THE INSTITUTION OF ENGINEERS - BIOTECHNOLOGY, MANIPAL CHAPTER (IE-BT),
MANIPAL BIOMACHINES AND
DEPARTMENT OF BIOTECHNOLOGY, MIT MANIPAL

2nd International Conference

SYMBIOT '25

(Symphony of Medicine, Biological Sciences & Omics Technologies)

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MAHE has branch campuses in **Bangalore, Malaysia, Dubai and Antigua** in the Caribbean Island. There is also a campus in Mangalore with a medical college, a dental college and a nursing college with attached teaching hospitals. MAHE has an international academic collaboration for twinning programmes in engineering with **universities in the US, UK, Australia and other countries**. Manipal Group institutions are located on scenic campuses, which provide a high- quality lifestyle and ideal environment for study. All campuses have excellent infrastructure for academic activities, sports and other extracurricular activities. The infrastructure includes air conditioned lecture halls, a skills lab, air-conditioned hostels, and a multi-cuisine food court. The state-of-the-art health sciences library is fully air-conditioned, accommodates **1300 learners** and has over **62,000 books and over 600 journals**. The library facilities include Medline, Proquest medical library of online databases, audio visual, Cochrane library, e-learning, computer and Internet services. The Skills Lab and Anatomy Museum are considered amongst the best in the world. The latest addition to the facilities, a Simulation Lab with computer-driven mannequins, is an achievement, which the university is proud of. It is of considerable help to students in the field of health care. MAHE believes in providing the **finest in infrastructure and facilities** to its students when it comes to learning and research. In fact, some of the facilities, like the Innovation Centre, have served as a valuable 'incubation centre' for industry and research. The state-of-the-art innovation centre bridges the gap between universities and industries for industrial-academic research. Other facilities on the campus include a gym, swimming pools, and football and cricket grounds. The new indoor sports complex is perhaps one of its kind in Asia. The complex has five badminton courts, four squash courts, three tennis courts, a basketball court, gymnasiums and a walking track. Besides being an ISO 9001:2008 and ISO 14001: 2004 certified University, it is home to many **top 10 ranked institutions of India**. MAHE has won the prestigious IMC Ramkrishna Bajaj National Quality Award and International Asia Pacific Quality Award during 2007- 2008. MAHE attained the **Institute of Eminence** by MHRD in 2018.

MANIPAL INSTITUTE OF TECHNOLOGY

Manipal Institute of Technology (MIT), one of the Premier Engineering Institutes in India, was among the first self–financed engineering colleges in the country. It was started in 1957 by **Padmashree late Dr. T.M.A Pai**, as Manipal Engineering College with an undergraduate course in Civil Engineering. In 1965, the institute got affiliated to the University of Mysore from Karnataka University. In 1974, it was renamed as Manipal Institute of Technology (MIT). In 1980 it got affiliated to the University of Mangalore. After the creation of the Visveswaraiah Technological University (VTU), MIT along with a number of other engineering colleges in the state got affiliated to the VTU in 1998. As the Manipal Academy of Higher Education (MAHE) had acquired a Deemed University status, MIT became a constitution institution of MAHE in May 2000. In 2003, MIT obtained full academic autonomy and adopted credit system with **10 point grading.** In 2007 MAHE was renamed as Manipal University and MIT retained its status as a constituent institution of Manipal University. With total student strength of over **7500**, MIT has emerged as the **largest institute of University**. MIT currently offers undergraduate programs (B.TECH) in 16 disciplines and postgraduate courses (M.TECH/MCA) in 24 different streams and Doctoral programs (Ph.D) in all streams of engineering, basic sciences, humanities and management. Academic programs offered by institute are approved by AICTE and have been accredited by the National Board of Accreditation (NBA). The institution plays a vital role in producing world class engineers tuned to the demands of a fast changing global village.

DEPARTMENT OF BIOTECHNOLOGY

The Department of Biotechnology, MIT, Manipal was founded in the year **2005**. The department has state-of-the-art infrastructure, well defined and updated curriculum, and wide range of electives to encourage interdisciplinary research. The faculty are highly qualified and experienced with research interests in diverse and emerging areas of biotechnology. The department has received **up to 5 crores in research grants** from various funding agencies. The vision of the department: Excellence in the **teaching-learning process and research**. The mission of the department: To impart and disseminate knowledge, develop competencies and to produce industry-ready and academically enriched engineers for the emerging areas of applied biotechnology.

IE-BT

The Institution of Engineers-Biotechnology, Manipal Chapter (IE-Bt) is a premier society of Indian engineers from MIT, Manipal, which organizes technical and non-technical activities relating to different aspects of biotechnology. **SYMBIOT** is an international-level symposium conducted **annually** by IE-Bt, Manipal, to provide participants with exposure to a real-life work environment. Every year, more than 100 students from all over the country take part in the event.

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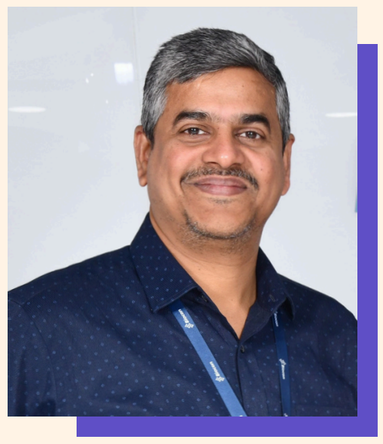
THE RISE OF BIOLOGICS

DR. RAMGOPAL RAO
SENIOR ACADEMIC MANAGER,
BIOCON ACADEMY BENGALURU, INDIA



The first guest lecture of Symbiot was delivered by Dr. Ramgopal Rao S from Biocon Academy on "The rise of biologics," highlighting that biopharmaceuticals and biologics are synonymous. Biologics are products derived from living organisms and are generally large molecules, including examples like immunoglobulins, erythropoietin, mAbs, filgrastim, calcitonin, and antibiotics. Antibodies have various applications, including therapeutics, detection, and diagnostics, such as CAR T-cell therapy and ATMP. The FDA approvals for new drugs have increased in the last 25 years. The workflow for developing biologics involves selecting a biological system, genetic enhancement, scale-up, purification, and sustainable product recovery. Monoclonal antibodies (mAbs) can be produced and humanized for targeted delivery of therapies, with types including naked mAbs, conjugated, and bispecific antibodies. The speaker also spoke about mechanisms used by mAbs to treat cancer- Block, Flag, Deliver. Biopharma manufacturing involves growing cultures, perfusion, continuous manufacturing, and chromatography, with DSP contributing significantly to production costs. The process from lab to industry has been accelerated greatly in recent years. The lecture also covered biosimilars, referencing insulin and the 351K pathway, multicolumn chromatography, and key concepts like quality by design and pharmaceutical digital twin platforms.

*Report written by the members of IE-Bt

IDENTIFICATION OF NOVEL KINASE INHIBITORS USING AI LED DRUG DISCOVERY AND PHYSICS-BASED SIMULATIONS

DR. SUNIL KUMAR
ASSOCIATE VICE PRESIDENT, CADD & INFORMATICS
AT AURIGENE PHARMACEUTICAL SERVICES LIMITED,
BENGALURU, INDIA

Recent breakthroughs in Artificial Intelligence (AI) and machine learning (ML) are transforming various fields, including drug discovery. Traditionally, developing a drug takes about >10 years and costs billions of dollars.1 This high cost makes these medicines unaffordable for many patients.

AI and ML are being used to streamline drug discovery, reducing both time and expense. AI-powered drug candidates show a significantly higher success rate in clinical trials compared to traditional methods.2 This success is due to combining fundamental scientific data, particularly physics simulations, with AI and ML. This approach optimizes the Design-Make-Test-Analyze (DMTA) cycle shorter, leading to faster and cheaper development.

We've demonstrated reduction in cost and development time through deployment of physics-based simulations along with AI/ML to identify of novel kinase inhibitors. This approach allows us to identify promising drug candidates (hits) in just 3 months, compared to the typical 6–9-month timeframe.

IMPROVED COMPUTATIONAL ANALYSIS OF BIOLOGICAL DATA FOR BETTER DIAGNOSTICS: A RECENT PROMISING CASE

MR. KSHITISH ACHARYA
FACULTY SCIENTIST,
INSTITUTE OF BIOINFORMATICS AND APPLIED BIOTECHNOLOGY,
BENGALURU, KARNATAKA, INDIA

Transcriptomics can be a gateway for biomarker discovery as well as for exploring the molecular basis of several biological phenomenon. While NGS has substantially enhanced the efficiency of gene expression profiling, there is still a scope to improve many aspects, especially the data analysis methods. The primary work in our group focused on a type of male infertility (non-obstructive azoospermia) where spermatogenesis has failed. In a recently completed study, we short-listed 87 potential mRNA candidates by applying the new method to differential transcriptomic analysis. We then identified 19 promising RNA biomarkers by RT-qPCR and validated them with meta-analysis. These RNAs included 16 mRNA isoforms and 3 chimeric transcripts. The biomarker candidature of 19 RNAs is so strong that we patented them and initiated efforts to develop a diagnostic assay. The work has been recognized by national awards and funding (via BIG) for developing a diagnostic kit. It should be noted that the strategies used in the research, viz., the data compilation and computational meta meta-analysis, are universal. They can be applied to multiple areas of application. Indeed, currently efforts are on to apply these approaches to certain cancer types and the PCOS condition.

FROM BENCH TO CLINIC: THE JOURNEY OF ANTIBODY DRUG DEVELOPMENT

MS. SHOHINI SHOME
MANUFACTURING BUSINESS PROCESS MANAGER, ABCELLERA
VANCOUVER, BRITISH COLUMBIA, CANADA

This talk will provide an end-to-end overview of drug discovery, development, through to bringing a drug to market, with a particular focus on the development part of the process where at-scale manufacturing of antibodies for first-in-human clinical trials will be discussed. Tools, methodologies, technology and ways of collaboration - both within the industry and with regulators - are constantly evolving. With this evolution, stakeholders are looking at bringing drugs to market faster to serve addressable unmet needs and ultimately patients. There is also an evolution in expanding the different modalities to make safer, more effective and longer-lasting drugs.

