving lipid profiles, reducing blood pressure, and preventing platelet aggregation, polyphenols lower risk of heart attacks and strokes. For instance, High-polyphenol olive oil increases *Lactobacillus* and *Bifidobacterium* levels, which enhances HDL's "cholesterol efflux capacity" to actively remove plaque-forming fats from artery walls. High intake of polyphenols linked to 15-25% lower risk of coronary heart disease (CHD), hypertension. Polyphenols promote inhibition of harmful compounds like Trimethylamine N-oxide (TMAO) leading to a reduced risk of plaque formation in the coronary arteries and slower atherosclerosis progression. These cardioprotective effects are mediated through key molecular pathways including NF-κB, Nrf2, MAPK, and JAK–STAT signaling pathways, along with gut microbiota-derived SCFA signaling. Taken together, dietary polyphenols offer a promising avenue for promoting cardiovascular health through their beneficial effects on gut microbiota and direct cardio-protective mechanisms.

Keywords: *Dietary Polyphenols; Gut Microbiota Modulation; Cardiovascular Health; Short-Chain Fatty Acids (SCFAs); Oxidative Stress And Inflammation; Atherosclerosis Prevention.*

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THE GUT-BRAIN AXIS: MICROBIAL MODULATION OF MENTAL HEALTH

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Abstract

The gut-brain axis (GBA) is an intricate, bidirectional network that links the central nervous system with the gastrointestinal tract via neuronal, endocrine, immunological, and metabolic pathways. Advance research highlights the critical role of gut microbiota in regulating brain function, behavior, and overall mental health. The human gut hosts trillions of microorganisms, predominantly from Firmicutes and Bacteroidetes phyla, which contribute to physiological homeostasis and influence neurodevelopment and cognitive processes. Dysbiosis, or changes in microbial composition, has been closely connected with psychiatric diseases such as major depressive disorder (MDD), anxiety disorders, and autism spectrum disorders. Key metabolites produced by gut microorganisms include short-chain fatty acids (SCFAs) and neurotransmitters like serotonin and GABA, which affect mood and behaviour via numerous signalling pathways. Dysbiosis can disrupt intestinal barrier integrity, resulting in systemic inflammation, stimulation of the hypothalamic-pituitary-adrenal (HPA) axis, and subsequent neuroinflammation, all of which can impair brain function. Furthermore, gut microbiota regulates immune responses by influencing cytokine production, which plays a significant role in the pathophysiology of mental disorders. Emerging therapeutic approaches, including probiotics, prebiotics, and symbiotic, show potential in restoring microbial balance and alleviating psychiatric symptoms. Additionally, growing evidence suggests that psychotropic medications can alter gut microbial diversity, indicating a bidirectional interaction between microbiome composition and drug efficacy. Thus, GBA represents a critical interface integrating microbial, neural, and immune signals. Understanding its mechanisms provides crucial insights into the development of mental illnesses and opens new avenues for microbiome-based therapies. Further research is essential to translate these findings into effective clinical interventions.

Keywords: *Gut-Brain Axis; Gut Microbiota; Dysbiosis; Mental Health; Probiotics; Microbiome-Based Therapy.*

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TARGETING BIOFILM FORMATION IN ESKAPE PATHOGENS: EMERGING THERAPEUTIC STRATEGIES

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Abstract

ESKAPE pathogens include *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* species. These bacteria cause serious hospital infections. They often resist many antibiotics. These pathogens form biofilms. Biofilms are groups of bacteria that live together in a protective layer. This layer helps them survive harsh conditions. It blocks antibiotics from reaching the cells. It also helps bacteria share resistance genes. In addition, it protects them from the human immune system. Targeting biofilm formation offers a useful treatment strategy. One method blocks quorum sensing. Quorum sensing is the way bacteria communicate and control biofilm growth. Compounds like furanones act as quorum sensing inhibitors. It reduces biofilm formation without strong pressure for resistance. Enzymes like proteases and DNases degrade the protective matrix. This process allows antibiotics to enter and work better. Nanotechnology also improves treatment. Liposomes and nanoparticles deliver drugs directly to biofilms. They increase drug stability and release it slowly. New therapies also show promise. Antimicrobial peptides kill bacteria and disturb biofilms. Bacteriophage therapy targets specific bacteria and disrupts their structure. Natural compounds (essential oils and plant polyphenols) reduce biofilm formation. Combination therapy works well. It uses biofilm-disrupting agents with antibiotics. This approach improves treatment outcomes. In conclusion, biofilm formation plays a major role in ESKAPE infections. Understanding and targeting biofilms help fight antibiotic resistance and can develop effective treatments. Current study encompasses therapeutics for targeting biofilm formation in ESKAPE pathogens.

Keywords: *ESKAPE Pathogens, Biofilm Formation. Antimicrobial Resistance, Quorum Sensing Inhibition, Novel Therapeutics.*

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INTEGRATED NEUROENGINEERING APPROACHES TO BRAIN REPAIR USING BIOELECTRONIC INTERFACES, STEM CELL-BASED SCAFFOLDS, AND NANOTECHNOLOGY

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Abstract

Neural engineering applies quantitative engineering principles to understand, repair, replace, or enhance neural function, offering promising avenues for brain repair after trauma, stroke, or neurodegenerative disease. Although the adult brain exhibits limited intrinsic regenerative capacity, advances in neuroengineering seek to harness neural stem cells, neuroplasticity, and bioelectronic modulation to restore lost function. This work reviews key methodologies and challenges in contemporary neuroengineering for brain repair. Deep Brain Stimulation (DBS) employs chronically implanted electrodes to deliver targeted electrical pulses, effectively re-tuning dysfunctional circuits in movement disorders such as Parkinson's disease and epilepsy. Brain-Computer Interfaces (BCIs) decode neural activity to control external devices, functionally bypassing damaged pathways and enabling motor restoration in paralyzed individuals. Complementary approaches include nanotechnology-based constructs, such as carbon nanotubes and nanowires, designed to interface at the single-neuron level to guide axonal growth and enable localised drug delivery, as well as stem cell-laden scaffolds that support the survival, integration, and network formation of transplanted neural stem cells. Despite substantial progress, major limitations persist. Mechanical mismatch and foreign-body responses to rigid implants provoke glial scarring and signal degradation. Ethical concerns surrounding identity, agency, privacy of neural data, and potential neurohacking remain insufficiently resolved. Furthermore, the high cost and restricted availability of these technologies risk exacerbating healthcare inequities. In this abstract, we conclude that the future of brain repair lies in adaptive, soft bioelectronic systems capable of dynamic bidirectional communication with evolving neural circuits. By more closely matching the brain's mechanical and biological properties, next-generation neuroengineering platforms may transform neurological damage from a largely irreversible condition into a tractable engineering problem.

Keywords: *Neural Engineering; Brain-Computer Interfaces (BCIs); Deep Brain Stimulation (DBS); Neural Regeneration And Repair; Neuroplasticity; Bioelectronic Medicine.*

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SYNERGISTIC ACTION OF PLANT PHYTOCHEMICALS AGAINST MULTIDRUG RESISTANT PATHOGENS

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Abstract

Antibiotic resistance in pathogenic microorganisms is a critical global public health concern, driven by mechanisms such as target modification, enzymatic degradation, efflux pumps, and biofilm formation. This study explores plant-derived phytochemicals as potential alternatives or adjuncts to conventional antibiotics against multidrug-resistant (MDR) pathogens. Phytochemicals including allicin (garlic), plumbagin (Plumbago spp.), and polyphenols (green tea) were extracted using solvent-based methods. For the first two, those were crushed in the mortar with a pestle and mixed with 100ml of cold ethanol slowly to extract the proteins. These mixtures were placed in refrigerator for overnight. Next day these solutions were reduced to 35ml in magnetic stirrer. The entire crude solution was poured in MCTs. These were centrifuged at 10000rpm for 10 minutes. Then the debris form a pellet under the MCTs. The supernatant was collected in a falcon and used for future experiments. For green tea bags, those were dipped in CH3OH. Then the beaker with the solution was incubated at 4 degrees for 24 hours with occasional agitation. The extracts were partially purified through centrifugation and subjected to chromatographic characterization using thin-layer chromatography (TLC) and column chromatography to confirm the presence of bioactive metabolites. Preliminary profiling indicated successful extraction of phytochemical compounds with diverse metabolite signatures. These compounds are known to interfere with resistance mechanisms such as efflux pump activity, quorum sensing, and biofilm formation. The findings suggest that plant-derived phytochemicals hold significant potential as natural antimicrobial agents or synergistic enhancers of existing antibiotics, offering a promising strategy to combat MDR pathogens.