We will explore the key stages of drug development, beginning with how a project is selected and what guides the discovery and development process, dive into development where we take the drug candidates and scale-up the processes from bench scale to manufacturing scale. Following manufacturing, we will further explore what clinical trials execution entails and how we are able to successfully bring a drug to market. To illustrate these concepts, we will examine a recent case study of an antibody drug, highlighting the milestones and challenges encountered along the way.

100,000L SCALEUP ROADMAP: CIRCULAR FERMENTATION.

DR. VINAYAK PACHAPUR
PRODUCTION OPERATIONS LEAD, DISPERSA,
NOVA SCOTIA-CANADA

Small and medium enterprises (SMEs) and early-stage startups are increasingly prioritizing sustainability and the circular economy, with fermentation emerging as a key enabler. This approach allows for the utilization of diverse feedstocks, ranging from pure substrates to industrial wastes, and offers low-energy conversion of complex substrates into simple monomers for value-added products using microorganisms.

Strategic planning is critical by, focusing on key elements, perform Design of Experiments (DoE), process optimization for upstream and downstream processes (USP/DSP), simulation and validation runs on bioreactors, risk mitigation, and addressing scale-up challenges.

The roadmap for scaling up to 100,000L emphasizes efficient process flexibility, aiming to enhance product yield, quality control and achieve higher recovery rates. This approach ensures a robust and sustainable pathway to circular fermentation at commercial scaleup.

CONFLICT OF THE MOLECULAR TITANS

DR. SABARI SANKAR THIRUPATHY
SCHOOL OF BIOLOGY, IISER THIRUVANANTHAPURAM

Conflicts between DNA replication and transcription are inevitable because both processes occur simultaneously on the same DNA template. This is especially true in rapidly dividing bacterial cells, where the machinery for each process frequently collides. Depending on the relative orientation of DNA and RNA polymerases, these collisions can happen in a co-directional (for leading strand genes) or head-on (for lagging strand genes) manner. Both types of collisions can disrupt the replisome, cause DNA breaks, and lead to spontaneous mutations. However, head-on collisions are more harmful, resulting in a pronounced genome-wide preference for co-directional gene-strands. Our lab focuses on exploring the molecular mechanisms behind collision-induced mutations, with the goal of establishing these collisions as a key mutational force influencing genome structure and evolution in bacteria.

ADVANCES IN BIOMATERIALS, 3D BIOPRINTING AND ORGAN ON CHIPS.

MR. CHAITANYA DOSHI
CHIEF EXECUTIVE OFFICER,
KORE ADDITIVE MANUFACTURING AND MEDICAL RECONSTRUCTION PVT.LTD,
MAHARASHTRA, INDIA

This lecture explores the latest advances in biomaterials, 3D bioprinting, and organ-on-chips, transforming healthcare and medicine. Novel biomaterials enable functional tissue substitutes and implantable devices. 3D bioprinting fabricates complex tissue structures and organs with precision. Organ-on-chips mimic human organs for drug discovery, toxicity testing, and personalized medicine. Attendees will gain insights into technological advancements, challenges, and opportunities, highlighting their transformative potential for human health and medicine.

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HYDROGEL BASED ANTIBACTERIAL DRUG DELIVERY STUDY FOR VETERINARY AND HUMAN APPLICATION : A COMPARATIVE STUDY.

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ABSTRACT

Controlled drug delivery (CDD) technology represents one of the most rapidly advancing areas of science. Such delivery systems offer numerous advantages compared to conventional dosage forms including improved efficacy, reduced toxicity, and improved patient compliance and convenience. Drugs with controlled release often combine with other safe substances which includes gels composed of organic polymers, either synthetic or natural. Soft materials known as hydrogels are often composed of networks of insoluble, cross- linked, three-dimensional polymers with a high absorption capacity for water molecules.

Recent proposals in this subject have drawn a lot of interest from the scientific community. One such innovation is the use of natural polymers that are renewable and biodegradable, such as gelatin, to create hydrogels for controlled drug release. Gelatin is a pure protein food ingredient, obtained by the thermal denaturation of collagen, and serves as a matrix for gelatinisation, due to the presence of reactive groups. Gelatin has been cross-linked with chemicals such as glyoxal, epoxides, isocyanates, and formaldehyde. Hydrogels are an effective method of drug administration because they allow for the long-term, regulated distribution of medications to the site of action. Human and veterinary dermal patches are used to treat small cuts and wounds on the skin's dermal layer. With their antibacterial properties, these patches aid in the direct delivery of medication into the wound and aid in the quicker healing process by killing microorganisms on the surface. Therefore, by treating them without any outside influences interfering with the healing process, these medicated biodegradable hydrogels aid in effective action against the damage.

ENHANCING NATURAL KILLER CELL ACTIVITY AGAINST CIRCULATING TUMOR CELLS: THE ROLE OF INTERFERON-ALPHA IN OVERCOMING PLATELET-MEDIATED IMMUNE EVASION

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ABSTRACT

Natural killer (NK) cells play a vital role in the innate immune system, known for their ability to identify and eliminate cancer cells without prior sensitization. These lymphocytes secrete various cytokines and chemokines to target cancer cells, particularly in the context of metastasis, where tumor cells migrate from the primary site to distant tissues via the circulatory system. Importantly, circulating tumor cells (CTCs) are shielded from immune surveillance by platelets, which can cloak CTCs and protect them from NK cell attacks. We investigated the immune-based treatment utilizing interferon-alpha (IFN-α) to address this challenge. In our in vitro experiments, we used K562, a chronic myeloid leukemia cell line, which was pre-co-cultured with platelets before incubation with NK cells pre-treated with IFN-α. The expression of NK cell activation markers was quantified using flow cytometry. Our results demonstrated that treatment with IFN-α significantly upregulated the NK cell degranulation marker CD107a and enhanced the production of interferon gamma (IFN-γ). This novel assessment platform allows for the evaluation of autologous platelet effects on personalized NK cell therapy, potentially improving the effectiveness of immunotherapeutic strategies against cancer.

KEYWORDS

Natural killer, circulating tumor cells, interferon-alpha, autologous Platelet

PLASTIC–ASSOCIATED MICROBIOMES: INSIGHTS INTO BACTERIAL ABUNDANCE AND RESISTOME PROFILING

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ABSTRACT

Background: Plastic pollution is a global issue, with 15-51 trillion plastic particles floating on the ocean's surface, particularly in rivers. Plastic waste has been overlooked as a potential source of infectious agents. It is possible that plastic waste acts as a vector for human infections and antimicrobial-resistant bacteria and a threat to food safety and marine species. The potential for plastic waste to act as a gateway for these infections raises concerns.

Objective: To investigate abundance and resistome profiles of bacterial assemblages on plastics collected from the estuarine environment.

Methods: Water samples were collected from the Nethravathi and Gurupur estuaries during the summer and monsoon seasons. Physicochemical parameters were estimated, and the obtained micro and macro plastics were characterized. Metagenomic analysis of the bacterial assemblages on the plastic debris was carried out.

Results: The study discovered a higher prevalence of micro and macroplastics during the summer compared to the rainy season at the isolation stage. FT-IR spectroscopy identified various polymer types, with polypropylene and polyamide being the most abundant.
Metagenomic analysis revealed that Enterobacteriaceae was the dominant taxon, exhibiting highest resistance to fluoroquinolone drug class.

Conclusion: Plastic pollution is a global environmental and health emergency, as plastic waste can harbour harmful pathogens and resistance genes. This study examines the diversity and resistome profiles of bacteria and the factors that facilitate their attachment to plastic surfaces. The research aims to shed light on the indirect consequences of plastic pollution and the growing issue of antibiotic resistance.

KEYWORDS
Estuary, Microplastics, Macroplastics, Metagenomics

INVESTIGATING THE ROLE OF PROGNOSTIC MITOPHAGY-RELATED GENES IN NON-SMALL CELL LUNG CANCER PATHOGENESIS VIA MULTIOMICS AND NETWORK-BASED APPROACH

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ABSTRACT

Background: Lung cancer (LC) is the leading cause of cancer-related deaths worldwide. Among its subtypes, Non-Small Cell Lung Carcinoma (NSCLC) is the most common and is broadly classified into lung adenocarcinoma (LUAD) and lung squamous cell carcinoma (LUSC).
Mitochondria, when damaged or under specific developmental conditions, are selectively degraded through mitophagy, a specialized form of autophagy. Mitochondrial dynamics play a crucial role in tumor development and metastasis.

Study design: In this study, we extracted paired normal and tumor tissue samples from LUAD and LUSC cohorts in TCGA, followed by differential expression analysis (DEA).
We identified differentially expressed mitophagy-related genes (DEMRGs) in both cohorts and performed soft clustering, overall survival (OS), and mutational analyses.

Study results: We analyzed 98 (49 pairs) and 92 (46 pairs) paired samples from LUAD and LUSC cohorts, respectively, identifying 986 and 1714 differentially expressed genes (DEGs).
A total of 5 and 9 DEMRGs were found in LUAD and LUSC cohorts. Soft clustering analysis revealed 7 genes in both cohorts. However, OS analysis identified TDRKH as the most prognostically significant gene.
Mutation analysis of TDRKH in the LUAD cohort showed a 14% amplification frequency and downregulation in tumor samples compared to adjacent normal tissue.

Conclusions: TDRKH is a highly conserved protein domain primarily involved in the piRNA biogenesis pathway and spermatogenesis. However, its role in LUAD requires further validation through in vitro studies.

KEYWORDS
NSCLC, TDRKH, mitophagy

EXTRACTION OF ANDROGRAPHIS PANICULATA AS A ANTISEPTIC FOR DEVELOPING SOAPS AND SANITIZER

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ABSTRACT

The aim of this work is to analyze the quantitative study of chemical properties of different *A. paniculata* extracts obtained from extraction methods such as ethanol extracts by maceration and Soxhlet extraction. This consists of antioxidant activity, total phenolic content (TPC), and total flavonoid content (TFC).