Keywords: *Antibiotic Resistance; Multidrug-Resistant (MDR) Pathogens; Phytochemicals; Antimicrobial Activity; Efflux Pump Inhibition; Biofilm Inhibition*

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DESIGNING NOVEL CLINICALLY RELEVANT BIOMARKERS FOR ACCELERATED WOUND HEALING AND REGENERATION

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Abstract

The economic expenditure of wound healing and management exceeds 5 billion pounds per annum for the National Health Service (NHS). This coupled with limitations of the current treatment regime opens up a promising opportunity for improvisation of wound management strategies using novel biomarkers and modulators in the process. Based on healing time and pathogenesis, wounds can be classified into acute or chronic categories and hence may require different medical interventions for progressive healing. Intermediate or deep and extended skin wounds prevent the *status quo* restoration, resulting in hypertrophic scars or keloids. This warrants a need for biomarkers for detection and devising effective strategies for amelioration of similar covert infections. Biomarkers are indicators of pathogenesis and help determine the inflammatory, proliferative, or infectious state of a wound to aid healing. IL-6 and IL-10 primarily act as an early marker for sepsis and a chronic infection, respectively. The molecules, like IL-10 may be integrated into hydrogel to create functional units, that provide a medium for both healing and sensing (superficial biosensors). Studies have indicated the use of microorganisms/microbiome of wound microenvironment in ameliorating chronic wounds and their potential as biosensors. Recent reports have indicated a prominent role of *Dunaliella bardawil,* a unicellular microalga, to act as biomarker and accelerate wound healing and regeneration simultaneously. In conditions such as Diabetic Foot Ulcers (DFU) a higher abundance of *Escherichia* and *Prevotella* was reported while the predominant presence of *Acinetobacter* and *Morganella* was reported in non-DFU wounds. Healed DFUs were characterized by higher levels of Alcaligenes and *Corynebacterium* while increased abundance of *Enterococcus* and *Serratia* was reported in worsening conditions. Taken together, the microbiome can potentially act as a biomarker as well as modulators in wound healing.

Keywords: *Wound Healing Biomarkers; Chronic Wounds; Cytokines; Wound Microbiome; Diabetic Foot Ulcers (DFU); Hydrogel-Based Biosensors.*

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ENGINEERED MICROBES AS TOOLS FOR MICROPLASTIC BIOREMEDIATION: MECHANISMS AND APPLICATIONS

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Abstract

Micro-plastic pollution has emerged as a significant global environmental and health issue. These particles accumulate in soil through multiple routes, such as agricultural activities, breakdown of larger plastic materials, and disposal of wastewater. Once present, they can interfere with food chains and create potential health hazards for living organisms. Bioremediation offers a sustainable and effective approach to address MP contamination. It involves the use of soil microbes, particularly bacteria and fungi, capable of degrading microplastics. They produce enzymes like laccase, esterase, peroxidase, oxidoreductase, and hydrolases that de-polymerize the larger polymer chains into smaller compounds such as carbon dioxide, water and methane. Among these, *Ideonella sakaiensis* has emerged as a significant bacterium known for its ability to degrade polyethene terephthalate (PET), a widely used plastic in bottles and packaging materials. It produces specialized enzymes that break the ester bonds present in PET. This enzymatic degradation highlights the potential of microbial systems in addressing plastic pollution. Our review work summarizes the sources and transport of microplastics, its impact on the environment and emerging approaches for microplastic remediation.

Keywords: *Microplastic Pollution; Bioremediation; Microbial Degradation; Enzymatic Depolymerization; Ideonella Sakaiensi; Polyethylene Terephthalate (PET).*

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ASTROBIOLOGY: EXOPLANETARY BIOSIGNATURES AND MIRRORING THE COSMOS

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Abstract

Following the establishment of NASA in 1958, the organization embarked on an effort to answer unsolved questions about origin of life, evolution, distribution of life in the universe and to detect the presence of life, beyond Earth. Astrobiology serves as a multidisciplinary field, transforming the search for extraterrestrial life from speculations to strong theoretical probability, backed by scientific data. Regarding habitable domains, astrobiology investigates potential locations beyond the periphery of Earth, that could support life, such as Mars, Europa, and exoplanets, through research on extremophiles, found in the austere environments on Earth. Europa, one of Jupiter's 95 moons, is believed to harness a vast ocean under its thick crust of ice, which poses as one of the potential hotspots to pinpoint extraterrestrial life. The extremophilic resilience of *Deinococcus radiodurans, Halobacterium salinarum,* and tardigrades provides a biological analog for potential life forms that can possibly thrive on Europa and Mars. Catalogued exoplanets, largely found by NASA missions, such as TESS (Transiting Exoplanet Survey) and Kepler Space Telescope, help in providing planetary models capable of potentially sustaining life. Anoxygenic phototrophs and hyperthermophiles are used as potential models for life on catalogued Kepler exoplanets. Biosignatures, which are substances that provide scientific evidences of past or present forms of life and crucial for locating extraterrestrial life, are detected through imaging, mass spectrometry, or remote sensing using telescopes to capture organic molecular patterns, such as atmospheric methane and carbon dioxide. Molecular biosignatures, such as lipid biomarkers, serve as molecular fossils, which are very helpful in detecting life in outer space. With advancing methodologies in this field, the gap between the Great Silence and the potential discovery of a resilient life form, progressively closes in.

Keywords: *Biosignatures; Extremophiles; Habitability; Planetary Analogs; Deinococcus Radiodurans; Halobacterium Salinarum; Tardigrades; NASA.*

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HARNESSING BACTERIAL LACCASES FOR SUSTAINABLE REMOVAL OF XENOBIOTIC POLLUTANTS

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Abstract
Industrial growth and modernization have caused a problem. They have spread chemicals like synthetic pollutants all over the environment. Many of these chemicals are called Endocrine Disrupting Chemicals. They are really bad for the environment and all the living things in it. Bisphenol A is a chemical used to make plastic. It is found in a lot of waste. Another chemical called Reactive Yellow 15 is used in the textile industry to color fabrics. The old ways of cleaning up these chemicals are not very good. They are expensive. Can even create more pollution. So, we need to find ways to clean up the environment. We are looking for eco-friendly ways to do this. One way is to use a kind of helper called bacterial laccases. These helpers are better than others because they work well in different conditions. They can even work in hot temperatures. Bacterial laccases are good at breaking down kinds of bad chemicals. They can even break down chemicals that're hard to get rid of. When we add some helpers to the mix these bacterial laccases can break down bad chemicals like Bisphenol A and Reactive Yellow 15 very quickly. In fact, they can break down than 90 percent of these chemicals in just one day. This is a good way to clean up industrial waste. It can even be used in wastewater treatment plants. This study is important because it can help us find ways to clean up the environment. We want to use helpers like bacterial laccases to make the environment cleaner and healthier. We want to create a sustainable future for our planet. The use of laccases and other biocatalytic technologies can help us get rid of bad chemicals like xenobiotics. This can help us move towards a circular economy that is good, for the environment.
Keywords: *Bacterial laccases; Xenobiotic Degradation; Bioremediation; Sustainable Future; Biocatalytic Technologies; Wastewater Treatment.*

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FOOD WASTE THAT FIGHTS BACK: ANTIMICROBIAL POWER OF PUMPKIN BYPRODUCTS

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Abstract

Natural matrices have been increasingly investigated as sources of bioactive molecules because of their technological applications in food and cosmetic products as well as their advantages for human health and food waste management has become an important concern also. Pumpkin (*Cucurbita spp.*) processing generates large amounts of byproducts including peels, seeds, and fibrous strands, these materials may contain valuable bioactive compounds. This study evaluates the antioxidant and antimicrobial potential of pumpkin byproducts. Hydroethanolic extracts were prepared from peels, seeds, and fibrous strands. Phenolic compounds were analyzed using HPLC-DAD-ESI/MS. Antioxidant activity was assessed using TBARS and OxHLIA assays, while antimicrobial activity was tested against selected foodborne microorganisms using the minimum inhibitory concentration (MIC) method. Cytotoxicity was also evaluated to ensure safety. According to the findings, of all the byproducts, pumpkin peels had the highest phenolic content. This suggests that bioactive chemicals are abundant in peels. One important molecule was found to be (-)-Eepicatechin. This compound is known for having potent antioxidant qualities. Seed extracts showed strong antioxidant activity. This may be due to the presence of phenolics and other bioactive molecules. In some cases, the activity was comparable to standard antioxidant compounds. This suggests that pumpkin seeds could serve as an effective natural alternative. The extracts also inhibited the growth of microorganisms including *Staphylococcus aureus* and *Yersinia enterocolitica*. This indicates that pumpkin byproducts possess antimicrobial activity against common foodborne pathogens. The effect was mainly bacteriostatic, means that the extracts were able to stop or slow down bacterial growth. They did not completely kill the bacteria. This activity may be due to the presence of phenolic compounds. These compounds are known to interfere with microbial cell functions. This suggests that the extracts are safe at the tested concentrations, as no cytotoxic effects were observed. Pumpkin byproducts show potential as natural antioxidant and antimicrobial agents. Their use may help reduce waste and support sustainable practices.

Keywords: *Pumpkin Byproducts (Cucurbita spp.); Phenolic Compounds; Antioxidant Activity; Antimicrobial Activity; HPLC-DAD-ESI/MS Analysis; Food Waste Valorization.*

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ANTIOXIDANT-BASED DISEASE MODULATION AND THE THERAPEUTIC POTENTIAL OF AYURVEDIC *RASAYANA* HERBS

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Abstract

Ayurveda adopts a disease-preventive and health-promotive paradigm that considers the integrated functioning of the body, mind, and spirit in the maintenance and restoration of health. Within this holistic framework, classical Ayurvedic physicians developed specific dietary regimens and therapeutic interventions aimed at delaying the onset of aging and rejuvenating overall physiological function. This comprehensive revitalization process is termed *Rasayana chikitsa* (rejuvenation therapy). *Rasayana* formulations have traditionally been employed in the management of a wide spectrum of clinically heterogeneous disorders that, from the perspective of modern biomedicine, may not share an obvious common pathophysiological basis. Many plants categorized as *Rasayana* exhibit pronounced antioxidant properties; however, only a limited subset has been subjected to rigorous pharmacological and mechanistic evaluation. To date, more than 100 disease conditions, including rheumatoid arthritis, haemorrhagic shock, cardiovascular disorders, cystic fibrosis, metabolic syndromes, neurodegenerative diseases, gastrointestinal ulceration, and AIDS, have been implicated as being mediated, at least in part, by reactive oxygen species (ROS) and oxidative stress. This review briefly summarizes the role of free radicals and oxidative damage in the pathogenesis of these disorders. It further examines Ayurvedic *Rasayana* plants with potent antioxidant activity, highlighting their traditional therapeutic indications and the current understanding of their mechanisms of antioxidant action. Fifteen key *Rasayana* plants are discussed in detail, and additional species with comparatively limited experimental characterization are also noted.