This project also aims to study the chemical and physicochemical properties of the developed soaps and sanitizer in order to evaluate the quality of the products. The properties of the original extracts were compared with the products to investigate the improvement of the antioxidant contents of the products upon the addition of the *A. paniculata* extract.

The antioxidant activity is evaluated using the 2,2-diphenyl-1-picrylhydrazyl test. TPC is determined using the Folin-Ciocalteu calorimetric method. TFC is quantified by following the aluminum chloride calorimetric method. All tests are quantified using a spectrophotometer.

A simple antimicrobial assay using the hand-printing method on agar plate media was also conducted to analyze the efficiency of the sanitizers against human pathogens on hands. The results showed that the *A. paniculata* macerated methanol extract exhibited the highest antioxidant activity at 76.027%, as well as the highest TPC and TFC with 0.222 mg GAE/ml and 7.500 mg QE/ml, respectively.

The results also showed that both products were able to retain similar antioxidant content, higher TPC, and lower TFC compared to the original plant extract used in their preparation. The findings demonstrated an improvement in the antioxidant content of soap and sanitizer upon the addition of *A. paniculata* extracts.

Therefore, *A. paniculata* extracts are potent natural ingredients with antioxidant properties and can be used to replace harmful synthetic ingredients in product formulations.

KEYWORDS

A. paniculata, Folin-Ciocalteu, maceration, picrylhydrazyl, Soxhlet

COMPUTATIONAL BIOLOGY DIVULGES HEPATOPROTECTIVE MECHANISMS OF TRADITIONAL MEDICINAL PLANTS AGAINST INH–RIF INDUCED TOXICITY

SURTHI RAVEDAR [1,2], DARASAGUPPE R. HARISH [1], FAIZAN A. BEERWALA [1,2], SWARUP S. GUJARATHI [1,2], ADILMEHADI KARIKAZI [1,2], JYOTHI BHAT [1]

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ABSTRACT

Background: Isoniazid (INH) and Rifampicin (RIF) are crucial anti-TB drugs but often cause hepatotoxicity with prolonged use. Traditional medicinal plants from the Western Ghats of Karnataka have been used for hepatoprotection. Arylacetamide deacetylase (AADAC) plays a key role in metabolizing INH and RIF, making it a potential target for mitigating drug-induced liver toxicity.

Objective: This study aims to identify non-toxic, druggable phytocompounds that interact with AADAC to counteract INH and RIF-induced hepatotoxicity using in-silico methods.

Materials and Methods: Phytocompounds from 10 medicinal plants were retrieved from chemical databases and literature. Drug-likeness scores (DLS) were predicted using Molsoft DB ($p \geq 0.5$), and potential targets were identified using SuperPred ($p \geq 70\%$). Molecular docking with AutoDock Vina via PAOP pipeline screened prioritized compounds against AADAC. Stability was assessed through a 100 ns molecular dynamics (MD) simulation using GROMACS. Gene set enrichment and pathway networks were analyzed using KEGG and Cytoscape.

Results: Among 697 screened compounds, 97 showed positive DLS. Withanolide P and Nicotiflorin exhibited high binding affinity to AADAC (-11.7 and -10.8 kcal/mol). MD simulations confirmed their stability and interactions. Enrichment analysis highlighted key hepatoprotective pathways, including PI3K-Akt, IL-17, and drug metabolism-related signaling.

Conclusion: This study identified promising phytocompounds from traditional herbs that target AADAC, suggesting their potential role in alleviating INH- and RIF-induced hepatotoxicity. Further experimental validation is warranted to confirm their efficacy.

KEYWORDS

Isoniazid, Rifampicin, Hepatotoxicity, Arylacetamide Deacetylase (AADAC), Phytocompounds, Molecular docking and dynamics.

EXPLORING THE HEPATOPROTECTIVE ACTIVITY OF ALLIUM CEPA PHYTOCOMPOUNDS AGAINST HEPATITIS B VIRUS–INDUCED LIVER INFLAMMATION: A SYSTEMS BIOLOGY APPROACH

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ABSTRACT

Background: Hepatitis B virus (HBV) remains a significant global health challenge in 2024, often leading to severe liver conditions with limited effective treatments available. Traditional medicines such as Allium cepa have been reported for their hepatoprotective activity. However, its mechanism of action against HBV is still unknown.

Objective: To explore Allium cepa phytoconstituents with a non-toxic and druggable profile against therapeutic targets involved in anti-HBV activity using computational approaches.

Methods and Materials: The study utilized the IMMPAT Database and Molsoft online web server to identify 256 phytocompounds and their drug-likeness scores (DLS) in Allium cepa. Phytocompounds with a target prediction probability greater than 70% were selected. GeneCards was employed to identify disease targets. Gene enrichment analysis was performed to predict modulated pathways, and a network was constructed using Cytoscape version 6.1. Molecular docking was conducted using AutoDock Vina via the POAP pipeline to assess binding modalities. A GROMACS simulation was run for 100 ns to verify stability through analyses of RMSD, RMSF, Rg, SASA, and MMPBSA.

Results: Based on the analysis, 39 phytocompounds met the target probability criterion. GeneCards identified 100 potential targets involved in HBV pathogenesis. Gene enrichment revealed modulation in 115 pathways, with 23 directly associated with HBV. Among these, HBV pathways showed the highest edge count via NFκB1, TNF, TLR4, and COX. Docking analysis produced binding affinities greater than -5 kcal/mol, and MD simulations confirmed molecular stability up to 100 ns.

Conclusion: This study highlights the potential of Allium cepa phytoconstituents as effective agents against HBV-induced liver inflammation, providing a strong foundation for further in vitro and in vivo validations.

KEYWORDS

Hepatitis B Virus (HBV), Allium cepa, Phytoconstituents, Molecular Docking, Molecular Dynamics, Gene Enrichment.

EVALUATION OF NATURAL DYE FOR DNA VISUALIZATION IN AGAROSE GEL

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ABSTRACT

Curcumin, a natural polyphenol extracted from turmeric, has been explored as a novel DNA stain for molecular biology applications. This study aims to extract the curcumin from turmeric and the extracted curcumin is confirmed by analytical techniques. Further the curcumin is studied for its application as natural dye for staining the DNA in Agarose gel. A solvent extraction method using ethanol was employed, followed by purification using column chromatography. The purified curcumin was characterized using HPLC and spectroscopic techniques. The extracted curcumin was then evaluated as a DNA stain for agarose gel electrophoresis, demonstrating superior sensitivity and specificity compared to conventional DNA stains. This study provides a robust and efficient method for extracting and purifying curcumin for DNA visualization, paving the way for its potential applications in molecular biology and genomics.

KEYWORDS

Agarose gel, Ethidium Bromide, Curcumin , Natural Dye, Molecular Biology.

SICKLE CELL TRAIT AND MALARIA RESISTANCE: A BIOCHEMICAL AND EVOLUTIONARY PERSPECTIVE

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ABSTRACT

Sickle cell trait (HbAS) is one of the most well-characterized genetic adaptations conferring resistance to *Plasmodium falciparum* malaria. The prevalence of HbAS in malaria-endemic regions, particularly in Africa, exemplifies natural selection favoring a heterozygote advantage. The protective effect of HbAS against malaria is attributed to multiple physiological and biochemical mechanisms, including impaired cytoadherence of infected erythrocytes, increased phagocytosis of parasitized cells, potassium leakage-induced parasite death, and immune response modulation. HbAS erythrocytes exhibit reduced surface expression of *P. falciparum* erythrocyte membrane protein-1 (PfEMP-1), a key factor in vascular sequestration, thereby lowering the risk of severe complications such as cerebral malaria.

Furthermore, oxidative stress in HbAS red blood cells promotes heme oxygenase-1 (HO-1) expression, conferring additional protection through anti-inflammatory effects. Immune system modulation also plays a crucial role, as HbAS individuals exhibit enhanced antibody responses to malarial antigens and increased dendritic cell recruitment, accelerating acquired immunity. These combined effects reduce both parasite load and disease severity, highlighting HbAS as a model for studying host-pathogen interactions and potential therapeutic targets. Understanding these mechanisms can provide insights into malaria resistance strategies and inform new approaches to combating this disease.

KEYWORDS

Malaria, Sickle Cell, Vascular Sequestration, Cytoadherence, Natural Selection.

INVESTIGATING THE STRUCTURAL DYNAMICS OF POSACONAZOLE SEDDS: A COMPUTATIONAL STUDY OF WATER–MEDIATED SELF–ASSEMBLY

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ABSTRACT

Posaconazole (PSC), a Biopharmaceutics classification system-II (BCS II) antifungal drug, faces challenges in achieving therapeutic plasma levels due to its lipophilicity and low water solubility. Self- emulsifying drug delivery systems (SEDDS) incorporating eugenol, polysorbate 20, and polyethylene glycol (PEG 200) enhance PSC solubility, stability, and bioavailability by forming stable oil-in-water emulsions. Understanding the self-assembly, drug localization, and interfacial properties of SEDDS is crucial for optimizing formulation efficiency. Molecular dynamics (MD) simulations provide valuable insights into these aspects. This study employs MD simulations to investigate the water-dependent phase behaviour of a PSC SEDDS comprising Eugenol, PEG 200, and Tween 20. Simulations were performed at different water mole percentages (0%, 1%, 70%, and 90%) over 400 ns in an NVT ensemble (number of particles (N), volume (V), and temperature (T) are kept constant) to analyze structural and dynamic transitions. Density profiles illustrate a shift from a dispersed state at low water content to micellar organization at higher concentrations, indicating water-driven self-assembly. Radial distribution functions (RDFs) quantify intermolecular interactions, revealing preferential associations among PSC, Tween 20, Eugenol, and PEG 200. Solvent-accessible surface area (SASA) and diffusion coefficients further characterize molecular exposure and mobility, correlating with observed phase transitions. Visualizations confirm a progressive transition from a non-solvated system to a well-defined micellar phase at high water content. These findings highlight the critical role of water in modulating component distribution and intermolecular interactions, providing essential insights for optimizing PSC SEDDS formulation and enhancing drug delivery efficiency.

KEYWORDS

posaconazole, SEDDS, molecular dynamics simulation, phase behaviour.

NITROPLAST INCORPORATION AS A POTENTIAL SOLUTION TO FIXED NITROGEN FOR AGRICULTURAL CROPS

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ABSTRACT

Nitrogen is indispensable for plant growth, with its natural rate of fixation being one of the main limiting factors for agricultural productivity. This has led to the rise of massive industries that produce synthetic fertilizers to address this issue, yet these fertilizers are energy-intensive to manufacture, and a large portion is wasted due to leaching and runoff.

Candidatus Atelocyanobacterium thalassa (UCYN-A) is a nitrogen-fixing cyanobacterium that exists in an endosymbiotic relationship with the unicellular marine haptophytic algae, *Braarudosphaera bigelowii*, exhibiting organelle-like characteristics. UCYN-A shows a coordinated cell cycle with *B. bigelowii* and a phylogenetically conserved size ratio between it and its host, with a large portion of proteins vital for the nitroplast being produced by the algae.

By engineering UCYN-A to function within crops through protoplast fusion, reliance on external nitrogen inputs could be dramatically reduced. The resulting self-sustaining system holds the potential to decrease greenhouse gas emissions, protect water quality by lowering nitrate runoff, and reduce farming costs, particularly for resource-limited communities. Moreover, improved soil structure and increased biodiversity may follow from reduced fertilizer application, fostering more resilient agroecosystems. Ultimately, this approach could transform conventional farming into a more sustainable model, supporting both productivity and environmental conservation.

KEYWORDS

Biological Nitrogen Fixation, Nitroplasts, Endosymbiosis, Sustainable Agriculture.

DEVELOPMENT OF A THIN LAYER CHROMATOGRAPHY METHOD TO DETECT THE PRESENCE OF STERIODS IN THE HERBAL DRUGS

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ABSTRACT

This study aimed to develop a fast and efficient thin-layer chromatography (TLC) method for detecting steroids in herbal samples. The steroids dexamethasone and prednisolone were taken as adulterants and spiked into herbal samples. Optimization of the mobile phase and spray reagent for visualization was performed using various combinations. Methanol was used as the solvent for extracting both the herbal sample and the steroids. Chloroform and methanol in the ratio 9:1 v/v was determined as the best mobile phase among the different combinations of the solvents tried out. The spray reagent made of methanol : sulphuric acid in the ratio 9:1 gave good results. The same condition were applied and another drug prednisolone was tested which was also successful with this method. The method was also able give separate spots in the TLC plate when the two drugs were mixed together in the same ratio. The Rf of the steroids were matching in the spiked samples and the detection limit was also better compared to previous studies. The process was easy without any complications in sample preparation and experimental set up and the future work by combining TLC with other analytical techniques are also discussed in this study.

KEYWORDS

Herbal Medicines, Adulteration, Thin Layer Chromatography, Steroids, Retention Factor, Lowest Detection Limit.

NURTURING WITH SCIENCE: ALTERNATIVE SOLUTIONS FOR HUMAN MILK OLIGOSACCHARIDES IN INFANT NUTRITION

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ABSTRACT

Human Milk Oligosaccharides (HMOs) are bioactive carbohydrates found in human milk that play a crucial role in infant health, including immune modulation, gut microbiome development, and disease prevention. However, factors such as maternal health conditions and socio-economic barriers can limit breastfeeding, necessitating alternative HMO sources.

This review explores various natural and synthetic HMO alternatives, including bovine, goat, and camel milk oligosaccharides, as well as plant-derived and marine oligosaccharides. Additionally, advanced biotechnological approaches such as microbial fermentation, enzymatic synthesis, and chemical synthesis are discussed alongside purification and characterization methods for large-scale HMO production. Challenges related to structural complexity, biosynthetic efficiency, purification, and economic viability are also analyzed.

Future advancements in genetic engineering, process optimization, and regulatory considerations will be critical for enhancing the scalability and application of HMOs in infant nutrition, pharmaceuticals, and functional foods. By addressing these challenges, alternative HMOs can provide essential health benefits to non-breastfed infants, bridging the nutritional gap and ensuring optimal early-life development.

KEYWORDS

Human Milk Oligosaccharides, Infant Nutrition, Prebiotic, Plant-Derived Oligosaccharides, Microbial Fermentation, Enzymatic and Chemical Synthesis, Large-Scale Production.

IMMOBILIZED ENZYMES: A BOON FOR THE BIODIESEL INDUSTRY

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ABSTRACT

The growing concerns over global warming and carbon emissions call for sustainable solutions in the fuel industry. Biofuels offer a viable alternative, with enzymatic transesterification using immobilized enzymes emerging as an efficient and eco-friendly method for biodiesel production. Conventional thermochemical transesterification relies on chemical catalysts like NaOH/KOH, requires a 60–65°C energy input, and generates significant wastewater. In contrast, the enzymatic process replaces chemical catalysts with biocatalysts (enzymes) that function at room temperature. This process efficiently converts both triglycerides and free fatty acids (FFAs) into fatty acid methyl esters (FAMEs), i.e., biodiesel. Additionally, it yields high-purity glycerin as a by-product, reducing purification steps and minimizing waste.

A key advantage of immobilized enzymes is their reusability, making biodiesel production more cost-effective. Replacing chemical catalysts with biocatalysts also mitigates environmental hazards associated with chemical disposal, contributing to cleaner fuel production. With advancements in enzyme engineering and immobilization techniques, enzymatic biodiesel synthesis holds great potential for large-scale adoption. This biocatalytic approach enhances biodiesel yield and quality while aligning with global efforts to transition toward green energy. The proposed process demonstrates efficient biodiesel production of up to 93% using immobilized lipase, contributing to sustainable biodiesel production.

KEYWORDS

Immobilized Enzyme, *Lysinibacillus macroides FS1*, Biodiesel, Pure Glycerin.

EFFECT OF BACTERIAL RESISTANCE TO NANOPARTICLES

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ABSTRACT

Antimicrobial resistance is a global challenge contributing to millions of deaths worldwide. To address this issue, researchers are exploring alternative therapeutic strategies such as phage therapy, vaccines, immunotherapy, and nanobiotics. Among these, nanotechnology has emerged as a particularly promising and widely applicable field. Nanoparticles can serve as both targeted drug delivery systems and antimicrobial agents.

In this study, we investigated whether bacteria can develop resistance to quantum dots—semiconductor nanoparticles used in medical applications. Antimicrobial susceptibility patterns and the presence of copper and silver metal efflux genes were analyzed in *Escherichia coli*, *Salmonella Typhi*, and *Klebsiella pneumoniae* (both ATCC reference strains and clinical isolates). Bacteria exhibiting significant susceptibility to quantum dots were selected for the development of nanoparticle-resistant strains. The selected bacterial populations were exposed to increasing concentrations of quantum dots.

Following treatment, antibiotic susceptibility profiling and biofilm formation assays were conducted, comparing treated bacteria to untreated controls. The results revealed an increase in antibiotic resistance by 17%, 40%, and 35% in *E. coli, S. Typhi, and K. pneumoniae* across different tested antibiotics. Additionally, modifications in biofilm formation were observed, with some strains exhibiting stronger biofilm formation while others lost this ability. These findings suggest that bacterial resistance to nanoparticles may contribute to cross-resistance against antibiotics and influence biofilm formation, potentially exacerbating the challenge of antimicrobial resistance.

KEYWORDS

Antimicrobial Resistance, Quantum Dots, Biofilm

FERMENTATIVE PRODUCTION OF MICROBIAL EXOPOLYSACCHARIDE

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ABSTRACT

This research focuses on the microbial production of exopolysaccharide (EPS). The selected bacterial strain was cultured on a sucrose-based medium supplemented with NH_4Cl, K_2HPO_4, $MgSO_4{\cdot}7H_2O$, $MnSO_4{\cdot}H_2O$, $CaCl_2{\cdot}2H_2O$, and $FeCl_3$ and incubated under optimized conditions for EPS production. Initial screening of EPS was performed using the phenol-sulfuric acid method. The EPS was extracted through solvent precipitation to ensure efficient recovery. The characterization was performed using Fourier-transform infrared spectroscopy (FTIR) to identify functional groups and thermogravimetric analysis (TGA) to assess thermal stability. These preliminary findings provided insights into the structural and thermal properties of the EPS. Further optimization of production parameters and detailed characterization will be conducted to enhance yield and functional properties.

KEYWORDS

Exopolysaccharide, Solvent Precipitation, Characterization

DEVELOPMENT OF POLYMER NANOCOMPOSITES FROM MICROBIAL SOURCE AND THEIR APPLICATION IN REMOVING PHARMACEUTICAL WASTE.

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ABSTRACT

The problem of micro-pharmaceutical waste, which is growing in our environment, leads to serious risks to ecosystems and human health and emphasizes the need for effective bioremediation strategies. Through an innovative microbial method that is also sustainable, this research has managed to create eco-friendly polymer-silver nanoparticle (polymer-AgNP) nanocomposites. After incorporating nanoparticles, we have biopolymer-based stable nanocomposites with reactivity enhanced. The UV-Vis spectroscopy, FTIR, XRD, SEM, and TEM techniques were all used to measure the physicochemical properties of the synthesized polymer-AgNP nanocomposites. These composites were also tested for their antimicrobial and adsorption properties and their efficiency in removing pharmaceutical waste, such as antibiotics, nonsteroidal anti-inflammatory drugs (NSAIDs), and endocrine disruptor chemicals (EDCs) under controlled environmental conditions. The results revealed a high adsorption and removal efficiency due to the synergistic bond between the biopolymer and silver nanoparticles, which increased adsorption capacity. They made the pollutants easier to be absorbed. The research suggests the application of microbial-derived polymer-silver particles as one of the green and practical methods for the bioremediation of pharmaceutical waste, thus contributing to sustainable environmental management and pollution control.

KEYWORDS

Microbial Nanocomposites, Polymer nanocomposites, Microbial nanotechnology, Sustainable materials, pharmaceutical waste removal.