Keywords: *Rasayana chikitsa; Ayurveda; Oxidative Stress; Reactive Oxygen Species (ROS); Antioxidant Phytochemicals; Neurodegenerative and Metabolic Disorders.*

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SUSTAINABLE BIOFUELS PRODUCTION USING HOUSEHOLD AND INDUSTRIAL WASTES

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Abstract
Interest in biofuel production from household and industrial waste increases due to the rising demand for sustainable energy and the environmental problems caused by waste accumulation. This approach reduces dependence on fossil fuels and helps manage waste effectively while producing renewable energy. Organic wastes such as food scraps, agricultural residues, used cooking oil, and industrial byproducts serve as abundant and low-cost raw materials for biofuel production. Different biological and thermochemical methods convert waste into useful biofuels like bioethanol, biodiesel, and biogas. Anaerobic digestion produces biogas from organic matter, while microbial fermentation converts carbohydrate-rich waste into bioethanol. Transesterification converts waste oils into biodiesel. These processes reduce landfill burden and lower greenhouse gas emissions. They also improve energy recovery from waste materials. Waste-to-energy technology supports the concept of a circular economy by turning waste into valuable resources. But large-scale implementation impairs due to variability in feedstock. It requires process optimization to reduce economic barriers. Enzyme engineering, bioengineered microbial cell factories help to address aforementioned pitfalls to ameliorate biofuel production. Current study depicts ameliorative impact of sustainable biofuel production from household and industrial wastes. It focuses on environmental, economic, and social benefits. This approach supports energy security and promotes sustainable development by encouraging efficient waste management and renewable energy generation. Future research focuses on improving conversion efficiency and developing scalable systems to make waste-based biofuel a strong alternative to conventional energy sources.

Keywords: *Biofuels, Waste Valorisation, Renewable Energy, Microbial Fermentation, Circular Economy.*

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UNLOCKING THE PHARMACOLOGICAL POTENTIAL OF SECONDARY METABOLITES THROUGH NANOBIOTECHNOLOGY

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Abstract

Drug development depends on secondary metabolites. These are natural bioactive compounds. Microbes, plants, and marine organisms produce them. They show strong medicinal value. However, these compounds face many challenges. They have poor solubility. They show low bioavailability. They are often unstable. They degrade quickly. These problems limit their use in medicine. Nanobiotechnology offers a practical solution. It combines nanotechnology with biological systems. It helps scientists design advanced drug delivery systems. These systems include nanoparticles, liposomes, dendrimers, and nanoemulsions. These carriers improve stability and solubility. They also help in targeted drug delivery. As a result, they increase drug efficiency and reduce toxicity. Nanocarriers improve compounds like curcumin, resveratrol, and alkaloids. They enhance pharmacokinetic behaviour. They allow slow and controlled drug release. Nanobiotechnology also supports site-specific drug delivery. This approach reduces side effects. It improves treatment accuracy. It works well for diseases like cancer, neurological disorders, and infections. It also allows the delivery of multiple compounds together. This improves therapeutic results. Green nanotechnology promotes eco-friendly production of nanoparticles. It uses biological sources. This method supports sustainable and cost-effective processes. Artificial intelligence and high-throughput screening speed up drug discovery. This study highlights the role of nanobiotechnology. It improves the use of secondary metabolites. It helps develop safer, more effective, and targeted drug delivery systems.

Keywords: *Secondary Metabolites, Nanobiotechnology, Drug Delivery, Bioavailability, Nanocarriers.*

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IN VITRO EVALUATION OF ANTIBACTERIAL ACTIVITY OF METHANOLIC EXTRACTS FROM POTENTIAL PLANT SPECIES

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Abstract

The emergence of antimicrobial resistance has led to increased investigation of therapeutic agents, and natural sources are being explored for this purpose. Plant-derived compounds, which are rich in bioactive compounds, are potential sources of antimicrobial activity. The current investigation aims to assess the antimicrobial activities of certain plant materials, such as leaves of *Nyctanthes arbor tristis*, *Bacopa monnieri*, and *Tradescantia pallida*, along with peels of *Punica granatum*, against bacterial strains. The plant materials were collected, washed, shade-dried, and subjected to methanolic extraction to obtain bioactive compounds. The crude extracts were investigated for their antimicrobial activity using the Minimum Inhibitory Concentration (MIC) method against certain bacterial isolates. The results revealed that certain plant extracts possessed varying levels of antibacterial activity. Among these, pomegranate peel and *Nyctanthes* leaf extracts possessed strong levels of antimicrobial activity. The *Nyctanthes* leaves when tested on *Staphylococcus aureus* showed 1.6 cm zone of inhibition at 50 mg/ml concentration followed by 1cm zone at 25mg/ml and no such zones at 12.5 and 6.25 mg/ml concentrations and the peels of pomegranate showed a zone of inhibition - 2cm at 50 mg/ml, 1.7 cm at 25mg/ml, 1.4 cm at 12.5 mg/ml and 1cm at 6.25 mg/ml. The methanolic extracts of the leaves of *Bacopa* and *Tradescantia* were also treated on the bacterial strains of *Salmonella typhi* and *Pseudomonas* but no such results have yet been observed. The antimicrobial activity of these extracts can be attributed to the presence of phytochemicals such as flavonoids, tannins, alkaloids, and saponins, which may act through multiple mechanisms including disruption of cell membranes and inhibition of essential metabolic processes.

Keywords: *Antimicrobial Activity, Plant Extracts, Methanolic Extraction, Minimum Inhibitory Concentration, Phytochemicals.*

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ENZYMATIC BIOREMEDIATION OF TEXTILE POLLUTANT AZO DYES USING LACCASE: A SUSTAINABLE APPROACH FOR WATER POLLUTION CONTROL

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Abstract

This study shows how white rot fungi can remove color from synthetic dyes using the laccase enzyme. Azo dyes are major pollutants because they are persistent organic compounds primarily discharged from textile, leather, and paper industries. They pollute water by creating intense colors that limits sunlight penetration, which affects the aquatic life, reducing oxygen level and breaking down into mutagenic, carcinogenic, aromatic amines that endanger aquatic life and human health. White rot fungi are well known for their outstanding ability to produce extracellular oxidative enzymes like laccase, lignin peroxidase, lip, horseradish. Laccase enzyme was purified from bacterial culture by filtration and dialysis. It was further purified using DEAE ion exchange chromatography. Its size and activity were analyzed using SDS-PAGE and staining methods. Molecular weight loss determined by comparing with standard protein. Purified laccase was tested for decolorizing five textile dyes using ABTS as a mediator. Decolorization was monitored via UV-visible spectrophotometry. Post-degradation products were extracted with ethyl acetate and analyzed using HPLC and GCMS to identify metabolites with compounds confirmed via the NIST library to access phytotransformation.

Keywords: *Laccase-Mediated Dye Decolorization; White Rot Fungi; Azo Dye Biodegradation; Enzymatic Bioremediation; ABTS-Mediated Oxidation; HPLC-GCMS Metabolite Analysis.*

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BIOSORPTION AND DECOLORIZATION OF TEXTILE DYES USING A NOVEL BIOCOMPOSITE MATERIALS

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Abstract

Nowadays as industries grows rapidly thus releasing large amount of different organic and inorganic wastes like synthetic dyes into water bodies. These dyes create serious environmental and health problems. Many dyes are toxic, non-biodegradable, and difficult to remove with traditional treatment methods. This study examines a new biocomposite material for dye removal from water. Researchers prepare the biocomposite by combining natural biomaterials with functional components. This combination improves adsorption capacity and structural stability. Scientists perform batch experiments under different conditions. They test pH, temperature, contact time, and initial dye concentration. The results show that the biocomposite strongly attracts dye molecules. It removes color from water in a short time. Adsorption studies follow the Langmuir isotherm model. This result suggests monolayer adsorption on a uniform surface. Kinetic analysis follows a pseudo-second-order model. This finding indicates that chemisorption controls the process. The material also shows good reusability. It works well over several adsorption and desorption cycles. This characteristic makes it cost-effective and sustainable for our environment. Different interactions like electrostatic attraction, hydrogen bonding, and surface complexation helps to remove the dye. These mechanisms improve the efficiency of the process. This study shows that the biocomposite works as an eco-friendly solution for dye-contaminated wastewater. It offers high efficiency, low cost, and good stability. In conclusion, this biocomposite provides a practical method for environmental cleanup. It supports sustainable wastewater treatment and offers strong potential for large-scale industrial use.