NANOPARTICLE BASED THERAPEUTICS AGAINST CANDIDA SPP : AN EMERGING APPROACH IN ANTIFUNGAL TREATMENT

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ABSTRACT

Candida species represent a significant cause of opportunistic infections ranging from superficial mucocutaneous infections to life-threatening systemic diseases, particularly in immunocompromised individuals. The rise of antifungal resistance and biofilm-associated infections poses substantial therapeutic challenges. Traditional antifungal treatments often fail due to toxicity, limited efficacy against biofilms, and resistance development.

This review explores the potential of nanoparticle-based therapeutics as an innovative approach to combat *Candida* infections. Nanoparticles, including metal-based (silver, gold, copper), metal oxide-based (zinc oxide, copper oxide), carbon-based (carbon nanotubes, graphene oxide), and polymeric nanoparticles (chitosan), demonstrate enhanced antifungal properties. These nanoparticles exhibit mechanisms such as disrupting fungal cell walls, interfering with biofilm formation, generating reactive oxygen species, and enhancing drug delivery.
Chitosan nanoparticles, in particular, show promise due to their biofilm penetration ability and gene regulation effects, making them effective against resistant strains. The integration of nanoparticles in antifungal therapy not only improves drug efficacy but also offers solutions to overcome resistance mechanisms. This highlights the promising role of nanoparticles in antifungal therapy, potentially paving the way for new, more effective treatments against resistant fungal infections.

KEYWORDS

Candidiasis, Biofilm, Antifungal Resistance, Nanoparticles, Fungal Diagnosis

NANOPARTICLES AS DELIVERY VEHICLES FOR CRISPR/CAS-9

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ABSTRACT

CRISPR-based genome editing holds significant therapeutic potential, but its clinical application is limited by challenges in delivering the CRISPR-associated protein and single-guide RNA safely and efficiently. Viral vectors, such as adeno-associated viruses (AAVs), have been commonly used for CRISPR delivery, but their long-term presence in vivo raises concerns about off-target effects, immunogenicity, and insertional mutagenesis. Furthermore, AAVs have a limited cargo capacity, restricting their ability to deliver large CRISPR components.

To overcome these challenges, non-viral delivery systems, particularly nanoparticle-based approaches, have emerged as promising alternatives. Nanoparticles offer advantages such as specific targeting, high customization potential, scalability, and reduced immune stimulation. Among these, lipid nanoparticles (LNPs) and polymeric nanoparticles have shown particular promise. Polymeric nanoparticles provide benefits such as prolonged blood circulation, enhanced bioavailability, and protection of CRISPR components from immune responses and nuclease degradation. These nanoparticles can traverse the cell membrane via endocytosis, enabling efficient gene editing.

A notable study demonstrated the successful knockdown of the oncogene lipocalin-2 in human triple-negative breast cancer (TNBC) cells using polymeric nanocarriers to deliver CRISPR/Cas9. Such advances highlight the growing potential of nanoparticle-based delivery systems in therapeutic applications. This review will explore recent innovations in nanoparticle-mediated CRISPR delivery, focusing on challenges, advantages, and potential strategies for both clinical and industrial applications. By addressing these aspects, nanoparticle-based CRISPR delivery systems could revolutionize gene therapeutics, offering a safer and more effective alternative to traditional viral vectors.

KEYWORDS

CRISPR/Cas9, Nanocarriers, Lipid Nanoparticles (LNPs), Polymeric Nanoparticles, Genome Editing, Non-Viral Delivery Systems

COMPUTATIONAL IDENTIFICATION OF BIOMARKERS FROM THE BLOOD AND SALIVA SAMPLES OF BREAST CANCER

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ABSTRACT

Breast cancer is a multi-faceted disease and the most prevalent cancer among women worldwide. Despite recent advancements in breast cancer management, it remains a major cause of cancer-related mortality in women. While breast imaging and biopsy serve as the gold standards for breast cancer screening and diagnosis, these procedures can be expensive and invasive. Consequently, the discovery of blood and saliva biomarkers for diagnostics and prognostics is vital for improving patient outcomes. Non-invasive techniques have the potential to provide crucial insights into cancer progression and therapeutic response.

This study aims to identify potential biomarkers for breast cancer by leveraging computational approaches and utilizing publicly available transcriptome datasets from Gene Expression Omnibus (GEO). Differentially expressed genes (DEGs) were identified in blood and saliva samples using tools such as EdgeR and Limma. Top DEGs (logFC greater than 1.50 and P-value less than 0.05) were selected for further investigation.

Our analysis identified two significantly overexpressed genes (RPS24 and XIST) in blood samples and one significantly overexpressed gene (S100A8) in saliva samples of breast cancer patients. While these findings highlight promising biomarker candidates, further validation and functional studies are required to establish their diagnostic and prognostic utility.

By integrating transcriptomic data, we aim to uncover novel biomarkers and therapeutic targets, contributing to the development of more effective strategies for breast cancer management. This approach underscores the potential of computational biology in advancing non-invasive diagnostic tools and personalized treatment options.

KEYWORDS

Transcriptome, Breast Cancer, Biomarker

MARINE FUNGI AS A SOURCE OF NOVEL BIOACTIVE COMPOUNDS

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ABSTRACT

Marine fungi are generally an underexplored reservoir of bioactive compounds, which hold immense value in the fields of pharmaceuticals and biotechnology. These microbes thrive in harsh marine environments, leading to the production of structurally diverse secondary metabolites with antibacterial, antifungal, antiviral, anticancer, and anti-inflammatory properties. Current bioprospecting efforts have identified novel bioactive compounds in marine fungi, demonstrating significant therapeutic potential. The unique ecological niches of marine fungi, such as deep-sea sediments, mangrove forests, and coral reefs, contribute to their distinct metabolic profiles, making them a promising source for drug discovery.

This review highlights the potential of marine fungi as a major source of novel bioactive compounds relevant to pharmaceutical research. It explores methods for isolating, characterizing, and analyzing these metabolites and their diverse pharmacological applications. Recent advancements in biotechnological techniques have accelerated the discovery and production of these compounds. However, challenges such as limited culturable diversity and sustainable harvesting remain obstacles in marine fungal bioprospecting.

With the rise of antibiotic resistance and emerging diseases, the demand for new therapeutic compounds is increasing. Marine fungi offer a promising and effective alternative to traditional sources of bioactive metabolites. Future research should focus on optimizing cultivation techniques, enhancing metabolite yields through genetic engineering, and exploring fungal symbiotic relationships in marine ecosystems. Continued exploration of marine fungi could revolutionize drug discovery, leading to significant advancements in medicine, agriculture, and industrial biotechnology.

KEYWORDS

Marine Fungi, Bioactive Compounds, Bioprospecting

ADIPOSE-DERIVED STEM CELL THERAPY IN PARKINSON'S DISEASE: A THERAPEUTIC POTENTIAL IN TREATING PD

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ABSTRACT

Parkinson's Disease (PD) is one of the fastest-growing neurodegenerative disorders, primarily affecting motor, sensory, and visual functions due to the progressive loss of dopaminergic neurons in the Substantia Nigra pars compacta (SNc) and the accumulation of misfolded α-synuclein into Lewy bodies. PD is estimated to affect nearly 8.5 million people globally. Current therapies, including dopamine agonists, monoamine oxidase-B (MAO-B) inhibitors, and deep brain stimulation, mainly focus on managing symptoms rather than addressing the underlying neurodegeneration, limiting their effectiveness.

Adipose-derived Mesenchymal Stem Cell (AD-MSC) therapy has emerged as a promising approach for PD treatment, particularly in elderly patients. AD-MSCs have the potential to differentiate into dopaminergic neurons, promoting the repair and regeneration of damaged nerve tissue. The treatment process involves extracting pericytes, adipocytes, endothelial cells, hematopoietic cells, progenitor cells, and stem cells (SCs) from adipose tissue, followed by isolation and purification using surface markers (CD44, CD90, CD105, CD45, and CD34) before injecting AD-MSCs into PD patients. This approach has shown improvements in memory and motor symptoms.

Beyond their minimally invasive nature, high plasticity, and low immunogenicity, AD-MSCs pose no ethical concerns. Clinical studies have also demonstrated their safety, making AD-MSC transplantation a promising therapeutic strategy for Parkinson's Disease.

KEYWORDS

Parkinson's Disease, Adipose-Derived Mesenchymal Stem Cells, Dopaminergic Neurons.

THE DRUG RESPONSE ON SEQUENTIAL ANEUPLOIDY STRAINS IN CANDIDA ALBICANS

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ABSTRACT

Background: *Candida albicans* is an opportunistic fungal pathogen that predominantly survives as a diploid organism but may adapt to environmental stresses through aneuploidy—the reversible loss and gain of chromosomes. This chromosomal modification plays a critical role in gene expression regulation and cellular adaptability. This study investigates the effects of chromosomal alterations in *C. albicans* strains derived from *Candida strain C15* (csu51Δ/CSU51) on antifungal drug sensitivity.

Methods: *Candida albicans* strains C19, C29, C3, C36, and C42, each carrying a truncated chromosome 5 in one homologue, were assessed for susceptibility to fluconazole (FLZ), itraconazole (ITZ), voriconazole (VRZ), amphotericin B (AMB), and caspofungin (CAS). Wild-type CAF4-2 and C15 (csu51Δ/CSU51) served as control strains. Plate assay, disc diffusion, and minimum inhibitory concentration (MIC) testing were used to evaluate antifungal susceptibility.
The results demonstrated differences in drug susceptibility across the aneuploidy strains, with specific strains exhibiting altered resistance to triazoles and echinocandins. Chromosome 5 deletion and truncations impacted antifungal resistance patterns, possibly due to regulatory elements on chromosome 5.

Conclusion: Our study highlights the significant role of chromosomal alterations in determining antifungal drug efficacy in *C. albicans*. These findings enhance the understanding of aneuploidy-driven adaptability in fungal pathogens and could guide treatment strategies for drug-resistant *C. albicans* infections.

KEYWORDS

Candida albicans, Aneuploidy, Chromosome 5, Antifungal Susceptibility, Drug Resistance, Chromosomal Truncation.