Keywords: *Biosorption, Textile Dye Decolorization, Biocomposite Material, Environmental Remediation, Adsorption Kinetics.*

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SCOOP SMART LIVE LIGHT: A PROMISING SOLUTION FOR PREMIUM CALORIE RICH ICE-CREAM

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Abstract

Commercially available ice cream products offered by prominent brands are highly appreciated for their taste and flavor. Nevertheless, these products are high in calorie content and contain high amounts of sugar, making them inappropriate for consumption by people suffering from diabetes, obesity, and those who wish to maintain a fitness lifestyle. Although a number of brands are offering low-calorie and sugar-free ice cream products, these are highly priced and hence may not be within the reach of the masses. In this context, a low-calorie, cost-effective ice cream product containing zero sugar was formulated, targeting fitness enthusiasts, gym-goers, and people suffering from diabetes. The formulated product contains natural and nutrient-rich ingredients such as soya seeds, bananas, soft dates, raisins, cashew nuts, almonds, low-fat milk, cocoa powder, and dark chocolate, which are known to improve the nutritional content while adding natural sweetness and a creamy texture to the product without adding refined sugar to it. A controlled laboratory study was designed, and ten different individuals aged 40-50 years, including five diabetics and five non-diabetics, were chosen for the study. The formulated ice cream and a premium low-calorie commercial ice cream product were provided to both groups of individuals at equal amount, and the levels of the glucose level were measured before and after consumption of each product. The results showed that the glucose levels for both diabetic and non-diabetic individuals increased slightly higher for the commercial product compared to the formulated ice cream product. The results indicate that the formulated product is highly acceptable and lies within the moderate range, proving that the formulated ice cream product is an appropriate alternative for the masses, effectively meeting the requirements of health-conscious individuals.

Keywords*: Low-Calorie Cost-Efficient Ice Cream; Fitness Enthusiasts; Blood Sugar Level.*

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STUDY OF THE PREVALENCE AND RESISTANCE PROPERTY OF *E. COLI*: SEARCHING NOVEL PLANT

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Abstract

Generally, *E. coli* is present in our intestine and also acts as a pollution indicator species. *E. coli* is an emerging pathogen of the greatest concern as it is the leading cause of various severe infections of the stomach, urinary tract, ear, wounds, etc. in humans. Billions of *E. coli* are secreted per day from a healthy person through faeces. Therefore, *E. coli* acts as a pollution indicator species. So, increasing rates of antibiotic resistance among *E. coli* is another foremost concern worldwide. This problem is more traumatic when water bodies are getting contaminated by faecal pollution and inappropriate use of antibiotics that leads to the emergence of multi-drug-resistant strains of this normal microbiota of the human intestine. The aim of this study was to gather information on the antibiotic resistance property of *E. coli* collected from different water samples like rivers, wells, tube wells, ponds, industrial wastewater, hospital drain water, municipal drain water, and fishery water. *E. coli* was isolated on selective media (EMB, MacConkey). The isolated colonies were characterized by pink-colored colony formation on MacConkey agar and metallic green sheen formation on EMB agar, followed by CFU counting and colony morphology by Gram staining. CFU count shows the *E. coli* content in the order: Simlapal drain water > Medinipur hospital wastewater > Simlapal tubewell water > Midnapore drain water > Kharagpur hospital wastewater > Sarenga tubewell water > Moyna deep tubewell water > Sarenga domestic pond water > Srerampore deep tubewell water. These bacteria were tested for resistance and susceptibility patterns against six frequently prescribed clinically relevant antibiotics (Ampicillin, Cefraxome, Ceftazidime, Vancomycin, Amoxicillin, Gentamicin). Tested *E. coli* strains showed multiple resistance (to two or more antibiotics). Frequent resistance was observed for Vancomycin, Ampicillin, Amoxicillin, Cefraxome, Ceftazidime, and Gentamicin. This bacterium was also tested for resistance and susceptibility patterns against 21 different herbal dried leaf extracts (Guava, Neem, Thankuni, Tea, Basak, Shiuli, Tulsi, Akanda, Marigold, Nayantara, Orange, Jasmine, Mango, Karabi, Durba, Heliotropium, Chromolaena, Mikania micrantha, Blumea, Euphorbia, Mahua flower).

Keywords: *Faecal-Borne; Antibiotics Resistance; Multi-Drug Resistant; Selective Media and Herbal Dried Leaf Extract.*

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ROLE OF MICROBES IN MAINTAINING SOIL HEALTH AND FERTILITY

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Abstract

Microorganisms in soil constitute a critical part of microbial systems that support soil fertility and plant productivity, with taxon-specific contributions based on proven biochemical mechanisms. One such beneficial organism is a diverse group of free living diazotrophic bacterium, Azotobacter which has drawn much attention for its multifunctional role in agroecosystems. Azotobacter species show the nitrogen-fixation activity with help of atmospheric nitrogen limited to bioavailable forms of ammonia enhancing soil nitrogen content without needing synthetically manufactured fertilizers, as studied by Singh et al. in 2021. In addition to nitrogen fixation, Azotobacter also produces and releases a variety of bioactive metabolites such as indole-3-acetic acid (IAA), gibberellins, cytokinin, siderophores, and exopolysaccharides. These include hormones that promote plant growth through root elongation, improve nutrient uptake and soil aggregation. Therefore, understanding the metabolic and ecological functions of Azotobacter is crucial for developing eco-friendly strategies aimed at maintaining soil health and ensuring long-term agricultural sustainability. Such iron chelation is complemented by the production of siderophores, which are used to either increase available iron for plants or suppress phytopathogens through competitive exclusion as studied Sahu et al. in 2022. Besides, Azotobacter enhances soil structure through exopolysaccharide production that increases soil aggregates causing higher water retention and aeration. Its antagonistic function, producing antimicrobial molecules to prevent soil-borne pathogens, and thus enhance plant health and yield is also remarkable. Bhattacharyya et al report on recent studies indicating that Azotobacter application as a biofertilizer increases crop yield, while promoting sustainable agriculture practices through reduction in chemical fertilizer inputs and improved soil resilience. This indeed interprets that the metabolic and ecological functionalities of Azotobacter need to be praised so as to develop bio-sustainable strategies for maintaining soil health and agricultural sustainability in the long run.

Keywords: *Azotobacter; Soil Fertility; Nitrogen Fixation; Plant Growth.*

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UNRAVELLING DRUG RESISTANCE NETWORKS THROUGH WHOLE GENOME SEQUENCING AND SYSTEMS BIOLOGY MODELING

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Abstract

Drug-resistant microbes spread fast across the world. This problem threatens global health. Scientists need better ways to control it. This accelerated study explains how whole genome sequencing and systems biology help us study drug resistance. Whole genome sequencing studies the complete DNA of microbe. It finds changes like single nucleotide polymorphisms and gene transfer. These changes often cause drug resistance. However, drug resistance does not depend on one gene alone. Many genes and pathways work together. Systems biology studies these complex interactions carefully. It uses data from genomics, transcriptomics, proteomics, and metabolomics. It builds models to explain how genes and proteins interact. These models include gene regulatory networks, protein interaction networks, and metabolic pathways. They help us find key genes and important pathways. Researchers combine genome sequencing with computational models. This approach builds predictive models. These models simulate drug resistance and microbial adaptation. Scientists also use machine learning and artificial intelligence. These tools improve prediction accuracy and detect hidden patterns. Recent advances improve sequencing tools and modeling methods. These advances help researchers study drug resistance more effectively. This combined approach offers strong benefits. It explains how drug resistance develops. It also helps identify new targets for diagnosis and treatment.

Keywords: *Whole Genome Sequencing (WGS); Drug Resistance Networks; Systems Biology Modelling; Bioinformatics; Antimicrobial Resistance (AMR).*

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TARGETING ORF6 AND PP1A OF SARS-COV-2 FOR EPITOPE BASED VACCINE DEVELOPMENT

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Abstract

This study aims to explore lesser studied but important proteins of SARS-CoV-2, namely ORF6 and PP1a, which are conserved across different viral strains. Instead of focusing only on commonly targeted proteins, this work tries to identify key immunodominant epitopes using computational tools. The main goal is to find suitable B-cell and T-cell epitopes that are stable, antigenic, and non-allergenic, which can be further used in designing a multi-epitope vaccine. A step-by-step immunoinformatics approach was followed to analyze the proteins and their derived peptides. The stability and basic physicochemical properties were checked using the Expasy ProtParam tool. Antigenicity was predicted using VaxiJen (v2.0), while allergenicity was evaluated using AllerTOP (v2.1). B-cell, CD8+ T-cell, and CD4+ T-cell epitopes were identified with the help of the Immune Epitope Database (IEDB). To make the results more applicable to a wider population, two commonly occurring alleles, HLA-A*02:01 and HLA-DRB1*07:01, were selected for the analysis. The study identified several epitopes from ORF6 and PP1a proteins that showed good stability, strong antigenic properties, and non-allergenic nature. These findings suggest that the selected epitopes can be combined to form a multi-epitope vaccine construct. Such a vaccine may provide broader protection against different strains of SARS-CoV-2 and help in reducing future outbreaks. In conclusion, ORF6 and PP1a proteins appear to be promising alternative targets for vaccine development. The identified epitopes provide a strong base for designing a multi-epitope vaccine. However, further laboratory and clinical studies are needed to confirm their effectiveness and practical use.

Keywords: *SARS-CoV-2; ORF6 Protein; PP1a Protein; Immunoinformatics; Epitope Prediction; Multi-Epitope Vaccine Design.*

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MICROBIAL BIOREMEDIATION: A SUSTAINABLE APPROACH FOR ENVIRONMENTAL POLLUTION CONTROL

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Abstract

Environmental pollution is a significant global issue. It stems from rapid industrial growth, urban expansion, and improper waste management. Contaminants such as heavy metals, hydrocarbons, and synthetic chemicals threaten ecosystems and human health. Conventional methods of pollution control often tend to be costly and may generate secondary pollutants, making them less sustainable. Cleaning up the environment is of paramount importance. Bioremediation is an ecologically sound and state-of-the-art technique that employs natural biological processes to completely eliminate toxic contaminants. Based on the site of treatment, bioremediation strategies are classified as in situ and ex situ processes. In situ bioremediation involves treating the contaminated material at the site while ex situ involves the removal of the contaminated material to be treated elsewhere. Some examples of bioremediation technologies are bioventing, land farming, bioreactor, compositing, bioaugmentation, rhizofiltration, and bio-stimulation. Microorganisms that perform the function of bioremediation are known as Bioremediators. Not all contaminants, however, are easily treated by bioremediation using microorganisms. For example, heavy metals such as cadmium and lead are not readily absorbed or captured by organisms. Microorganisms possess metabolic pathways that let them utilize pollutants as energy sources. They can transform toxic compounds into less harmful or non-toxic forms. Techniques such as bioaugmentation and biostimulation have shown promising results, enhancing the efficiency of bioremediation processes. We attempt to recapitulate the different facets and nuances of bioremediation and give a conceptual and contemporary overview of the process.

Keywords: *Bioremediation; Environmental Pollution; Microbial Degradation; In Situ and Ex Situ Remediation; Bioaugmentation and Biostimulation; Heavy Metal Contamination.*

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LAG-3 AS A DUAL BIOMARKER: BRIDGING PROGNOSTIC STRATIFICATION AND IMMUNOTHERAPEUTIC TARGETING IN BREAST CANCER

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Abstract

The identification of precise therapeutic targets and reliable prognostic biomarkers remains critical for improving cancer outcomes. Despite significant advances, the vast repertoire of potential molecular targets continues to pose a challenge for comprehensive exploration. Immune exhaustion, marked by the upregulation of inhibitory checkpoint molecules such as PD-1, PD-L1, LAG-3, TIM-3, and CTLA-4, has emerged as a key mechanism in tumor immune evasion and a promising focus in cancer immunotherapy. Among these, Lymphocyte Activation Gene-3 (LAG-3) is a relatively underexplored immune checkpoint with considerable potential. In this study, we aim to evaluate the therapeutic relevance and prognostic significance of LAG-3 in breast cancer, one of the most prevalent and life-threatening malignancies affecting women globally and in India. The murine 4T1 breast cancer cell line was cultured and orthotopically implanted into the mammary fat pad of 6-week-old female BALB/c mice. LAG-3 expression in peripheral blood mononuclear cells (PBMCs) was analyzed using RT-PCR in tumor-bearing and control groups (n = 10 each) at 40 days post-inoculation. Tumor growth parameters, body weight, and survival were monitored throughout the study. Tumor-bearing mice demonstrated a marked increase in LAG-3 expression in PBMCs compared to controls. This elevation was associated with increased tumor burden, progressive weight loss, and decreased survival, indicating a correlation between LAG-3 expression and immune exhaustion. LAG-3 shows promise as both a prognostic biomarker and a therapeutic target in breast cancer. Targeting LAG-3-mediated immune dysfunction may contribute to the development of more effective precision immunotherapy strategies.

Keywords: *LAG-3 (Lymphocyte Activation Gene-3); Breast Cancer; Immune Checkpoint; Tumor Immune Evasion; Prognostic Biomarker; Cancer Immunotherapy.*

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GOLD NANOPARTICLE FOR PHOTOTHERMAL THERAPY IN CANCER

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Abstract

The efficacy of Gold Nanoparticle-based therapy for treating various forms of cancer has been seen to be more pronounced for superficial and accessible forms of malignancies like Skin Cancer, Breast Cancer, and Oral Cancer. This is due to efficient uptake of Gold Nanoparticles through the Enhanced Permeability and Retention Effect and efficient penetration of light. Antibodies like Trastuzumab, in combination with drugs like Folic acid and Transferrin, can be utilized for efficient targeting of cancerous cells, a process known as active targeting. Gold Nanoparticles respond to near-infrared rays through Surface Plasmon Resonance, converting them to heat through intrinsic properties of Gold, where Gold ions act as heat-generating agents for destroying cancerous cells without harming healthy tissues. However, for inaccessible forms of malignancies like Brain Cancer, Pancreatic Cancer, and Bone Cancer, it was seen that efficacy was low. To overcome this problem, efficient techniques like drug delivery systems for key chemotherapeutic agents like Doxorubicin, Paclitaxel, and Cisplatin have been incorporated for efficient targeting of tumor tissues and evasion of the Blood-Brain Barrier. In addition, internal sources of light like fiber optic probes and endoscopic laser systems have been developed for efficient penetration of near-infrared rays. The prolonged retention of Gold Nanoparticles was seen to be toxic, where accumulation of Gold in the liver and spleen was influenced by particle size and dose. Green synthesis techniques have been developed, where plant extracts like tulsi, neem, and green tea have been utilized for efficient synthesis of Gold Nanoparticles, where bioactive compounds like alkaloids, proteins, and phenolics have been seen to be beneficial for synthesis of Gold Nanoparticles.

Keywords*: Gold Nanoparticles (GNPs); Photothermal Therapy; Enhanced Permeability and Retention Effect; Surface Plasmon Resonance; Targeted Drug Delivery.*

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GREEN FABRICATION AND STRUCTURAL CHARACTERIZATION OF SILVER NANOSTRUCTURES DERIVED FROM *AVERRHOA CARAMBOLA* LEAVES

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Abstract

Green nanotechnology embodies combining the principles used by green chemistry and green engineering to formulate biocompatible nanoassemblies to combat the problems faced by the human body and the environment and green synthesis of metal nanoparticles is a significant part of green nanotechnology, it utilizes natural resources for synthesizing nanoparticles, therefore, it is highly advocated as a superior alternative to conventional methods. Nanotechnology provides solution to different global problems by giving rise to different metallic nanoparticles which has unique physiochemical and antimicrobial properties, among them silver nanoparticles gain significant interest due to their remarkable applications in it. Growing drug-resistant microorganisms and burgeoning variety of adversely mutated pathogenic strains of bacteria led to the exploitation of many plants to explore their antimicrobial capability. The conventional methods of silver nanoparticle synthesis employ hazardous chemicals as reducing agents and capping agent and it also produces harmful byproducts, the exigency to overcome these limitations cause researchers to utilize phytochemicals for silver nanoparticle (AgNPs) fabrication. This study reports the bio-fabrication of silver nanoparticles using a utilizing the aqueous leaf extract of *Averrhoa carambola* as a potent reducing and stabilizing agent. To evaluate the properties of the synthesized nanomaterials, we conducted a thorough structural and physicochemical characterization. The UV-Visible spectroscopy showed a distinct absorption peak between 420 and 450 nm, which confirmed the formation of AgNPs. FTIR analysis identified functional groups like polyphenols and flavonoids in the *A. carambola* extract, indicating their role in reducing and capping the metal ions. Furthermore, the crystalline nature of the particles was established through XRD, revealing a face-centered cubic (FCC) lattice.

Keywords: *Silver Nanoparticles; Averrhoa Carambola; Green Synthesis; Characterization.*

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EFFECTS OF NATURAL PRODUCTS ON HUMAN HEALTH

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Abstract

In recent years scientific studies have confirmed that natural products which have been used for a long time to support health and treat diseases are very important. Inflammation, oxidative stress, metabolism, apoptosis, cell communication and fibrosis are key processes that are maintained by natural products as it manages the body's internal balance. Natural compounds such as Rubi Fructus, *Mokko lactone*, YG-1 extract, *Dracocephalum moldavica*, lactoferrin, *Sparassis crispa*, and *Sargassum plagiophyllum* and others have been found to help reduce inflammation, protect body cells from damage, support heart and brain functions, treat cancer, and strengthen the immune system. As a result, the secondary metabolites formed such as polyphenols and flavonoids (Rubi Fructus), terpenoids (Mokko Lactone), polysaccharides, alkaloids and glycoproteins (lactoferrin) contribute to these therapeutic properties. These metabolites act by regulating signaling pathways such as MAPK, JAK/STAT and NLRP3 inflammasome, thereby reducing disease progression in critical conditions such as cancer, cardiovascular diseases, liver disorders, respiratory inflammation and metabolic syndromes. Apart from these natural products play a vital role in maintaining gut microbiota, enhancing immune responses and improving in physiological functions. For example, *Saussurea pulchella* produces phytochemicals which act with anti-ulcerative properties and helps in gastrointestinal motility. Despite promising preclinical research further studies are required to ensure their safety and efficacy. Overall natural products represent a valuable and sustainable source for developing therapeutic agents and functional foods required for improving human health and disease management.

Keywords*: Natural Products; Disease Prevention; Secondary Metabolites; Inflammation; Oxidative Stress; Flavonoids; Antioxidants, Cancer, Phytochemicals, Therapeutics.*

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METAGENOMIC ANALYSIS OF ANTIBIOTIC RESISTANCE GENES IN PHARMACEUTICAL INDUSTRY EFFLUENTS

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Abstract

Antibiotics are among the most important drugs for treating infectious diseases in humans and animals and are widely and often heavily prescribed worldwide. However, improper and excessive use of antibiotics increases selective pressure, favouring the survival and spread of antibiotic-resistant bacteria (ARB) and antibiotic resistance genes (ARGs). Pharmaceutical and hospital wastewaters frequently contain substantial antibiotic residues, contributing to the emergence and proliferation of ARB and ARGs. Pharmaceutical effluents carry diverse ARGs, including clinically relevant ones. Biological treatment processes with high bacterial densities in pharmaceutical wastewater treatment plants (PWWTPs) create ideal conditions for horizontal gene transfer (HGT) of ARGs from non-pathogenic to pathogenic bacteria. Traditional methods for ARG investigation, such as culture-based approaches and quantitative PCR, are limited by the inability to culture many microbes and by targeting only known genes. These limitations are overcome by metagenomics, which enables comprehensive profiling of taxonomic composition and the resistome, and identification of potential pathogenic ARB and their ARG hosts. Metagenomic studies of pharmaceutical wastewater show that ARG persistence and higher relative abundance in effluents are often associated with mobile genetic elements (MGEs). The most common resistance mechanisms identified include antibiotic target alteration, antibiotic inactivation, and efflux-mediated resistance. Metagenomic analyses further reveal that conventional wastewater treatment can substantially reduce antibiotic concentrations but does not completely eliminate ARGs. These findings underscore the need for systematic study and monitoring of ARGs in influents and effluents from different pharmaceutical industries and environmental compartments.