MACHINE LEARNING–ASSISTED PREDICTION OF ANTICANCER ACTIVITY USING SMILES REPRESENTATIONS

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ABSTRACT

Cancer is a syndrome that arises as a resultant of multitude of molecular aberrations facing drug failure due to lack of efficacy and severe side effects. CADD (Computer Aided Drug Discovery) recommended drugs employing protein and ligand structure representations could be tailored to overcome drug failure. Simplified molecular input line entry system (SMILES) is alphanumeric representation with symbols embedding rings and scaffold patterns that could imply biological property. We have developed a machine learning model (ML) using drug SMILES of NCI-60 cancer growth inhibition data to predict anticancer property. Characters of Drug SMILES were one-hot encoded and trained in a multilayer perceptron (MLP) network with two hidden layers. Synthetic Minority Oversampling TEchnique (SMOTE) was employed to normalize class imbalance between anticancer and non-anticancer classes. The MLP model was trained and evaluated with a 25% independent test split. The developed model classified drug SMILES with an accuracy of 0.92 and was validated with 5-fold cross-validation resulting in mean accuracy of 0.89. Benchmarking with other ML algorithms viz., support vector classifier (SVC), logistic regression, decision tree, AdaBoost, CatBoost and XGBoost showed better performance of MLP with good performance metrics. MLP model also outperformed existing methods CDRUG and pdCSM-cancer which had AUROC of 0.88 and 0.49 respectively. Furthermore, top 8 frequently occurring molecular scaffolds were identified in NCI-60 cancer growth inhibition and ChEMBL drug data endorsing preference of certain molecular patterns. Thus, our developed model effectively predicts anticancer property using molecular SMILES notation compared to other methods based on high-level descriptors or representations.

KEYWORDS

SMILES, Anticancer Activity, MLP, Machine Learning

RESTORING EFFICACY OF DOCOSAHEXAENOIC ACID [DHA] IN PERINATAL MATERNAL SEPARATION STRESS–INDUCED ALTERED EMOTIONAL LEARNING &MEMORY AND AMYGDALA NEURAL CELL COUNTS IN WISTAR RAT PUPS

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ABSTRACT

Background: Perinatal maternal separation stress (PMSS) has been shown to cause changes in brain morphology, learning, and memory. The present study explores the neuroprotective benefits of DHA in alleviating PMSS-induced changes in the brain.

Purpose: To study the effect of DHA supplementation in PMSS rat pups on:
a. Avoidance learning and memory
b. Basolateral amygdala (BLA) neural cell counts

Materials & Methods: Inbred pregnant Wistar female rats were grouped as: Control, PMSS, and PMSS + DHA (n = 9 rats/group). PMSS was given from post-natal day (PND) 2-25, for 6 hours/day, and DHA supplements were administered to respective groups. On day 28, all rat pups were tested for avoidance learning and memory using a passive avoidance apparatus, after which they were sacrificed, and brain tissues were processed for cresyl violet staining.

Results: During the retention test (24 hours after foot shock):

- Latency to enter the dark chamber significantly decreased ($p<0.001$, $p<0.01$) in PMSS rats compared to the control and DHA group.
- Time spent in the dark chamber significantly increased ($p<0.01$, $p<0.05$) in PMSS rats.
- Number of crossings between the dark and bright chambers significantly increased ($p<0.001$, $p<0.05$) in PMSS rats.
- BLA neural cell counts significantly increased ($p<0.001$, $p<0.05$) in the PMSS group compared to the control and DHA groups.

Conclusion: PMSS caused poor avoidance learning, impaired memory retention, increased anxiety, and heightened activation of the BLA, as indicated by increased neural cell counts. DHA supplementation restored stress-induced changes, providing neuroprotection against PMSS-induced alterations in emotional learning, memory, and BLA neural cell counts.

KEYWORDS

DHA, PMSS, basolateral amygdala, passive avoidance

INNOVATIONS IN DECELLULARIZATION TECHNIQUES FOR TRACHEAL TISSUE ENGINEERING

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ABSTRACT

The rising prevalence of congenital and acquired disorders of the trachea, such as tracheomalacia, tracheoesophageal-fistula, tracheal-stenosis, airway ischemia, infections, and tumors, frequently results in respiratory failure that necessitates medical treatment. Nevertheless, there are currently no tracheal grafts available that provide a lasting solution to restore respiratory function in patients. Tissue engineered tracheal grafts have become increasingly popular in the field of regenerative medicine. This approach addresses the shortcomings of traditional methods by facilitating the repair and regeneration of tracheal tissues. Among various techniques, decellularization is the most common, as it retains the original extracellular matrix components while eliminating cellular and nuclear materials from the tissue. Relevant articles were identified using targeted keywords in ScienceDirect and Google Scholar. The authors created a comprehensive list of decellularization methods utilized throughout the years and compared outcomes of different physical, chemical, and enzymatic techniques. They analyzed the impact of decellularization on both the mechanical integrity and immunogenicity of the acellular scaffold. Recent advancements in decellularization include detergent-enzymatic, vacuum- assisted, and laser-pore-based techniques. Additionally, new alternatives to traditional detergents, such as supercritical carbon dioxide, have been introduced. For effective tracheal tissue transplantation, the grafts must possess sufficient mechanical properties, blood supply, epithelial lining, and exhibit no immunogenicity.

Thus, decellularized tracheal scaffolds exhibit significantly lower immunogenicity and retain the biomechanical and proangiogenic properties of native tissue, creating a foundation for tracheal regeneration. Though decellularization is one of the best approaches for producing biomimetic tracheal scaffolds, further refinements are required for generating clinically applicable tracheal grafts.

KEYWORDS:
Trachea, decellularization, recellularization, scaffolds, transplantation

SMART PVA FILMS WITH BIOACTIVE COMPOUNDS FOR RAPID WOUND HEALING

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ABSTRACT

Polymer-based thin films are widely used in biomedical applications due to their ability to absorb wound exudates, maintain moisture balance, and facilitate a high water vapor transmission rate, all of which promote wound healing. Additionally, these films act as protective barriers against microbial contamination, reducing infection risks. However, there remains a need for novel material combinations with enhanced properties, including improved mechanical strength, biocompatibility, and antimicrobial activity.

This study focuses on developing biocompatible thin films by synthesizing polyvinyl alcohol (PVA) with other naturally available biopolymers and incorporating the bioactive compound curcumin. Curcumin is well known for its antioxidant, antimicrobial, and anti-inflammatory properties, making it highly beneficial for wound healing applications. However, previous studies have not optimized polymer proportions in these systems.

Our research aims to overcome these limitations by developing an optimized polymer matrix that ensures sustained and enhanced curcumin release while maintaining film stability. The optimized film is expected to demonstrate a higher curcumin release rate while maintaining superior tensile strength and flexibility, preventing breakage. This study contributes to the advancement of wound healing biomaterials by combining natural, safe, and functionally superior polymeric systems. The findings could lead to the development of more effective, non-toxic, and mechanically stable wound dressings with enhanced therapeutic potential.

KEYWORDS

Curcumin, Film, Wound healing, Antimicrobial, Anti-inflammatory

HARNESSING PHYTOCHEMISTRY TO COMBAT INDOLEAMINE 2,3–DIOXYGENASE 1 AND TRYPTOPHAN 2,3–DIOXYGENASE 2 IN RESTORING TRYPTOPHAN HOMEOSTASIS IN OVARIAN CANCER

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ABSTRACT

Polymer-based thin films are widely used in biomedical applications due to their ability to absorb wound exudates, maintain moisture balance, and facilitate a high water vapor transmission rate, all of which promote wound healing. Additionally, these films act as protective barriers against microbial contamination, reducing infection risks. However, there remains a need for novel material combinations with enhanced properties, including improved mechanical strength, biocompatibility, and antimicrobial activity.

This study focuses on developing biocompatible thin films by synthesizing polyvinyl alcohol (PVA) with other naturally available biopolymers and incorporating the bioactive compound curcumin. Curcumin is well known for its antioxidant, antimicrobial, and anti-inflammatory properties, making it highly beneficial for wound healing applications. However, previous studies have not optimized polymer proportions in these systems.

Our research aims to overcome these limitations by developing an optimized polymer matrix that ensures sustained and enhanced curcumin release while maintaining film stability. The optimized film is expected to demonstrate a higher curcumin release rate while maintaining superior tensile strength and flexibility, preventing breakage. This study contributes to the advancement of wound healing biomaterials by combining natural, safe, and functionally superior polymeric systems. The findings could lead to the development of more effective, non-toxic, and mechanically stable wound dressings with enhanced therapeutic potential.

KEYWORDS

Curcumin, Film, Wound healing, Antimicrobial, Anti-inflammatory

BBB REBOOT: EXOSOME–AAV GENE THERAPY FOR PARKINSON'S NEUROPROTECTION

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ABSTRACT

The Blood-Brain Barrier (BBB) is a protective endothelial barrier that selectively allows ions and small molecules to enter the central nervous system. Moreover, it separates the delicate neural environment from the peripheral blood. The tight junctions, composed of transmembrane and membrane-associated proteins, help maintain the integrity of the blood-brain barrier.

One of the main proteins in regulating the tight junction is claudin 5, expressed by the CLDN5 gene. In neurodegenerative disorders like Parkinson's Disease (PD), downregulation of claudin 5 is a primary cause of BBB integrity loss, leading to further disease progression.

Through our proposed therapy, we aim to upregulate claudin 5 expression via the CLDN5 gene. This therapy includes the integration of exosomes and adeno-associated vectors (AAV), which would carry our gene of interest. We are designing an AAV carrying a claudin 5 cDNA, a BBB-specific promoter (Tie2 or VE-Cadherin), and an enhancer, coupled with an exosome engineered by overexpressing CD9 for efficient AAV loading. Purification involves ultracentrifugation along with an iodixanol gradient to obtain purified Exo-AAV. These Exo-AAV-CLDN5 can be administered intrathecally for targeted BBB repair.

This dual-modality gene therapy offers a highly targeted and efficient strategy for restoring BBB integrity, potentially reducing neuroinflammation, slowing dopaminergic neurodegeneration, and mitigating disease progression in PD. By improving BBB function, Exo-AAV-CLDN5 therapy could enhance the delivery of neuroprotective agents while addressing both motor and non-motor symptoms. This approach represents a transformative step in gene therapy-based neurovascular repair strategies for Parkinson's and other neurodegenerative diseases.