Keywords: *Antibiotic Resistance Genes (ARGs); Metagenomics; Pharmaceutical Effluents; Wastewater Microbiome; Environmental Antibiotic Resistance.*

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BIODEGRADATION OF PLASTIC AND MICROPLASTIC: A CURRENT REVIEW ON RELATED PATHWAYS AND AFFECTING FACTORS

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Abstract
Plastic pollution is the evaluation of plastic waste in the environment. Due to its complex and stable structure, it cannot naturally decompose, harming humans, animals, and the environment. Plastics persist in soil and water for extended periods of time and contribute to the rapid rise of pollution, which destroys ecosystems and poses major health hazards. In addition to this difficulty, there is significant potential in the biodegradation of plastics. Many scientists are investigating how bacteria can break down plastics, which is crucial for environmental protection. Bacteria break down plastic through the use of their enzymes and convert it into less toxic molecules. Bacteria adhere to the plastic's surface, release enzymes that break down complicated polymer chains into monomers, that can be used as energy source. However, this process may also result in intermediate pollutants with varying degrees of environmental effect. This review highlights the promising possibilities of using several types of bacteria to break down plastics.

Keywords: *Plastic Pollution; Biodegradation of Plastics; Microbial Degradation; Plastic-Degrading Bacteria; Enzymatic Polymer Breakdown; Environmental Bioremediation.*

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AI/ML FRAMEWORKS IN THE DETECTION AND MANAGEMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE

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Abstract

Chronic Obstructive Pulmonary Disease (COPD) is a long-term and often complicated respiratory condition that gradually worsens over time, leading to persistent airflow limitation, frequent flare-ups, and a steady decline in quality of life. On top of it, late diagnosis, difficulty in maintaining patient adherence to treatment, and uneven application of clinical guidelines, especially in low- and middle-income countries (LMICs) makes the situation worse. However, the availability of large data, (including clinical records, imaging results, and biomarkers such as eosinophil levels) integrated with the evolving efficacy of artificial intelligence (AI)/machine learning (ML) frameworks can help in early diagnosis and prognosis of the disease with greater accuracy. In addition, AI-supported digital health tools make it easier to monitor patients remotely and encourage better self-care. However, issues like limited digital awareness and challenges in integrating these systems into existing healthcare frameworks still need to be addressed. Exacerbations continue to be a major factor contributing to the overall burden of COPD, affecting not only lung function but also everyday activities and general well-being. The effectiveness of treatment varies from one patient to another. For example, inhaled corticosteroids (ICS) tend to work better in individuals with higher eosinophil counts, while long-acting muscarinic antagonists (LAMA) are particularly useful in improving lung function in patients with ACO. Biologic therapies that target Type 2 inflammation show only modest benefits, and although systemic corticosteroids are effective, they may lead to unwanted side effects. Alongside medications, non-pharmacological approaches, such as encouraging physical activity, improving air quality, and providing nursing support play a crucial role in reducing flare-ups and enhancing quality of life. Overall, processing large data with AI/ML and integrating it with advanced technologies in personalized and supportive care may be a critical step towards achieving better outcomes in COPD management.

Keywords: *AI/ML; COPD; Personalized Medicine; Early Diagnosis; LAMA.*

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PHANEROCHAETE CHRYSOSPORIUM MEDIATED REMEDIATION: AN ECO-FRIENDLY PERSPECTIVE

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Abstract

Mycoremediation, utilizes fungi and their enzymatic repertoire to reduce, transform, and abolish environmental contaminants. Conventional remediation techniques, while effective, are often costly and may produce secondary pollutants against which a sustainable and eco-friendly alternative is looked forward. *Phanerochaete chrysosporium* (white rot fungi) of the Basidiomycetes phylum are naturally occurring fungal strains widely used for large-scale remediation due to their adaptability and resilience in diverse environmental conditions. Fungi possess highly active ligninolytic enzymes like laccases and peroxidases, which enable the breakdown of complex organic pollutants like textile dyes, petroleum hydrocarbons, endosulfans, pesticides, petroleum refineries and heavy metals. The fungal biomass has the capability to adsorb and gather these pollutants through their hyphal spread and thereby reduce toxicity and movement in polluted environments. The mycelial mat extends surface area interaction, refining pollutant degradation. Moreover, fungi can form synergistic associations with bacteria forming biofilm and Mycorrhizal association with plants, enhancing the overall bioremediation efficiency. Advanced techniques like engineering genetic pathways, consortium approach and enzyme immobilization can further be explored to enhance the degradative capacity of *Phanerochaete chrysosporium*. The fungal remediation is cost-effective, environmentally safe, and contributes to the restoration of ecological balance and agricultural productivity. The study highpoints the mycoremediation capacity as a green approach for successful management of diverse environmental contaminants.

Keywords: *Phanerochaete chrysosporium; Environmental Pollution; Bioremediation; Ligninolytic Enzymes; Fungal Biomass.*

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MICROBIAL PIGMENT-BASED BIOSENSORS FOR ENVIRONMENTAL MONITORING

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Abstract

The escalating global industrialization has triggered the need for rapid in-situ detection of environmental pollutants leading to the development of pigment-based biosensors as a high-precision and eco-friendly alternative to conventional analytical environmental monitoring methods. By liaising the distinct chromogenic properties of microbial pigments, sensitive detection of diverse analytes from heavy metals to neurotoxic pesticides can be done on-site. Biosensors provide speedy visual information without any pre-hand sample preparation. The biosensors function through a variety of mechanisms mainly involving direct chemical reactions between microbial pigment and the analyte with a quantifiable output signal. This method allows for cheap, no-equipment, and on-field detection, as the colour change can be visualized with naked eye within seconds. Microbial pigments act as the sensing element and detects the analyte or environmental pollutants present in the sample. The interaction triggers change in the pigment colour which can be analysed or quantified by various spectroscopic techniques such as colorimetry or fluorimetry. Surface modifications of the pigment or genetic engineering can enhance pigment synthesis and lower nonspecific interactions. The blue pigment indigoidine was biosynthesized in *E. coli* with synergistic expression of both gene BpsA responsible for a non-ribosomal peptide synthetase and a dependent gene like PcpS. Even for a dual-color visual detection, metal-responsive regulators like MerR and PbrR which trigger for pigments like indigoidine and prodeoxyviolacein are clubbed up for detection of specific pollutants. The microbial pigment-based biosensors study demonstrates the limitless potential of in-situ environmental monitoring in resource limited settings and in real time.

Keywords: *Pigment; Biosensors; Environment; Monitoring; Genetic Engineering.*

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REPROGRAMMING IMMUNITY: THE RISE OF CAR-T CELLS IN PRECISION ONCOLOGY

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Abstract

One significant development in the treatment of cancer is chimeric antigen receptor (CAR) T-cell therapy. With this treatment, the patient's own T cells are altered to selectively identify and eliminate cancer cells. The patients T cells are first collected using leukapheresis, expand outside the body, and then modified genetically with viral vectors to introduce the car construct. Structurally, the CAR contains an external scFv that binds tumour antigen without relying on MHC, a hinge and transmembrane region, and an internal signalling domain. Inside the cell it carries CD3ζ activation motif with co-stimulatory domains like CD28 or 4-1BB. they together promote strong T-cell activation upon antigen binding. Downstream signaling induces calcium influx and activates transcription regulators like NF-κB and NFAT, promoting cytokine release (IL-2, IFN-γ, TNF-α) and ultimately killing of target cells through perforin and granzyme pathways. After lymphodepleting chemotherapy, the infused CAR T cells can multiply and stay active in the body. This helps create a strong and lasting remission in B-cell cancers that have come back or haven't responded to other treatments. Treatments like tisagenlecleucel have showed a high frequency of complete remissions in CD19-expressing leukaemia's and lymphomas. Despite its promise, its broader use is restricted by factors such as massive release of inflammatory cytokines, neurotoxicity, antigen escape, an immunosuppressive tumour microenvironment and poor movement of CAR-T cells into solid tumours. Emerging next-generation platforms, including multi- specific CARs, "armoured" CAR T cells with cytokine secretion, safety switches, and genome-edited allogeneic products, seek to enhance efficacy, durability, and safety, reinforcing the promise of CAR T-cell therapy in precision oncology.

Keywords: *Chimeric Antigen Receptor (CAR) T-cell therapy; CD19-Targeted Immunotherapy; Cytokine Release Syndrome (CRS); Tumour Microenvironment (TME); Genome-Edited CAR T Cells.*

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IN-SILICO EVALUATION OF ORAL MICROBIOME MODULATION IN ASTHMA: MOLECULAR DOCKING AND THERAPEUTIC TARGET IDENTIFICATION

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Abstract

Asthma is a chronic inflammatory disease affecting over 300 million individuals worldwide, with a complex etiology involving genetic and environmental factors. Recent evidence demonstrates a microbiome dysbiosis in Asthma patients, which may contribute to asthma pathogenesis. However, the underlying molecular mechanisms of this crosstalk are yet to be investigated. To address this knowledge gap, in this study, we investigated the potential role of oral microbiome proteins in asthma pathophysiology and sought to identify promising therapeutic candidates using in-silico approaches of structural homology and molecular docking. Sequence homology analysis was performed between select asthma-associated proteins and the microbial proteins of Human Oral Microbiome Database (HOMD) and the National Centre for Biotechnology Information (NCBI) database using BLAST. Three-dimensional structures of the proteins and their microbial counterparts were modelled using SWISS-MODEL and PyMOL, and molecular docking was performed using AutoDock4 and AutoDock Vina with five select therapeutic compounds: ciclesonide, zafirlukast, prednisolone, ozanimod, and cylindrin. Cut-off values of 50 % and 30% were considered for query cut-off and percent identity, respectively. Significant sequence homology was revealed between human and bacterial proteins, with 36.3% similarity between YKL-40 and *Bacillus anthracis* chitinase A1, and 39.1% similarity between MMP2 and *Tannerella forsythia* karilysin. Molecular docking studies of chitinase A1 and karilysin showed the highest binding affinity with zafirlukast (-12.225 kcal/mol) and ozanimod (-8.570 kcal/mol), respectively, followed by other tested molecules. Notably, Zafirlukast demonstrated consistent high affinity toward both chitinase A1 and karilysin, suggesting a potential dual-target inhibition. This study reveals structural similarity and binding affinity between the human proteins and the microbial proteins present in the oro-respiratory system, and reveals a binding affinity of the tested drugs. This is suggestive of the potential modulatory role of the microbial proteins in the onset and progression of asthma.

Keywords: *Asthma; Oral Microbiome; Molecular Docking; Chitinase; Karilysin; Zafirlukast; Ozanimod; In-Silico Analysis; Drug Discovery.*

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IN-SILICO EVALUATION OF HOST-MICROBIOME INTERACTION IN MANAGEMENT OF HYPERGLYCEMIA

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Abstract

Type 2 diabetes mellitus (T2DM) is distinguished by hyperglycemia, which is produced by altered gut microbiome dysbiosis and dysregulated host metabolic pathways that influence insulin signalling and glucose homeostasis. The gut microbiota governs metabolic illnesses through LPS/SCFAs, which influence energy balance and inflammation. This study investigates how berberine targets human adiponectin/PKC and their microbial homologs in T2DM-associated *Desulfovibrio piger* and *Clostridia* spp. In order to identify berberine as a dual-target therapeutic and identify host-microbiome interactions for improved management, this study will evaluate structural similarities between microbiome proteins and human proteins involved in the progression of hyperglycemia or immune evasion using in-silico homology modelling and molecular docking. BLAST used computational biology techniques to match microbial proteins in NCBI database with sequences of certain T2DM-associated proteins. The 3D structures of these proteins and their microbial homologs were modelled using SWISS-MODEL and PyMOL, and then berberine docking was done using AutoDock tools. For the query coverage and percent identity, cut-off values of 50% and 30%, respectively, were taken into consideration. Berberine exhibited moderate human PKC Beta 1 affinity, weaker human Adiponectin binding, significantly weaker *D. piger* Adiponectin contact, and extraordinarily strong *Clostridia* PKC Beta 1 binding. These findings support a host-microbiome precision medicine model in which berberine reduces host insulin resistance while selectively changing pro-diabetic microorganisms, paving the way for berberine-based therapies that require in vitro, metabolic, and clinical confirmation. These findings support a host-microbiome precision medicine model in which berberine reduces host insulin resistance while selectively changing pro-diabetic microorganisms, paving the way for berberine-based therapies that require in vitro, metabolic, and clinical confirmation.

Keywords: *Type 2 Diabetes mellitus; Gut Microbiome; Molecular Docking; Host-Microbe Interactions; Precision Medicine; Adiponectin; Protein Kinase C; Computational Biology.*

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JAK-STAT AND MAPK CELL SIGNALLING PATHWAYS IN HPV-ASSOCIATED CERVICAL CANCER

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Abstract

Human papillomavirus (HPV) is the principal cause of cervical cancer and a major global public health problem. Persistent infection with high-risk genotypes, particularly HPV-16 and HPV-18, drives carcinogenesis through continuous expression of the viral oncoproteins E6 and E7. These proteins inactivate the tumour suppressors p53 and retinoblastoma protein (pRb), disrupting cell-cycle regulation, promoting genomic instability, and enabling malignant transformation. Cervical cancer imposes substantial clinical, social, and economic burdens, affecting quality of life, fertility, and healthcare systems. According to the World Health Organization (WHO), it accounts for over 660,000 new cases and about 350,000 deaths annually worldwide, with India contributing nearly one-fifth of the global incidence and mortality, largely due to limited access to screening, vaccination, and timely treatment. HPV infection alters multiple signalling networks. The JAK–STAT pathway is hijacked to promote immune evasion, chronic inflammation, and dysregulated cytokine signalling, while aberrant activation of the mitogen-activated protein kinase (MAPK) cascade supports uncontrolled proliferation, survival, and resistance to apoptosis. Crosstalk between these pathways further amplifies oncogenic signalling and tumour progression. Conventional therapies, surgery, radiotherapy, and chemotherapy improve survival but often cause significant toxicity, infertility, and long-term immunosuppression. As a result, precision oncology and immunotherapy are gaining prominence. mRNA-based approaches, including prophylactic and therapeutic vaccines, show promise in eliciting antigen-specific immune responses and selectively targeting HPV-infected or transformed cells. This review focuses on JAK-STAT and MAPK signalling in HPV-induced cervical carcinogenesis and evaluates current and emerging preventive and therapeutic strategies.

Keywords: *Human Papillomavirus (HPV); Cervical Carcinogenesis; E6 and E7 Oncoproteins; JAK-STAT Signaling Pathway; MAPK Signaling Pathway; mRNA-based Vaccines*

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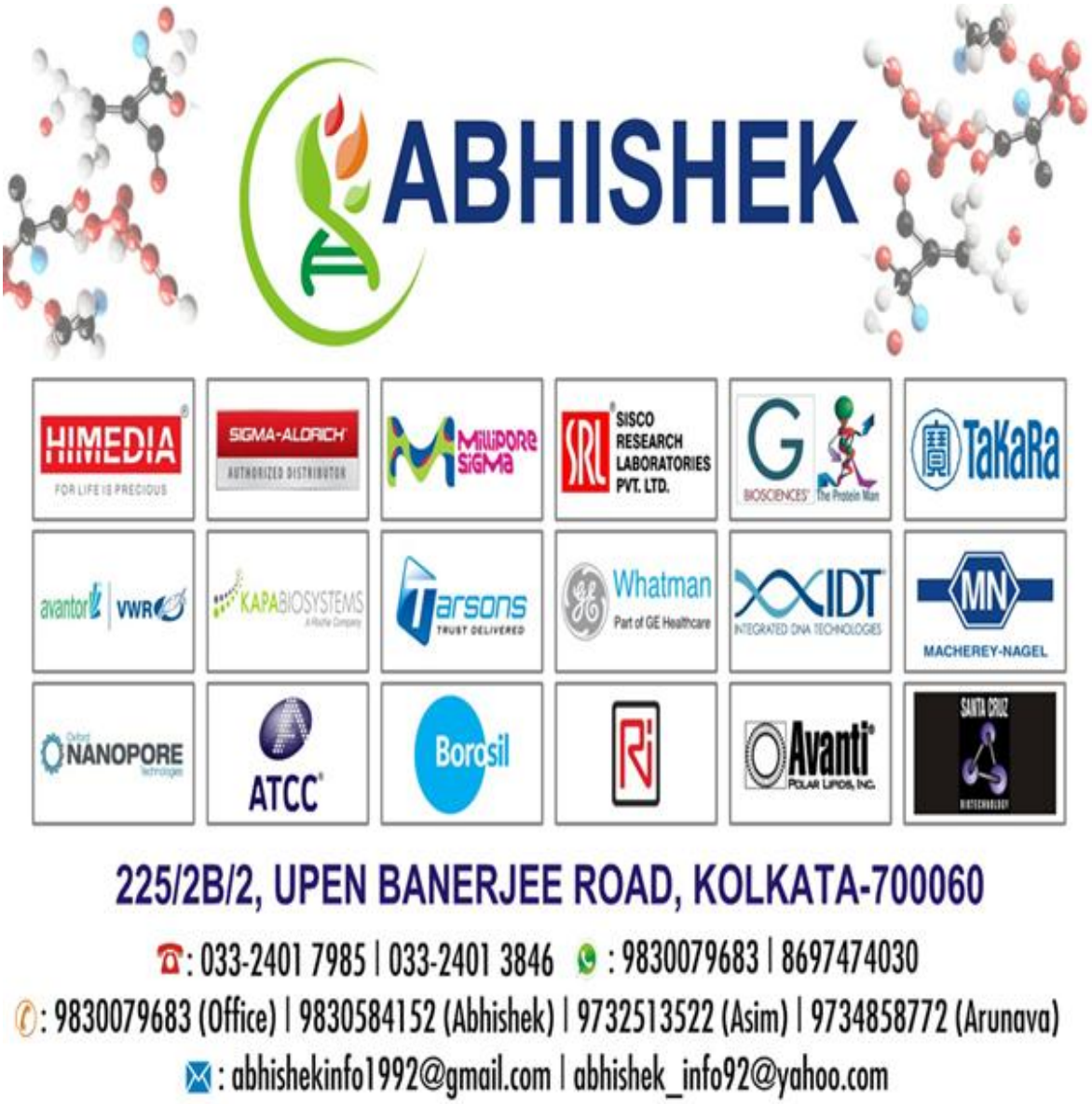