KEYWORDS

Blood-Brain Barrier (BBB), Tight Junctions (TJ), Claudin 5, Exosomes-AAV, Parkinson's Disease (PD).

MUCOADHESIVE PVA FILM ENRICHED WITH POLYPHENOLS FROM PINEAPPLE PEEL/CROWN

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ABSTRACT

Mucoadhesive drug delivery systems enhance drug retention at mucosal sites, improving therapeutic efficacy and patient compliance. Conventional mucoadhesives are often toxic, costly, and non-biodegradable, limiting their biomedical applications. To address these challenges, biopolymer-based alternatives are being explored. Among them, polyvinyl alcohol (PVA) is widely studied due to its biodegradability, biocompatibility, and ability to form flexible, durable films. When combined with plasticizers such as glycerol, PVA-based films can be tailored to exhibit desirable mechanical properties, swelling behaviour, and mucoadhesive characteristics, making them suitable candidates for controlled drug delivery applications. Pineapple (*Ananas comosus*) peel and crown, often discarded as agro-industrial waste, are rich in polyphenols known for their antioxidant and anti-inflammatory properties. These compounds, including ferulic acid, gallic acid, catechin, and epicatechin, have demonstrated potential in biomedical applications. By extracting and purifying these bioactive compounds, their integration into PVA-glycerol biofilms can enhance the therapeutic potential of the material while also contributing to waste valorization. The formulation of these biofilms is optimized to enhance their adhesion to mucosal surfaces, mechanical flexibility, and controlled release properties under physiological conditions. Their performance is assessed based on structural stability, biocompatibility, and drug release efficiency to ensure their suitability for therapeutic applications. By integrating plant-based bioactive compounds into polymeric films, this research contributes to both waste valorization and pharmaceutical advancements, promoting an eco-friendly approach to innovative drug delivery systems.

KEYWORDS

Poly Vinyl Alcohol, Mucoadhesives, Polyphenols, Anti-inflammatory

BIO-DERIVED SYNTHESIS OF SILVER DECORATED CARBON NANOCOMPOSITE FOR SENSISTIVE DETECTION OF AZO DYE IN FOOD

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ABSTRACT

Azo dyes are synthetic colorants used in various industries but pose health risks like carcinogenic and mutagenic effects. Strict regulations govern their use in food, and advanced sensors aid in their detection. Nanomaterial-based electrochemical sensors offer high sensitivity and selectivity for azo dye detection. This study synthesizes AgNPs using a green approach with *Cynodon dactylon* leaf extract as a reducing and stabilizing agent, eliminating hazardous chemicals for sustainability. Optimization by OFAT analysis was carried out for the synthesis process, and the optimum conditions were determined as follows

Temperature (40°C), Salt concentration (1mM), Extract concentration (20%), Rpm (100), and pH (10) and time (10 min).Four fold increase in nanoparticles synthesis was observed after OFAT optimization. The synthesized AgNPs will be incorporated with multi-walled carbon nanotubes (MWCNTs) to form a nanocomposite for modifying a glassy carbon electrode (GCE) for electrochemical detection of azo dyes. The AgNP/MWCNT nanocomposite will be characterized using XRD, UV-Visible spectroscopy, FTIR, zeta potential analysis, and SEM. Electrocatalytic activity towards azo dye oxidation will be assessed using cyclic voltammetry (CV) and square wave voltammetry (SWV), where CV provides insights into redox behavior, and SWV enhances detection sensitivity. A nano-electrochemical sensor will be developed with LOD and LOQ estimation, ensuring precise azo dye detection. The GCE modified with AgNP/MWCNT will be tested on a commercial food sample, demonstrating its potential as a sustainable, cost-efficient, and effective tool for food safety monitoring.

KEYWORDS

Azo dye, Green synthesis, Nanoparticles, Electrochemical sensor

IDENTIFICATION OF OVER EXPRESSED EXOSOMAL MICRO RNAS ASSOCIATED WITH INSULIN RESISTANCE FOR EARLY DETECTION OF TYPE 2 DIABETES MELLITUS

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ABSTRACT:
Diabetes is a major issue across the world and has been classified as an epidemic
due to its high occurrence and prevalence among the public. Type 2 Diabetes Mellitus (T2DM) is a chronic metabolic disease wherein either the body has become resistant to insulin (Insulin Resistance) or it is not capable of producing enough of it. Prediabetes, characterized by a fluctuating blood sugar level between normal and high, is a precursor to T2DM. Due to its high incidence rate, newer and more efficient detection methods are necessary. Various reviews and studies have been conducted which confirmed that microRNAs (miRNAs) play a significant role in metabolic homeostasis. This indicates that specific miRNAs are intricately linked with Insulin Resistance and would show noticeable changes in their levels with the progression of T2DM. miRNAs are the most significant active components transported by small membrane-bound nanovesicles called exosomes. This knowledge may be used to identify a potential biomarker for the early detection of the disease allowing for rapid treatment options. The current study aims to identify serum exosomal miRNAs for precise detection of prediabetes.

KEYWORDS: miRNA, biomarker, insulin resistance, prediabetes, Type 2 Diabetes mellitus

COMPUTATIONAL UNVEILING OF SYNTHETIC DERIVATIVES AS DUAL IDO AND TDO INHIBITORS FOR OVARIAN CANCER THERAPY: DOCKING, ADME, DFT, AND MD SIMULATIONS

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Background: Ovarian cancer, a deadly gynaecological malignancy, often presents with subtle symptoms and has a high recurrence rate, with 80% of patients relapsing post-treatment. Tryptophan catabolism via the kynurenine pathway, involving enzymes IDO1, IDO2, and TDO2, plays a crucial role in tumour progression and immune evasion. Elevated IDO1 expression in tumours is linked to myeloid-derived suppressor cell activation and resistance to immune checkpoint therapies, making, Indoleamine 2,3-dioxygenase (IDO) and tryptophan 2,3-dioxygenase (TDO) as potential therapeutic targets to combat immune suppressions and recurrence of the ovarian cancer. The overarching objective of this endeavour is to deploy in silico studies of novel synthetic dual IDO and TDO inhibitor.

Material and Methods: In this study, ten novel acridone derivatives were docked against the IDO1 (PDB code: 6E43) and TDO2 enzyme (PDB code: 8QV7) using Auto Dock 4.2.1 and the ligand-protein complex were visualized through Chimera software. Further molecular dynamics simulation was employed to investigate the interactions, stability, and dynamic behaviour of the complex with significant binding energy over a period of 200 ns. Additionally, the compounds were screened for DFT studies using Gaussian software and ADMET properties using pkCSM database.

Result and Conclusions: Docking study revealed that all ten novel compounds had stronger binding energies than the
standard drug, with AOZ-6 (-10.14) showing the most negative binding energy. Molecular dynamics simulations confirmed ligand-receptor stability over 200 ns. DFT analysis suggested favourable reactivity, likely due to the rigid acridone structure. ADMET analysis indicated good drug-like properties, supporting the potential of acridone derivatives against ovarian cancer.

KEYWORDS

Acridone, Kynurenine pathway, in silico studies, Indoleamine-2,3 dioxygenase ADMET

MANIPULATING LIPID CONTENT IN LIMNOSPIRA PLATENSIS VIA WAVELENGTH–SPECIFIC HEAVY METAL STRESS INDUCTION

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ABSTRACT

This research article investigates the wavelength-dependent lipid accumulation manipulation within *Limnospira platensis*, specifically through the application of controlled heavy metal stress induced by chromium and nickel salts. A detailed investigation was conducted to analyze the synergistic effects of varying metal concentrations, in conjunction with distinct light wavelengths, on crucial parameters including biomass production, as well as carbohydrate, protein, and lipid yields. Employing statistical analysis via ANOVA, a significant correlation was established between the applied light wavelength and the resultant biomolecule production. Notably, cultivation under blue light conditions yielded the most substantial overall production of carbohydrates, proteins, and lipids. Conversely, white light cultivation proved optimal for maximizing biomass production, particularly at a heavy metal salt concentration of 1 ppm. Specifically, a peak lipid yield of 390 mg/g was achieved under chromium stress at a concentration of 5 ppm, providing compelling evidence for the potential of targeted lipid enhancement. This study underscores the practical feasibility of harnessing *Limnospira platensis* for dual applications: bioremediation of heavy metal-contaminated environments and sustainable biofuel production, through the strategic and precise control of light and heavy metal exposure.

KEYWORDS

Microalgae, *Limnospira platensis*, light wavelength, heavy metal, bioremediation.

DEVELOPMENT OF ANTIBODY–BASED DIAGNOSTIC AND THERAPEUTIC REAGENTS AGAINST CARBAPENEM–RESISTANT ACINETOBACTER BAUMANNII

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ABSTRACT

Multi-drug resistant (MDR) strains of *Acinetobacter baumannii (A. baumannii*) are known for causing nosocomial infections globally resulting in significant mortality rates. Carbapenems are considered the last-resort treatment of choice for MDR *A. baumannii*. Due to the emergence of carbapenem-resistant *A. baumannii* (CRAB), WHO has listed it as the 'priority 1' pathogen for research and development to develop new antibiotics. Strategies to counter the emergence of CRAB should not only involve the development of newer antibiotics but should also include the development of reliable, rapid, and easy-to-use diagnostic reagents for timely treatment of the patients for improved clinical outcomes and to ensure controlled use of carbapenem drugs and effective management of infection spread. In this work, using a major carbapenemase as a target, we have developed specific monoclonal antibodies that can enable rapid detection of carbapenem resistance in drug-resistant *Acinetobacter baumannii*. The antibodies have been developed using phage display technology and have shown high reactivity against the target protein.

These antibodies are currently being explored for the development of rapid. Point-of-care tests against CRAB and inhibitors of carbapenemases.

Funding: The work is funded by the Department of Science and Technology – SERB (Start-up Research Grant to Vaishali Verma; SRG/2022/000486).