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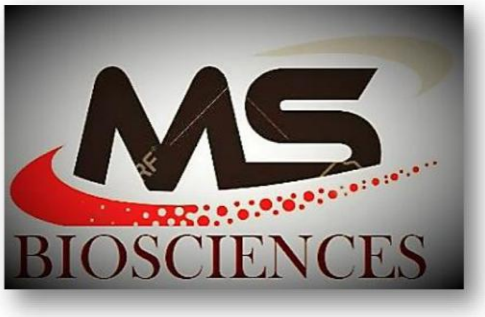

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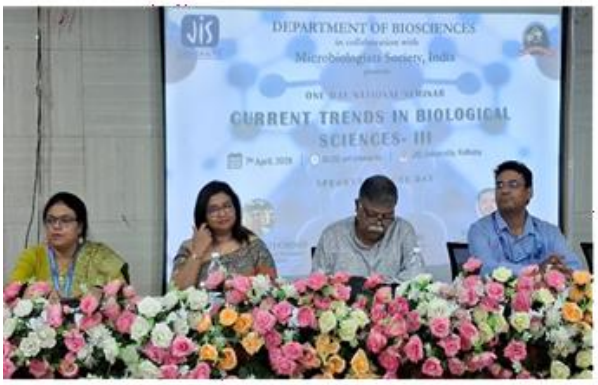







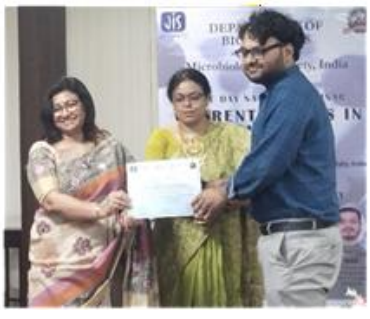

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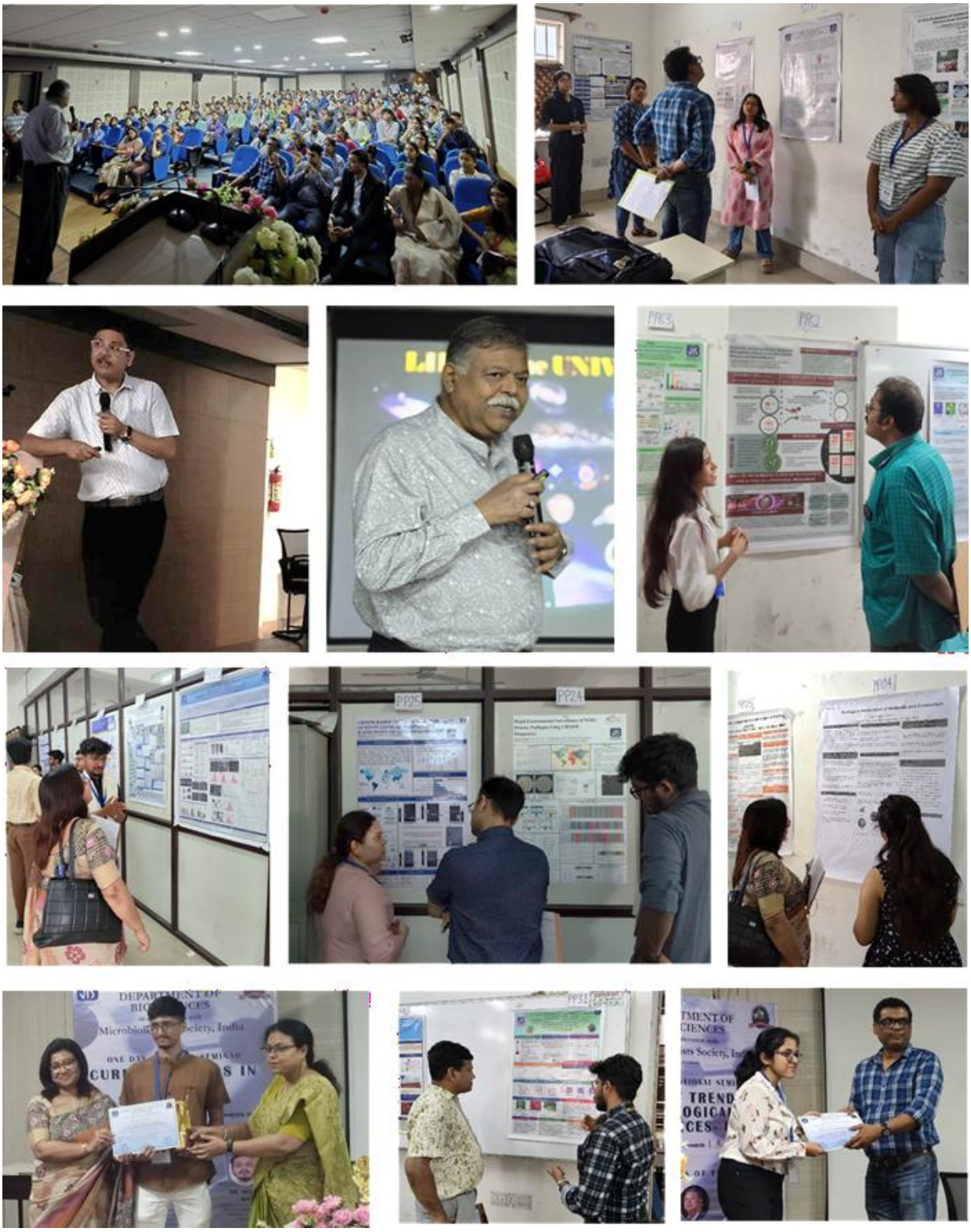

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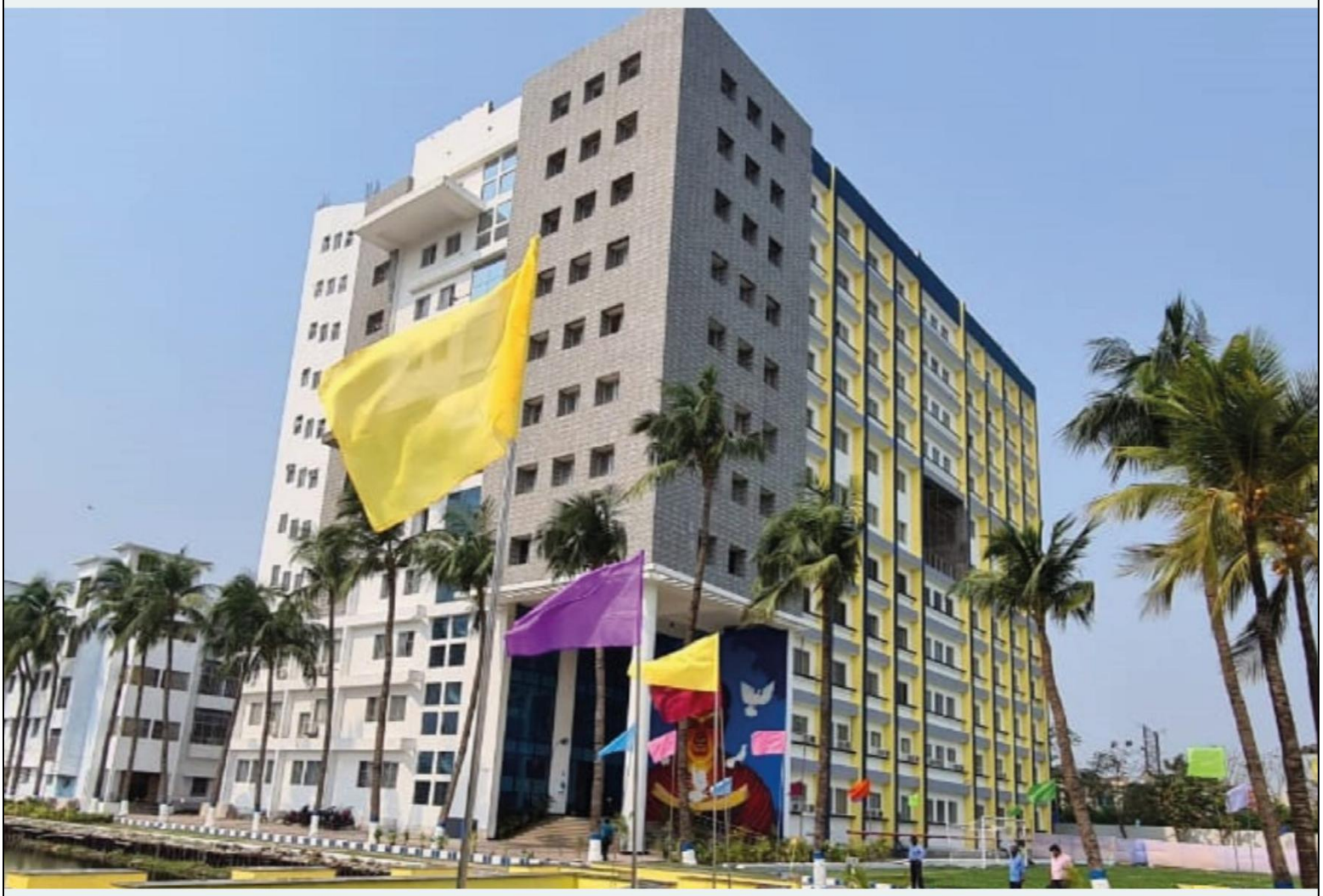

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