KEYWORDS

Acinetobacter baumannii, Phage display immunodiagnostics

CHARACTERIZING QUORUM SENSING MOLECULES IN CLINICAL ISOLATES OF ACINETOBACTER BAUMANNII

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ABSTRACT

Background: *Acinetobacter baumannii* is an opportunistic pathogen responsible for nosocomial infections. The production of virulence factors that govern bacterial pathogenicity is regulated by Quorum Sensing (QS), which is modulated by the secretion of Acyl Homoserine Lactones (AHLs). Therefore, this study aimed to detect and characterize the AHLs produced by clinical isolates of *A. baumannii*.

Objectives: To characterize quorum sensing molecules produced by isolates of *Acinetobacter baumannii*.

Methods: A cross-streak assay was performed to screen for the presence of QS molecules in 34 clinical isolates of *A. baumannii* using *A. tumefaciens* NTL4 as the reporter strain. AHLs were extracted using the ethyl acetate extraction method and detected using the TLC bioassay, comparing them with a reference AHL. The extracted AHLs were further characterized using High-Performance Liquid Chromatography (HPLC) and Gas Chromatography-Mass Spectroscopy (GCMS) analysis.

Results: The cross-streak assay confirmed the presence of AHLs in *A. baumannii* clinical isolates by the formation of blue pigmentation. Rf values of all 34 A. baumannii clinical isolates closely resembled standard 3-Hydroxy C12-HSL, indicating the presence of long-chain AHLs (3-Hydroxy C12-HSL). However, HPLC and GCMS analysis in one isolate revealed the presence of diketopiperazine.

Conclusion: This is the first study to report the presence of diketopiperazine as a QS molecule in a clinical isolate of *A. baumannii*. Further research is required to investigate its role in the QS system of *A. baumannii* and its other biological activities.

KEYWORDS

Acinetobacter baumannii, Quorum Sensing, *A. tumefaciens NTL4*, Diketopiperazine

CAS12A–BASED DIAGNOSIS OF X–DISEASE PHYTOPLASMA INFECTING TREE FRUIT (CHERRY)

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ABSTRACT

X-disease of sweet cherries is caused by *Candidatus Phytoplasma pruni* (X- disease phytoplamsa-XDP), a cell wall-less phytopathogenic bacterium, which infects agriculturally important *Prunus* species, including cherries, peaches, nectarines, almonds, plums, and chokecherries. XDP lives and replicates in the vascular phloem tissue of infected trees and the disease causes significant economic losses in Washington in recent years. Early diagnosis of XDP is critical due to its unculturable nature, uneven distribution, and low titer in plant tissues. In this study, we developed a DNA endonuclease-targeted CRISPR trans reporter (DETECTR) assay that combines recombinase polymerase amplification (RPA) and CRISPR/Cas12a-based transcleavage of fluorescently labelled oligonucleotides for highly sensitive, rapid, and specific detection of XDP. The DETECTR was capable of specifically detecting one copy of DNA of XDP and XDP infected cherry samples at the attomolar level within an hour by using a fluorescent microplate reader. Using this method, we also detected the presence of XDP in different weed samples, including dandelion, alfalfa, and buckhorn plantain. Our results showed that this method improves the detection sensitivity and has the potential for early diagnosis of X disease in cherries, which might limit the spread of disease in healthy plants, thus helping manage the disease and reduce the losses.

KEYWORDS

X-disease phytoplasma, cherry, RPA, Cas12a

UNDERSTANDING THE FUNCTIONAL ANALYSIS OF ERG 11 IN CANDIDA ALBICANS

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ABSTRACT

Antifungal resistance in *Candida albicans*, particularly to azoles, poses a significant challenge in treating fungal infections. This study aims to identify novel amino acid residues in ERG11 mediating azole resistance. We made the ERG11 gene bigger and cloned it into a YEP24 vector. Then we added mutations and changed it into the strain B8728 of *Saccharomyces cerevisiae*. Initial fluconazole resistance screening via MIC assays has been completed. The next steps are to make a genomic library, test for higher levels of azole resistance, and sequence mutated ERG11 genes from resistant clones. This research seeks to elucidate key residues involved in azole resistance, potentially informing new antifungal strategies.

KEYWORDS

ERG11, Antifungal Resistance, *Candida albicans*, Fluconazole, site-directed mutagenesis.

OBESITY–ASSOCIATED METABOLIC REPROGRAMMING DIFFERS BETWEEN HORMONE–POSITIVE AND NEGATIVE BREAST TUMORS

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ABSTRACT

Obesity is a significant risk factor for various cancers, including breast carcinoma, profoundly influencing its molecular landscape. This research is planned to explore the obesity-associated differential molecular alterations in breast cancer, aiming to uncover the specific signaling pathway alteration linked to obesity. By examining these alterations, the study seeks to enhance the understanding of how obesity accelerates the breast cancer progression and affects treatment outcomes. RNA and metabolic profiling were conducted on MCF-7 and MDA-MB-231 breast cancer cells cultured in adipocyte-conditioned media. Adipocyte-conditioned media significantly increased breast cancer cell proliferation and migration, altering 2204 genes in MCF7 and MDAMB231 cells. Metabolomic analysis showed significant differences in MCF7 but not MDAMB231 upon treatment. We analyzed transcriptomics data from The Cancer Genome Atlas (TCGA) using the TCGA R package to identify gene expression patterns linked to obesity in breast carcinoma. In TCGA-BRCA data, 101 genes were linked to poor prognosis. Fatty acid and glucose metabolic pathways were notably altered due to adipocyte secretions, affecting different pathways in triple-negative breast cancer cells. This suggests obesity-related factors uniquely influence the metabolic landscape of various breast cancers, potentially impacting progression and treatment responses. These findings may lead to tailored therapeutic strategies, improving
prognosis and patient care for obese breast carcinoma patients.

KEYWORDS

adipocyte-conditioned media, hormone positive breast cancer, triple-negative breast cancer, obesity

EXTENSIVE CHARACTERIZATION OF WITHANOLIDE A TAGGED CHITOSAN NANOPARTICLES

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ABSTRACT

WithanolideA (WNA) is a Steroidal lactone compound derived mainly from roots of *Withania somnifera* (Ashwagandha), which has tremendous anti-oxidant, anti-diabetic, anti-cancerous properties. However, the Clinical applications of WNA is often limited due to poor bioavailability resulting from low solubility and rapid metabolism. In this study, nanoencapsulation of WNA is performed using low molecular weight branched biopolymer like chitosan which overcome these limitations. Ionotropic gelation method is deployed to yield WNA tagged chitosan nanoparticles (CNPs) by cross-linking chitosan with Sodium tripolyphospate. The spherical and uniform dispersed WNA loaded CNPs average particle size was found to be 141.6 nm and polydispersity index (PDI) was found to be 0.241. The loading process achieved an encapsulation efficiency of 67%. Mean zeta potential value was found to be 34 mV. The optimized Nano encapsulation process resulted in spherical nanoparticles with appreciable encapsulation efficiency resulting in the narrow, uniform size distribution and moderate stability.

KEYWORDS

WITHANOLIDE A, CHITOSAN, NANO ENCAPSULATION, POLYDISPERSITY INDEX.

EVALUATION OF ANTIBACTERIAL AND DYE–DEGRADATION POTENTIAL OF SILVER NANOPARTICLES DERIVED FROM KLEBSIELLA PNEUMONIAE NSB–2 STRAIN

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The emergence of multidrug-resistant (MDR) pathogens in effluent water poses a significant threat to public health and environmental safety. The present study focuses on the biosynthesis of silver nanoparticles (AgNPs) using soil bacterium *Klebsiella pneumoniae NSB-2*. The synthesized AgNPs were characterized using UV-Visible spectrophotometry, X-ray diffraction (XRD), and Transmission Electron Microscopy (TEM) to confirm their structural and morphological properties.

The antimicrobial efficacy of AgNPs was evaluated by well diffusion method, against effluent-derived pathogens, including *Escherichia coli*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa*, which were identified through the VITEK system as pan-resistant. The highest antibacterial activity was observed against *E. coli* (22 mm), followed by *K.pneumoniae* (20 mm) and *P. aeruginosa* (20 mm). Additionally, the dye-degradation potential of AgNPs was assessed against industrial dyes, revealing a significant reduction in Crystal violet (94.06%) and Congo red (96.22%), as determined by spectrophotometric analysis.

These findings highlight the dual functionality of bacteriogenic AgNPs as both potent antimicrobial agents against MDR pathogens and effective catalysts for dye degradation. This study underscores the potential of biogenic nanoparticles in wastewater treatment and infection control, offering an eco-friendly and sustainable approach to mitigating environmental and microbial contamination. Further research into the mechanistic pathways of bacterial inhibition and catalytic degradation could enhance their applicability in industrial and biomedical sectors.

POTENTIAL OF SPONGE–DERIVED CHEMICALS IN COMBATTING ANTIBIOTIC–RESISTANT MICROBES AND EMERGING PATHOGENS

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ABSTRACT

With the rise of antibiotic-resistant bacterial outbreaks and the advent of pandemics, finding new, innovative strategies to combat microbial threats has become paramount.

Marine sponges, among the earliest multicellular organisms, have evolved sophisticated defense mechanisms to deter predation. These include structural adaptations such as spicules and the production of bioactive compounds that serve as chemical deterrents. Some of these secondary metabolites, including andramide and monoalide, have demonstrated potential in combating antibiotic-resistant bacteria [1]. Additionally, marine sponges have contributed to the discovery of critical antiviral drugs, such as Remdesivir [2], originally derived from *Tectitethya crypta*, and azidothymidine (AZT), used in HIV treatment [3].

With the increasing prevalence of antibiotic-resistant infections and viral outbreaks, marine sponges present a largely untapped reservoir of novel bioactive compounds [3]. However, climate change poses a significant threat to their survival [4], emphasizing the urgent need to preserve and harness these organisms. Given their proven role in discovering potent antibacterial and antiviral agents, sponges remain underutilized, and further research into their cultivation and metabolic profiling could provide invaluable resources for future drug development.

KEYWORDS

Marine sponges, antibiotic resistance, bioactive compounds, drug discovery.

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